

C	19	17	85.0	252467	14	AC108255	AC108255	Rattus	no
C	20	16.8	84.0	720	1	PSEIASRA1	D30812	Pseudomonas	AC0812
C	21	16.8	84.0	720	1	PSEIASRB	D30813	Pseudomonas	AC0813
C	22	16.8	84.0	720	6	BI224017	BD224017	Gene swit	BD224017
C	23	16.8	84.0	720	6	CQ839858	CQ839858	Sequence	CQ839858
C	24	16.8	84.0	720	6	CQ839862	CQ839862	Sequence	CQ839862
C	25	16.8	84.0	720	11	AY658192	AY658192	Synthetic	AY658192
C	26	16.8	84.0	802	10	BV638915	BV638915	S216P6135	BV638915
C	27	16.8	84.0	1725	1	PSEIASR	MS9425	Pseudomonas	AC0825
C	28	16.8	84.0	3444	2	ABGUCYC	X12874	Sea urc1in	AC0825
C	29	16.8	84.0	10238	1	AE004572	AE004572	Pseudomon	AC0825
C	30	16.8	84.0	36255	14	AC016208	AC016208	Hom sapi	AC016208
C	31	16.8	84.0	93714	14	AL161661	AL161661	Hom sapi	AL161661
C	32	16.8	84.0	111051	14	AC166715	AC166715	Hom sapi	AC166715
C	33	16.8	84.0	118396	8	AC073138	AC073138	Hom sapi	AC073138
C	34	16.8	84.0	131972	8	AC008794	AC008794	Hom sapi	AC008794
C	35	16.8	84.0	132063	14	AC142244	AC142244	Hom sapi	AC008794
C	36	16.8	84.0	147815	8	HS9986B	AC142244	Hom sapi	AC008794
C	37	16.8	84.0	149208	14	AC164137	AC164137	Human DNA	AC164137
C	38	16.8	84.0	162541	14	AC148601	AC148601	Gasferost	AC148601
C	39	16.8	84.0	162541	14	AC104460	AC104460	Hom sapi	AC104460
C	40	16.8	84.0	163701	14	AC073317	AC073317	Hom sapi	AC073317
C	41	16.8	84.0	163386	8	AC015722	AC015722	Hom sapi	AC015722
C	42	16.8	84.0	166703	8	AL135378	AL135378	Human DNA	AL135378
C	43	16.8	84.0	168087	14	AC157818	AC157818	Mus muscu	AC157818
C	44	16.8	84.0	187700	14	AC131061	AC131061	Mus muscu	AC131061
C	45	16.8	84.0	193104	14	AC001141	AC001141	Mus muscu	AC001141
C	46	16.8	84.0	195041	9	AC135809	AC135809	Hom sapi	AC135809
C	47	16.8	84.0	195767	9	AC127377	AC127377	Mus muscu	AC127377
C	48	16.8	84.0	201745	9	AC104205	AC104205	Mus muscu	AC104205
C	49	16.8	84.0	204393	14	AC145989	AC145989	Pan trogl	AC145989
C	50	16.8	84.0	206775	9	AC158309	AC158309	Mus muscu	AC158309
C	51	16.8	84.0	209285	14	AC013517	AC013517	Hom sapi	AC013517
C	52	16.8	84.0	219033	14	AC159830	AC159830	Mus muscu	AC159830
C	53	16.8	84.0	231764	14	AC119470	AC119470	Rattus no	AC119470
C	54	16.8	84.0	233445	14	AC129662	AC129662	Rattus no	AC129662
C	55	16.8	84.0	235703	9	AC113970	AC113970	Mus muscu	AC113970
C	56	16.8	84.0	303855	1	AE017230	AE017230	Mycobacte	AE017230
C	57	16.4	82.0	243	8	HS47B1R	Z61175	H. sapiens	C
C	58	16.4	82.0	246	6	AR673655	AR673655	Sequence	AY214609
C	59	16.4	82.0	487	3	AY214609	AY214609	Unculture	AY214609
C	60	16.4	82.0	606	10	G95328	G95328	S208P6750FA	G95328
C	61	16.4	82.0	1041	6	CQ741984	CQ741984	Sequence	CQ741984
C	62	16.4	82.0	17237	9	AP463761	AP463761	Mus muscu	AP463761

92	16.4	82.0	179705	9	AL627087	AL627087 Mouse DNA	c 165	16	80.0	1265	3	AY592491	AY592491 Unculture
93	16.4	82.0	183582	14	AC158891	AC158891 Bos tauru	c 166	16	80.0	1279	3	AF355045	AF355045 Unculture
94	16.4	82.0	183905	9	AC022682	AC022682 Mus muscu	c 167	16	80.0	1446	3	AF355044	AF355044 Unculture
95	16.4	82.0	186464	14	AC142067	AC142067 Rattus no	c 168	16	80.0	1564	6	AR507944	AR507944 Sequence
96	16.4	82.0	188292	9	AC156639	AC156639 Mus muscu	c 169	16	80.0	1734	3	AF092445	AF092445 Rattus no
97	16.4	82.0	188519	8	AC104041	AC104041 Homo sapi	c 170	16	80.0	2052	3	DQ009429	DQ009429 Unculture
98	16.4	82.0	189732	8	AC002303	AC002303 Homo sapi	c 171	16	80.0	2238	2	AY061199	AY061199 Drosophil
99	16.4	82.0	190256	9	AC121302	AC121302 Mus muscu	c 172	16	80.0	2335	2	BT001775	BT001775 Drosophil
100	16.4	82.0	191710	9	AC122489	AC122489 Mus muscu	c 173	16	80.0	2550	6	CQ599934	CQ599934 Sequence
101	16.4	82.0	191798	14	AC123952	AC123952 Mus muscu	c 174	16	80.0	2668	6	CQ584337	CQ584337 Sequence
102	16.4	82.0	192761	14	AC135939	AC135939 Rattus no	c 175	16	80.0	4972	6	CQ599933	CQ599933 Sequence
103	16.4	82.0	192872	9	AC140374	AC140374 Mus muscu	c 176	16	80.0	4989	6	CQ584336	CQ584336 Sequence
104	16.4	82.0	193572	9	AC140268	AC140268 Mus muscu	c 177	16	80.0	2668	6	CQ599934	CQ599934 Sequence
105	16.4	82.0	193934	14	AL646094	AL646094 Mus muscu	c 178	16	80.0	34740	8	CR931794	CR931794 Mouse sapi
106	16.4	82.0	197658	14	AC156543	AC156543 Mus muscu	c 179	16	80.0	36918	8	AC120116	AC120116 Homo sapi
107	16.4	82.0	199318	14	AC156543	AC156543 Mus muscu	c 180	16	80.0	65987	14	AC153871_3	AC153871_3 Continuation (4 of
108	16.4	82.0	199422	9	AC124180	AC124180 Mus muscu	c 181	16	80.0	74753	14	AC101565	AC101565 Mus muscu
109	16.4	82.0	199604	9	AC133902	AC133902 Mus muscu	c 182	16	80.0	87865	14	AC008477	AC008477 Homo sapi
110	16.4	82.0	203073	9	AC122322	AC122322 Mus muscu	c 183	16	80.0	89437	14	AC095424_3	AC095424_3 Continuation (4 of
111	16.4	82.0	208625	14	AC164605	AC164605 Mus muscu	c 184	16	80.0	96600	6	AX695710	AX695710 Sequence
112	16.4	82.0	208765	9	EX004985	EX004985 Mouse DNA	c 185	16	80.0	110000	14	AC095424_2	AC095424_2 Continuation (3 of
113	16.4	82.0	209751	9	AC154733	AC154733 Mus muscu	c 186	16	80.0	112643	14	AC11637_1	AC11637_1 Continuation (2 of
114	16.4	82.0	210180	14	AC110466	AC110466 Rattus no	c 187	16	80.0	127883	9	AC114434	AC114434 Rattus no
115	16.4	82.0	212974	14	AC121452	AC121452 Mus muscu	c 188	16	80.0	128760	9	AC153843	AC153843 Rattus no
116	16.4	82.0	214025	8	AC124578	AC124578 Mus muscu	c 189	16	80.0	129957	8	HS41562	HS41562 Human DNA s
117	16.4	82.0	214025	8	AC026782	AC026782 Homo sapi	c 190	16	80.0	133499	14	AC141969	AC141969 Rattus no
118	16.4	82.0	214060	9	AC131081	AC131081 Mus muscu	c 191	16	80.0	145263	13	AF030027	AF030027 Equine he
119	16.4	82.0	215532	14	AC152076	AC152076 Mus muscu	c 192	16	80.0	145597	13	AF030027	AF030027 Equine he
120	16.4	82.0	218085	14	AC094952	AC094952 Rattus no	c 193	16	80.0	146201	9	AC153942	AC153942 Mus muscu
121	16.4	82.0	218127	14	AC132713	AC132713 Rattus no	c 194	16	80.0	148167	9	AC141879	AC141879 Bos tauru
122	16.4	82.0	219872	14	AC126232	AC126232 Bos tauru	c 195	16	80.0	148555	14	AC126921	AC126921 Bos tauru
123	16.4	82.0	221159	14	AC163666	AC163666 Mus muscu	c 196	16	80.0	148650	5	EX323829	EX323829 Zebrafish
124	16.4	82.0	222156	14	AC122104	AC122104 Rattus no	c 197	16	80.0	148675	9	AC131769	AC131769 Mus muscu
125	16.4	82.0	222640	14	AC148797	AC148797 Rattus no	c 198	16	80.0	151596	9	AL669859	AL669859 Drosophil
126	16.4	82.0	224623	14	AC118994	AC118994 Rattus no	c 199	16	80.0	156905	14	AC020006	AC020006 Drosophil
127	16.4	82.0	224778	9	AC116071	AC116071 Rattus no	c 200	16	80.0	160034	9	AC131986	AC131986 Mus muscu
128	16.4	82.0	228201	5	AC145914	AC145914 Gallus ga	c 201	16	80.0	162472	14	AC118460	AC118460 Homo sapi
129	16.4	82.0	230212	14	AC095694	AC095694 Rattus no	c 202	16	80.0	166983	8	AC020894	AC020894 Homo sapi
130	16.4	82.0	230845	14	AC098415	AC098415 Rattus no	c 203	16	80.0	167822	14	AC155961	AC155961 Rattus no
131	16.4	82.0	231754	14	AC106163	AC106163 Rattus no	c 204	16	80.0	168152	14	AC145592	AC145592 Mus muscu
132	16.4	82.0	232885	14	AC106163	AC106163 Rattus no	c 205	16	80.0	170059	14	AC150005	AC150005 Mus muscu
133	16.4	82.0	233144	14	AC110317	AC110317 Rattus no	c 206	16	80.0	173049	8	AC008653	AC008653 Homo sapi
134	16.4	82.0	233303	14	AC114025	AC114025 Bos tauru	c 207	16	80.0	173049	8	AC0022142	AC0022142 Homo sapi
135	16.4	82.0	234217	14	AC162551	AC162551 Bos tauru	c 208	16	80.0	174186	9	AC155294	AC155294 Mus muscu
136	16.4	82.0	234300	14	AC162551	AC162551 Bos tauru	c 209	16	80.0	174186	9	AC131066	AC131066 Mus muscu
137	16.4	82.0	236344	14	AC1106126	AC1106126 Rattus no	c 210	16	80.0	174546	9	AC160464	AC160464 Mus muscu
138	16.4	82.0	240125	9	AL669982	AL669982 Mouse DNA	c 211	16	80.0	175195	9	AC160464	AC160464 Mus muscu
139	16.4	82.0	242728	14	AC154647	AC154647 Mus muscu	c 212	16	80.0	175716	9	AC117245	AC117245 Mus muscu
140	16.4	82.0	250169	14	CT010585	CT010585 Mus muscu	c 213	16	80.0	177775	9	AC161447	AC161447 Mus muscu
141	16.4	82.0	254493	14	AC095874	AC095874 Rattus no	c 214	16	80.0	182569	9	AC117206	AC117206 Mus muscu
142	16.4	82.0	256132	14	AC136623	AC136623 Rattus no	c 215	16	80.0	183385	9	AC117130	AC117130 Mus muscu
143	16.4	82.0	256367	14	AC124207	AC124207 Rattus no	c 216	16	80.0	184209	14	AC117130	AC117130 Mus muscu
144	16.4	82.0	257714	14	AC096219	AC096219 Rattus no	c 217	16	80.0	184794	9	AC129582	AC129582 Mus muscu
145	16.4	82.0	267067	14	AC096599	AC096599 Rattus no	c 218	16	80.0	184960	14	EX004757	EX004757 Mouse DNA
146	16.4	82.0	270699	14	AC133821	AC133821 Rattus no	c 219	16	80.0	189540	9	AL772264	AL772264 Mouse DNA
147	16.4	82.0	273595	14	AC095278	AC095278 Rattus no	c 220	16	80.0	189867	9	AC161888	AC161888 Mus muscu
148	16.4	82.0	298970	14	AC119651	AC119651 Rattus no	c 221	16	80.0	191017	14	AC034286	AC034286 Mus muscu
149	16.4	82.0	303008	14	AC158959	AC158959 Mus muscu	c 222	16	80.0	191060	14	AC021468	AC021468 Homo sapi
150	16.4	82.0	318959	14	AY657023	AY657023 Mus muscu	c 223	16	80.0	192053	9	AC132103	AC132103 Mus muscu
151	16.4	82.0	335283	14	AC020865	AC020865 Mus muscu	c 224	16	80.0	192748	9	AC158679	AC158679 Mus muscu
152	16.4	82.0	348971	1	BX572594	BX572594 Rhodosphe	c 225	16	80.0	192812	9	AC115303	AC115303 Mus muscu
153	16.4	80.0	510	3	AY165971	AY165971 Unculture	c 226	16	80.0	195129	9	AL627069	AL627069 Mouse DNA
154	16.4	80.0	512	3	AB046181	AB046181 Unculture	c 227	16	80.0	195132	9	AC139335	AC139335 Mus muscu
155	16.4	80.0	521	3	AB046184	AB046184 Unculture	c 228	16	80.0	195384	9	AC112149	AC112149 Mus muscu
156	16.4	80.0	521	3	AB046184	AB046184 Unculture	c 229	16	80.0	195582	14	AC105486	AC105486 Rattus no
157	16.4	80.0	793	3	AY960289	AY960289 Unculture	c 230	16	80.0	195625	14	AC133805	AC133805 Rattus no
158	16.4	80.0	793	3	AY960289	AY960289 Unculture	c 231	16	80.0	195987	9	AC122537	AC122537 Mus muscu
159	16.4	80.0	856	3	AF440701	AF440701 Unculture	c 232	16	80.0	197482	8	AL930119	AL930119 Human DNA
160	16.4	80.0	856	3	AF440713	AF440713 Unculture	c 233	16	80.0	198927	9	AC155273	AC155273 Mus muscu
161	16.4	80.0	856	3	AF440718	AF440718 Unculture	c 234	16	80.0	198992	14	AC147548	AC147548 Mus muscu
162	16.4	80.0	856	3	AF440721	AF440721 Unculture	c 235	16	80.0	199016	2	AC008204	AC008204 Drosophil
163	16.4	80.0	891	3	AY672472	AY672472 Unculture	c 236	16	80.0	201291	14	AC144996	AC144996 Rattus no
164	16.4	80.0	1071	3	AY373420	AY373420 Unculture	c 237	16	80.0	201437	9	AL807236	AL807236 Mouse DNA



238	16	80.0	204312	9	AL669943	311	16	80.0	300940	14	AC134267	AC134267 Rattus no
239	16	80.0	205599	9	AC137156	312	16	80.0	303008	14	AC158959	AC158959 Mus muscu
240	16	80.0	205702	9	AC140190	313	16	80.0	307435	1	AE016914	AE016914 Chromobac
241	16	80.0	206230	9	AC084272	314	15.8	79.0	542	6	CQ484046	CQ484046 Sequence
242	16	80.0	206747	2	AE003747	315	15.8	79.0	568	10	BV050994	BV050994 S212P6324
243	16	80.0	207157	9	AC147634	316	15.8	79.0	576	6	AR506666	AR506666 Sequence
244	16	80.0	207239	9	AC113107	317	15.8	79.0	592	6	CO513874	CO513874 Sequence
245	16	80.0	208715	14	AC158176	318	15.8	79.0	628	10	BV370666	BV370666 S231P6132
246	16	80.0	209071	14	AC134109	319	15.8	79.0	965	5	AY693582	AY693582 Hemitramp
247	16	80.0	209211	14	AC084883	320	15.8	79.0	965	5	AY693583	AY693583 Hemitramp
248	16	80.0	209799	9	AL671117	321	15.8	79.0	969	8	AH007006S1	U92317 Homo sapien
249	16	80.0	209838	9	AC102505	322	15.8	79.0	978	6	CO575691	CO575691 Sequence
250	16	80.0	210204	14	AC158174	323	15.8	79.0	1003	6	AF012467	AF012467 Colobus a
251	16	80.0	210257	14	AC135865	324	15.8	79.0	1023	11	AY659219	AY659219 Synthetic
252	16	80.0	210959	9	AC109606	325	15.8	79.0	1057	6	BD209546	BD209546 Compositi
253	16	80.0	211317	14	AC114505	326	15.8	79.0	1057	6	AR341352	AR341352 Sequence
254	16	80.0	212221	14	AC136126	327	15.8	79.0	1140	4	AF338683	AF338683 Pteronotu
255	16	80.0	213476	14	AC114589	328	15.8	79.0	1140	4	AF338684	AF338684 Pteronotu
256	16	80.0	213482	9	AC154633	329	15.8	79.0	1140	4	AY604461	AY604461 Pteronotu
257	16	80.0	216169	9	AC154633	330	15.8	79.0	1288	2	AY089582	AY089582 Drosophill
258	16	80.0	218758	9	AC109608	331	15.8	79.0	1408	3	AY922139	AY922139 Unculture
259	16	80.0	219379	9	AL627083	332	15.8	79.0	2004	6	BD209680	BD209680 Compositi
260	16	80.0	220622	9	AC111085	333	15.8	79.0	2004	6	AR341486	AR341486 Sequence
261	16	80.0	220742	14	AC105644	334	15.8	79.0	2040	6	BD158578	BD158578 Primer fo
262	16	80.0	220742	14	AC105644	335	15.8	79.0	2040	8	AK023694	AK023694 Sequence
263	16	80.0	221599	14	AC094756	336	15.8	79.0	2040	8	AK023694	AK023694 Homo sapi
264	16	80.0	221805	9	AC105515	337	15.8	79.0	2151	8	GG86L0P	X02314 Gorilla bet
265	16	80.0	222544	14	AC127923	338	15.8	79.0	2388	15	SCU62525	U62525 Saccharomyc
266	16	80.0	222775	9	AC084069	339	15.8	79.0	3026	13	MCU02500	U02500 Murine cyto
267	16	80.0	223344	14	AC106193	340	15.8	79.0	3074	2	BT011433	BT011433 Drosophill
268	16	80.0	223541	9	AC125010	341	15.8	79.0	3215	9	AF245476	AF245476 Mus muscu
269	16	80.0	224703	14	AC115510	342	15.8	79.0	3265	6	CO575690	CO575690 Sequence
270	16	80.0	224933	14	AC095378	343	15.8	79.0	3481	5	AY303542	AY303542 Takifugu
271	16	80.0	225308	14	AC098918	344	15.8	79.0	3540	5	AB182274	AB182274 Takifugu
272	16	80.0	225308	9	AC153909	345	15.8	79.0	7055	8	GORHBBG	K02543 Gorilla bet
273	16	80.0	227833	14	AC128446	346	15.8	79.0	8476	8	GIBBGL0ETA	M54965 H.lar pai-e
274	16	80.0	228191	14	AC094451	347	15.8	79.0	11593	1	AE004678	AE004678 Pseudom
275	16	80.0	228296	14	AL831751	348	15.8	79.0	12046	1	AE005017	AE005017 Halobacte
276	16	80.0	229761	14	AC123314	349	15.8	79.0	13961	1	AE004984	AE004984 Halobacte
277	16	80.0	229976	14	AC166359	350	15.8	79.0	15051	6	CO575081	CO575081 Sequence
278	16	80.0	230212	14	AC095694	351	15.8	79.0	15769	1	AY026914	AY026914 Pseudom
279	16	80.0	230394	14	AC098017	352	15.8	79.0	16440	1	AE001993	AE001993 Delinococ
280	16	80.0	230447	9	AL671866	353	15.8	79.0	22566	8	CERGL0BIN	M81409 Cebus albif
281	16	80.0	231295	14	AC097286	354	15.8	79.0	25913	15	SC9910	Z46708 S.cerevisia
282	16	80.0	231822	14	AC129612	355	15.8	79.0	27256	9	AF240003	AF240003 Mus muscu
283	16	80.0	233094	14	AC128479	356	15.8	79.0	45562	8	AL358512	AL358512 Human DNA
284	16	80.0	234351	14	AC135903	357	15.8	79.0	49197	15	AP006349	AP006349 Lottus cor
285	16	80.0	235453	9	AC133910	358	15.8	79.0	51111	14	AC100579	AC100579 Mus muscu
286	16	80.0	235938	14	AC121469	359	15.8	79.0	67987	9	AL672157	AL672157 Mouse DNA
287	16	80.0	236159	14	AC125553	360	15.8	79.0	73920	9	AC091397	AC091397 Rattus no
288	16	80.0	236502	14	AC098186	361	15.8	79.0	74507	8	AC004031	AC004031 Homo sapi
289	16	80.0	236933	14	AC111937	362	15.8	79.0	90801	8	AC025033	AC025033 Homo sapi
290	16	80.0	237754	9	AC125576	363	15.8	79.0	93156	8	AY640177	AY640177 Homo sapi
291	16	80.0	240411	14	AC162491	364	15.8	79.0	95537	14	AC021512	AC021512 Homo sapi
292	16	80.0	245853	14	AC125965	365	15.8	79.0	100120	8	AC090454	AC090454 Homo sapi
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C 550	15.4	77.0	1596	3	DQ088759	Unculture	C 623	15.4	77.0	110000	14	AC157600	AC157600 3
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C 583	15.4	77.0	63720	6	AX695971	Sequence	C 656	15.4	77.0	148291	14	AC135926	AC135926
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C 590	15.4	77.0	68780	14	AC135185	Mus muscu	C 663	15.4	77.0	150936	9	AC087722	AC087722
C 591	15.4	77.0	69055	14	AC090769	Mus muscu	C 664	15.4	77.0	151603	9	AL731731	AL731731
C 592	15.4	77.0	70872	14	AC114997	Homo sapi	C 665	15.4	77.0	151603	9	AC008161	AC008161
C 593	15.4	77.0	72274	14	AC145201	Mus muscu	C 666	15.4	77.0	151804	14	AC154271	AC154271
C 594	15.4	77.0	72319	14	AC139642	Rattus no	C 667	15.4	77.0	152095	9	AC147466	AC147466
C 595	15.4	77.0	73319	14	AL512843	Human DNA	C 668	15.4	77.0	152281	14	AL672066	AL672066
C 596	15.4	77.0	73319	14	AL512843	Human DNA	C 669	15.4	77.0	152308	14	AC135212	AC135212
C 597	15.4	77.0	73319	14	AL512843	Human DNA	C 670	15.4	77.0	152308	14	AC135212	AC135212
C 598	15.4	77.0	73319	14	AL512843	Human DNA	C 671	15.4	77.0	152308	14	AC135212	AC135212
C 599	15.4	77.0	73319	14	AL512843	Human DNA	C 672	15.4	77.0	152308	14	AC135212	AC135212
C 600	15.4	77.0	73319	14	AL512843	Human DNA	C 673	15.4	77.0	152308	14	AC135212	AC135212
C 601	15.4	77.0	73319	14	AL512843	Human DNA	C 674	15.4	77.0	152308	14	AC135212	AC135212
C 602	15.4	77.0	73319	14	AL512843	Human DNA	C 675	15.4	77.0	152308	14	AC135212	AC135212

C 676	15.4	77.0	153767	9	AC124981	Mus muscu	749	15.4	77.0	187418	14	AC156240	AC156240 Bos tauru
C 677	15.4	77.0	154298	9	AL831773	Musce DNA	C 750	15.4	77.0	187600	14	AC140360	AC140360 Mus muscu
C 678	15.4	77.0	154454	8	AC146056	Pan trogl	C 751	15.4	77.0	188880	9	AC092203	AC092203 Mus muscu
C 679	15.4	77.0	154542	14	AC079040	Mus muscu	C 752	15.4	77.0	189286	9	AC122336	AC122336 Mus muscu
C 680	15.4	77.0	155034	9	AL662803	Musce DNA	C 753	15.4	77.0	189454	14	AC141044	AC141044 Mus muscu
C 681	15.4	77.0	156280	14	AC079595	Homo sapi	C 754	15.4	77.0	189458	9	AC134908	AC134908 Mus muscu
C 682	15.4	77.0	158255	8	AC025695	Homo sapi	C 755	15.4	77.0	189892	14	AC091425	AC091425 Mus muscu
C 683	15.4	77.0	158972	14	AC160538	Mus muscu	C 756	15.4	77.0	189932	14	AC146117	AC146117 Mus muscu
C 684	15.4	77.0	160367	14	AC009542	Homo sapi	C 757	15.4	77.0	190048	14	AL591136	AL591136 Musce DNA
C 685	15.4	77.0	160697	14	AC023457	Homo sapi	C 758	15.4	77.0	190149	9	AL713913	AL713913 Rattus no
C 686	15.4	77.0	161647	8	AC079080	Mus muscu	C 759	15.4	77.0	190485	9	AL713913	AL713913 Rattus no
C 687	15.4	77.0	161652	9	AC140353	Mus muscu	C 760	15.4	77.0	190937	14	AC103477	AC103477 Rattus no
C 688	15.4	77.0	162087	14	AC115938	Mus muscu	C 761	15.4	77.0	191328	9	AC159886	AC159886 Mus muscu
C 689	15.4	77.0	162455	9	AC125540	Mus muscu	C 762	15.4	77.0	191723	9	AC121792	AC121792 Mus muscu
C 690	15.4	77.0	163800	9	AC122510	Mus muscu	C 763	15.4	77.0	191904	9	AC158524	AC158524 Mus muscu
C 691	15.4	77.0	165012	14	AC117782	Mus muscu	C 764	15.4	77.0	191920	14	AC129843	AC129843 Rattus no
C 692	15.4	77.0	165241	9	AC161455	Mus muscu	C 765	15.4	77.0	192062	9	AC121855	AC121855 Mus muscu
C 693	15.4	77.0	165781	9	AC101542	Mus muscu	C 766	15.4	77.0	192200	14	AC163629	AC163629 Mus muscu
C 694	15.4	77.0	167145	9	AC158748	Mus muscu	C 767	15.4	77.0	192282	8	AC010424	AC010424 Rattus no
C 695	15.4	77.0	167418	9	AC133944	Mus muscu	C 768	15.4	77.0	192367	14	AC121410	AC121410 Rattus no
C 696	15.4	77.0	167526	14	AC121622	Rattus no	C 769	15.4	77.0	192586	9	AL645972	AL645972 Musce DNA
C 697	15.4	77.0	167691	14	AC103349	Mus muscu	C 770	15.4	77.0	192586	14	AC129244	AC129244 Rattus no
C 698	15.4	77.0	167775	9	AC112268	Mus muscu	C 771	15.4	77.0	192687	14	AC097960	AC097960 Mus muscu
C 699	15.4	77.0	167775	9	AC123432	Mus muscu	C 772	15.4	77.0	193147	14	AC097960	AC097960 Mus muscu
C 700	15.4	77.0	168107	9	AC145082	Mus muscu	C 773	15.4	77.0	193469	9	AC128125	AC128125 Rattus no
C 701	15.4	77.0	169059	14	AC009790	Homo sapi	C 774	15.4	77.0	193811	14	AC142098	AC142098 Mus muscu
C 702	15.4	77.0	170321	9	AC132229	Mus muscu	C 775	15.4	77.0	194185	8	AC103705	AC103705 Mus muscu
C 703	15.4	77.0	170321	9	AC108484	Mus muscu	C 776	15.4	77.0	194209	9	AL929249	AL929249 Musce DNA
C 704	15.4	77.0	170737	9	AC129180	Mus muscu	C 777	15.4	77.0	194307	14	AC132042	AC132042 Rattus no
C 705	15.4	77.0	171697	8	AC119116	Rattus no	C 778	15.4	77.0	194593	9	AC116470	AC116470 Mus muscu
C 706	15.4	77.0	172449	14	AC146031	Pan trogl	C 779	15.4	77.0	194616	14	AC186629	AC186629 Mus muscu
C 707	15.4	77.0	172595	9	AC145297	Mus muscu	C 780	15.4	77.0	194627	9	AC150685	AC150685 Mus muscu
C 708	15.4	77.0	173022	9	AC140275	Mus muscu	C 781	15.4	77.0	195017	9	AC154667	AC154667 Mus muscu
C 709	15.4	77.0	173472	9	AC131760	Mus muscu	C 782	15.4	77.0	195129	9	AC105958	AC105958 Mus muscu
C 710	15.4	77.0	173493	14	AC136016	Rattus no	C 783	15.4	77.0	195305	9	AC140233	AC140233 Mus muscu
C 711	15.4	77.0	173810	9	AC083815	Mus muscu	C 784	15.4	77.0	195605	14	AC130953	AC130953 Rattus no
C 712	15.4	77.0	174768	8	AC009330	Homo sapi	C 785	15.4	77.0	196249	14	AC154418	AC154418 Mus muscu
C 713	15.4	77.0	174882	9	AC127273	Mus muscu	C 786	15.4	77.0	196260	14	AC116247	AC116247 Mus muscu
C 714	15.4	77.0	175144	14	AC010415	Mus muscu	C 787	15.4	77.0	196783	9	AC137855	AC137855 Mus muscu
C 715	15.4	77.0	175245	9	AC129188	Mus muscu	C 788	15.4	77.0	196783	9	AL844592	AL844592 Mus muscu
C 716	15.4	77.0	176038	15	AC135915	Mus muscu	C 789	15.4	77.0	197462	8	AC009554	AC009554 Mus muscu
C 717	15.4	77.0	176092	9	AC129329	Mus muscu	C 790	15.4	77.0	197639	14	AC124208	AC124208 Rattus no
C 718	15.4	77.0	176354	14	BX855600	Mus muscu	C 791	15.4	77.0	197658	14	AC185119	AC185119 Mus muscu
C 719	15.4	77.0	177047	14	AC138613	Mus muscu	C 792	15.4	77.0	198374	14	AC118420	AC118420 Rattus no
C 720	15.4	77.0	177326	14	AC138613	Mus muscu	C 793	15.4	77.0	198621	9	AC122828	AC122828 Mus muscu
C 721	15.4	77.0	177733	14	AC113908	Rattus no	C 794	15.4	77.0	198621	9	AC139243	AC139243 Mus muscu
C 722	15.4	77.0	177885	14	AC141947	Mus muscu	C 795	15.4	77.0	198921	14	AC159972	AC159972 Mus muscu
C 723	15.4	77.0	178098	14	AC040955	Mus muscu	C 796	15.4	77.0	199035	14	AB088420	AB088420 Pseudom
C 724	15.4	77.0	178562	14	AC152854	Mus muscu	C 797	15.4	77.0	199098	14	AC158302	AC158302 Mus muscu
C 725	15.4	77.0	178868	14	AC160124	Mus muscu	C 798	15.4	77.0	199204	14	AC131298	AC131298 Mus muscu
C 726	15.4	77.0	179162	14	AC132076	Bos tauru	C 799	15.4	77.0	199207	9	AC124762	AC124762 Mus muscu
C 727	15.4	77.0	179927	9	AC154616	Mus muscu	C 800	15.4	77.0	199240	9	AC124549	AC124549 Mus muscu
C 728	15.4	77.0	180079	9	AC114678	Mus muscu	C 801	15.4	77.0	199341	14	AC112386	AC112386 Rattus no
C 729	15.4	77.0	180136	9	AL732557	Musce DNA	C 802	15.4	77.0	199789	15	ATCRH189	ATCRH189 Mus muscu
C 730	15.4	77.0	180353	14	AC128288	Rattus no	C 803	15.4	77.0	200057	14	AC073810	AC073810 Mus muscu
C 731	15.4	77.0	180560	9	AC137605	Mus muscu	C 804	15.4	77.0	200412	14	AC15666	AC15666 Rattus no
C 732	15.4	77.0	181111	14	AC166857	Oryctolag	C 805	15.4	77.0	200653	14	CT025540	CT025540 Mus muscu
C 733	15.4	77.0	182058	9	AC154412	Mus muscu	C 806	15.4	77.0	200935	14	AC148834	AC148834 Pan trogl
C 734	15.4	77.0	182058	9	AC137950	Mus muscu	C 807	15.4	77.0	201075	14	AC166870	AC166870 Oryctolag
C 735	15.4	77.0	182309	9	AC121846	Mus muscu	C 808	15.4	77.0	201441	14	AC111527	AC111527 Rattus no
C 736	15.4	77.0	182439	9	AL805955	Musce DNA	C 809	15.4	77.0	202201	9	AC115295	AC115295 Mus muscu
C 737	15.4	77.0	182439	9	AL805955	Musce DNA	C 810	15.4	77.0	202404	8	AC104447	AC104447 Homo sapi
C 738	15.4	77.0	182445	14	AC132717	Rattus no	C 811	15.4	77.0	202554	14	AC163076	AC163076 Mus muscu
C 739	15.4	77.0	182962	14	AC132511	Rattus no	C 812	15.4	77.0	202553	14	AL670464	AL670464 Musce DNA
C 740	15.4	77.0	182990	14	AC141383	Rattus no	C 813	15.4	77.0	202768	9	AC108825	AC108825 Mus muscu
C 741	15.4	77.0	183129	14	AC133282	Mus muscu	C 814	15.4	77.0	203558	9	AL670464	AL670464 Musce DNA
C 742	15.4	77.0	184074	14	AC148560	Oryctolag	C 815	15.4	77.0	203558	9	AC093354	AC093354 Mus muscu
C 743	15.4	77.0	184174	9	AC121570	Mus muscu	C 816	15.4	77.0	204313	14	AC126304	AC126304 Rattus no
C 744	15.4	77.0	185232	9	AC127266	Mus muscu	C 817	15.4	77.0	205084	9	AC121859	AC121859 Mus muscu
C 745	15.4	77.0	185321	14	AC110324	Rattus no	C 818	15.4	77.0	206093	9	AC087330	AC087330 Mus muscu
C 746	15.4	77.0	185938	14	AC122037	Mus muscu	C 819	15.4	77.0	206924	9	AC087780	AC087780 Mus muscu
C 747	15.4	77.0	186673	14	AL590713	Homo sapi	C 820	15.4	77.0	206924	9	AC087780	AC087780 Mus muscu
C 748	15.4	77.0	187181	9	AL591854	Musce DNA	C 821	15.4	77.0	206924	9	AC087780	AC087780 Mus muscu

822	15.4	77.0	207429	9	AC150312	AC150312 Mus muscu	895	15.4	77.0	223497	14	AC15162	AC15162 Rattus no
823	15.4	77.0	207823	14	AC145542	AC145542 Oryctolag	896	15.4	77.0	223528	9	AC155636	AC155636 Mus muscu
824	15.4	77.0	208376	9	AC155160	AC155160 Mus muscu	897	15.4	77.0	223650	14	AC095283	AC095283 Rattus no
825	15.4	77.0	208483	9	AC107757	AC107757 Mus muscu	898	15.4	77.0	224019	14	AC131146	AC131146 Rattus no
826	15.4	77.0	208652	14	EX324228	EX324228 Mus muscu	899	15.4	77.0	224181	9	AC139671	AC139671 Mus muscu
827	15.4	77.0	208848	14	AC139608	AC139608 Rattus no	900	15.4	77.0	224344	14	AC108294	AC108294 Rattus no
828	15.4	77.0	208848	14	AC139608	AC139608 Rattus no	901	15.4	77.0	224522	14	AC106627	AC106627 Rattus no
829	15.4	77.0	209121	9	AC127589	AC127589 Mus muscu	902	15.4	77.0	225235	14	AC103102	AC103102 Rattus no
830	15.4	77.0	209234	14	AC148639	AC148639 Callithrix	903	15.4	77.0	225300	14	AC084798	AC084798 Mus muscu
831	15.4	77.0	209384	14	AC151295	AC151295 Mus muscu	904	15.4	77.0	226140	14	AC097415	AC097415 Rattus no
832	15.4	77.0	209419	14	AC154608	AC154608 Mus muscu	905	15.4	77.0	226361	14	AC094681	AC094681 Rattus no
833	15.4	77.0	209523	9	AC084386	AC084386 Mus muscu	906	15.4	77.0	226532	14	AC110662	AC110662 Rattus no
834	15.4	77.0	209835	9	AC160125	AC160125 Mus muscu	907	15.4	77.0	226795	9	AC161493	AC161493 Mus muscu
835	15.4	77.0	209907	9	AC118038	AC118038 Mus muscu	908	15.4	77.0	227026	14	AC136659	AC136659 Rattus no
836	15.4	77.0	210003	9	AC120144	AC120144 Mus muscu	909	15.4	77.0	227458	14	AC110137	AC110137 Rattus no
837	15.4	77.0	210695	14	AC159205	AC159205 Mus muscu	910	15.4	77.0	227555	9	AC108416	AC108416 Mus muscu
838	15.4	77.0	210891	14	AC153356	AC153356 Mus muscu	911	15.4	77.0	227679	9	AC109807	AC109807 Mus muscu
839	15.4	77.0	210959	9	AC109606	AC109606 Mus muscu	912	15.4	77.0	227918	9	AL672284	AL672284 Mouse DNA
840	15.4	77.0	211118	14	AC073752	AC073752 Mus muscu	913	15.4	77.0	227955	9	AC122669	AC122669 Rattus no
841	15.4	77.0	211209	9	AC125227	AC125227 Mus muscu	914	15.4	77.0	228363	9	AC116128	AC116128 Mus muscu
842	15.4	77.0	211414	9	AC104885	AC104885 Mus muscu	915	15.4	77.0	228532	14	AC132523	AC132523 Rattus no
843	15.4	77.0	211456	9	AL928926	AL928926 Mouse DNA	916	15.4	77.0	228644	9	AC102570	AC102570 Rattus no
844	15.4	77.0	211776	9	AC084821	AC084821 Mus muscu	917	15.4	77.0	228702	14	AC139522	AC139522 Rattus no
845	15.4	77.0	211906	14	AC084293	AC084293 Mus muscu	918	15.4	77.0	228820	14	AC106330	AC106330 Bos tauru
846	15.4	77.0	212484	9	AC151841	AC151841 Mus muscu	919	15.4	77.0	228873	14	AC160430	AC160430 Bos tauru
847	15.4	77.0	212491	9	AC105474	AC105474 Mus muscu	920	15.4	77.0	228917	14	AC106079	AC106079 Rattus no
848	15.4	77.0	212532	9	AC091274	AC091274 Mus muscu	921	15.4	77.0	228945	14	AC160177	AC160177 Bos tauru
849	15.4	77.0	213181	9	AC084800	AC084800 Mus muscu	922	15.4	77.0	229321	14	AC094185	AC094185 Rattus no
850	15.4	77.0	213348	9	AC134898	AC134898 Mus muscu	923	15.4	77.0	229427	14	AC155779	AC155779 Oryctolag
851	15.4	77.0	213625	14	AC140950	AC140950 Rattus no	924	15.4	77.0	230026	14	AC109847	AC109847 Rattus no
852	15.4	77.0	213817	14	AC123649	AC123649 Mus muscu	925	15.4	77.0	230116	9	AL732620	AL732620 Mouse DNA
853	15.4	77.0	214121	14	AC123649	AC123649 Mus muscu	926	15.4	77.0	230116	14	AC091604	AC091604 Mus muscu
854	15.4	77.0	214331	14	AL732312	AL732312 Mus muscu	927	15.4	77.0	230349	8	AC161608	AC161608 Pan trogl
855	15.4	77.0	214762	14	AC158652	AC158652 Mus muscu	928	15.4	77.0	230448	14	AC128463	AC128463 Rattus no
856	15.4	77.0	214840	9	AC007305	AC007305 Mus muscu	929	15.4	77.0	230635	14	AC128319	AC128319 Rattus no
857	15.4	77.0	214934	9	AC154235	AC154235 Mus muscu	930	15.4	77.0	230972	14	AC138530	AC138530 Mus muscu
858	15.4	77.0	215043	9	AC087229	AC087229 Mus muscu	931	15.4	77.0	230972	14	AC138530	AC138530 Mus muscu
859	15.4	77.0	215072	14	AC157585	AC157585 Mus muscu	932	15.4	77.0	231000	9	AC149593	AC149593 Mus muscu
860	15.4	77.0	215150	14	AC116438	AC116438 Mus muscu	933	15.4	77.0	231258	14	AC159277	AC159277 Mus muscu
861	15.4	77.0	215210	9	AL713989	AL713989 Mouse DNA	934	15.4	77.0	231258	14	AC112557	AC112557 Rattus no
862	15.4	77.0	215366	9	AL603836	AL603836 Mouse DNA	935	15.4	77.0	231260	14	AC073735	AC073735 Mus muscu
863	15.4	77.0	215384	9	AC125221	AC125221 Mus muscu	936	15.4	77.0	231382	14	AC095549	AC095549 Rattus no
864	15.4	77.0	215485	8	AC103681	AC103681 Homo sapi	937	15.4	77.0	231494	14	AC121204	AC121204 Rattus no
865	15.4	77.0	215488	9	AC099415	AC099415 Mus muscu	938	15.4	77.0	231785	14	AC094057	AC094057 Rattus no
866	15.4	77.0	215722	9	AC140457	AC140457 Mus muscu	939	15.4	77.0	232175	14	AC115380	AC115380 Rattus no
867	15.4	77.0	215921	14	AC130550	AC130550 Rattus no	940	15.4	77.0	232452	14	AC115399	AC115399 Rattus no
868	15.4	77.0	216255	14	AC118841	AC118841 Rattus no	941	15.4	77.0	232472	9	AC068907	AC068907 Mus muscu
869	15.4	77.0	217141	14	AC073998	AC073998 Homo sapi	942	15.4	77.0	232817	9	AC126686	AC126686 Mus muscu
870	15.4	77.0	217221	8	AC008682	AC008682 Homo sapi	943	15.4	77.0	232817	14	AC111790	AC111790 Rattus no
871	15.4	77.0	217636	9	AC127411	AC127411 Mus muscu	944	15.4	77.0	233367	9	AC118931	AC118931 Mus muscu
872	15.4	77.0	217735	9	AL596116	AL596116 Mouse DNA	945	15.4	77.0	233436	14	CT025569	CT025569 Mus muscu
873	15.4	77.0	217949	9	AC127582	AC127582 Mus muscu	946	15.4	77.0	233473	14	AC133034	AC133034 Rattus no
874	15.4	77.0	218381	9	AC155268	AC155268 Mus muscu	947	15.4	77.0	233948	14	AC135493	AC135493 Rattus no
875	15.4	77.0	218608	14	AC113754	AC113754 Rattus no	948	15.4	77.0	234347	14	AC127187	AC127187 Rattus no
876	15.4	77.0	219481	14	AC161435	AC161435 Mus muscu	949	15.4	77.0	234358	14	AC131612	AC131612 Rattus no
877	15.4	77.0	219865	9	AC131187	AC131187 Mus muscu	950	15.4	77.0	234431	14	AC130025	AC130025 Rattus no
878	15.4	77.0	219949	14	AC119687	AC119687 Rattus no	951	15.4	77.0	234797	14	AC130921	AC130921 Rattus no
879	15.4	77.0	220358	14	AC129036	AC129036 Rattus no	952	15.4	77.0	235574	9	AC133889	AC133889 Mus muscu
880	15.4	77.0	220524	14	AL591685	AL591685 Mus muscu	953	15.4	77.0	235978	14	AC127084	AC127084 Rattus no
881	15.4	77.0	220577	14	AC068497	AC068497 Mus muscu	954	15.4	77.0	235978	14	AC094209	AC094209 Rattus no
882	15.4	77.0	221049	14	AC137178	AC137178 Rattus no	955	15.4	77.0	236064	14	AC095318	AC095318 Rattus no
883	15.4	77.0	221077	14	AC160060	AC160060 Mus muscu	956	15.4	77.0	236198	14	AC108547	AC108547 Rattus no
884	15.4	77.0	221906	14	AC117634	AC117634 Mus muscu	957	15.4	77.0	236337	14	AC161806	AC161806 Mus muscu
885	15.4	77.0	221953	9	AC073435	AC073435 Mus muscu	958	15.4	77.0	236472	14	AC118297	AC118297 Rattus no
886	15.4	77.0	222328	14	AC162451	AC162451 Mus muscu	959	15.4	77.0	236486	14	AC138166	AC138166 Bos tauru
887	15.4	77.0	222356	14	AC137233	AC137233 Rattus no	960	15.4	77.0	236773	14	AC128389	AC128389 Rattus no
888	15.4	77.0	222398	14	AC151838	AC151838 Mus muscu	961	15.4	77.0	236778	14	AC129110	AC129110 Rattus no
889	15.4	77.0	222536	14	AC117919	AC117919 Rattus no	962	15.4	77.0	237067	14	AC118339	AC118339 Rattus no
890	15.4	77.0	2232763	14	AC098207	AC098207 Rattus no	963	15.4	77.0	237285	14	AC158303	AC158303 Mus muscu
891	15.4	77.0	223018	14	AC107558	AC107558 Rattus no	964	15.4	77.0	237359	14	AC127753	AC127753 Rattus no
892	15.4	77.0	223152	14	AC114994	AC114994 Mus muscu	965	15.4	77.0	237421	14	AC099103	AC099103 Rattus no
893	15.4	77.0	223292	14	AC133790	AC133790 Rattus no	966	15.4	77.0	237549	14	AC112451	AC112451 Rattus no
894	15.4	77.0	223438	9	AL662804	AL662804 Mouse DNA	967	15.4	77.0	237653	14	AC073760	AC073760 Mus muscu

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 C 969 15.4 77.0 237881 14 AC105704  
 C 970 15.4 77.0 238256 14 AC094282  
 C 971 15.4 77.0 238602 14 AC109002  
 C 972 15.4 77.0 238623 14 AC099087  
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 C 976 15.4 77.0 239653 9 AC147047  
 C 977 15.4 77.0 239758 9 AL591495  
 C 978 15.4 77.0 239796 14 AC119389  
 C 979 15.4 77.0 240200 14 AC103040  
 C 980 15.4 77.0 240918 14 AC137254  
 C 981 15.4 77.0 240931 14 AC107097  
 C 982 15.4 77.0 241705 14 AC118921  
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 C 990 15.4 77.0 242966 14 AC111931  
 C 991 15.4 77.0 243290 14 AC099378  
 C 992 15.4 77.0 243892 14 AC097933  
 C 993 15.4 77.0 245105 14 AC115325  
 C 994 15.4 77.0 245214 14 AC110825  
 C 995 15.4 77.0 245258 14 AC121737  
 C 996 15.4 77.0 245322 14 AC097538  
 C 997 15.4 77.0 245447 14 AC098666  
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 C 999 15.4 77.0 245878 14 AC125842  
 C 999 15.4 77.0 245907 14 AC095162

## ALIGNMENTS

## RESULT 1

AX104199 20 bp DNA linear PAT 30-APR-2001

LOCUS AX104199 Sequence 391 from Patent WO0122972.

ACCESSION AX104199

VERSION AX104199.1 GI:13920396

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1  
 Kriegl, A.M., Schletter, C. and Vollmer, J.C.  
 Immunostimulatory nucleic acids  
 Patent: WO 0122972-A 391 05-APR-2001;  
 UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical  
 GmbH (DE)

FEATURES  
 source location/Qualifiers

1..20  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"

## ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 83;  
 Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGUAAGCCAGACUACGA 20  
 DB 1 AGGTAAGCCAGACTACGA 20

RESULT 2  
 AX355040 20 bp DNA linear PAT 06-FEB-2002



DEFINITION Sequence 68 from Patent WO0197843.  
 ACCESSION AX355040  
 VERSION AX355040.1 GI:18619707  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1  
 Weimer, G. and Hartmann, G.  
 Methods for enhancing antibody-induced cell lysis and creating  
 cancer  
 Patent: WO 0197843-A 68 27-DEC-2001;  
 UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)  
 FEATURES  
 source location/Qualifiers  
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 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="Synthetic oligonucleotide"

## ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 83;  
 Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGUAAGCCAGACUACGA 20  
 DB 1 AGGTAAGCCAGACTACGA 20

## RESULT 3

AX547252 20 bp DNA linear PAT 01-MAR-2003

LOCUS AX547252 Sequence 391 from Patent WO02053141.

ACCESSION AX547252

VERSION AX547252.1 GI:25812396

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1  
 Bratzler, R.L.  
 Inhibition of angiogenesis by nucleic acids  
 Patent: WO 02053141-A 391 11-JUL-2002;  
 Coley Pharmaceutical Group, Inc. (US)

FEATURES  
 source location/Qualifiers  
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 /mol\_type="unassigned DNA"  
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 /note="Synthetic Sequence"

## ORIGIN

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QY 1 AGGUAAGCCAGACUACGA 20  
 DB 1 AGGTAAGCCAGACTACGA 20

## RESULT 4

AB012214 5253 bp mRNA linear ROD 05-FEB-1999

LOCUS AB012214 Rattus rattus mRNA for DNA cytosine 5 methyltransferase, complete

DEFINITION cds

AB012214 AB012214.1 GI:4160669

VERSION AB012214.1 GI:4160669

KEYWORDS DNA cytosine 5 methyltransferase.

SOURCE Rattus rattus (black rat)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



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QY      2  GTUACAGCCAGGACTUACG  19
          ||:|||||:|||||
Db      2679 GGTACAGCCAGGACTTACG  2696

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On June 19, 2005 this sequence version replaced gi:44775767.   
 Charles Street, Cambridge, MA 02141, USA   
 Submitted (V-UUW-2005) Broad Institute of MIT and Harvard, 320

Smlt, Å.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Broad Institute of MIT and Harvard

Center code: W18R

Web site: http://www-seq.wi.mit.edu

Contact: sequence\_submissions@broad.mit.edu

----- Project Information

Center project name: L26564

Center clone name: 187\_P\_1

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 6 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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1 10836: contig of 10836 bp in length
* 10837 10936: gap of unknown length
* 10937 41320: contig of 30384 bp in length
* 41320 41420: gap of unknown length
* 41420 101112: contig of 59692 bp in length
* 101112 101212: gap of unknown length
* 101212 104894: contig of 3682 bp in length
* 104894 104895: gap of unknown length
* 104895 134899: contig of 29995 bp in length
* 134899 135089: gap of unknown length
* 135089 192617: contig of 57528 bp in length
* 192617 192617: Location/Qualifiers
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/db\_xref="taxon:10090"

/chromosome="8"

/map="8"

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/estimated\_length=unknown

41321..41420

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10113..101212

/estimated\_length=unknown

104895..104895

/estimated\_length=unknown

134990..135089

/estimated\_length=unknown

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Best Local Similarity 88.9%; Pred. No. 4.5e+02;

Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GUACAGCCAGACGACCA 20

DB 24573 GTACAGCCAGACGACCA 24556

RESULT 6 AC135310 243411 bp DNA linear HTG 13-NOV-2002

AC135310 Rattus norvegicus clone CH230-11C16, \*\*\* SEQUENCING IN PROGRESS

LOCUS AC135310 243411 bp DNA linear HTG 13-NOV-2002

DEFINITION Rattus norvegicus clone CH230-11C16, \*\*\* SEQUENCING IN PROGRESS

AC135310 243411 bp DNA linear HTG 13-NOV-2002

AC135310 243411 bp DNA linear HTG 13-NOV-2002

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AC135310 243411 bp DNA linear HTG 13-NOV-2002

AC135310 243411 bp DNA linear HTG 13-NOV-2002

AC135310 243411 bp DNA linear HTG 13-NOV-2002

AC135310 243411 bp DNA linear HTG 13-NOV-2002

AC135310 243411 bp DNA linear HTG 13-NOV-2002

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AC135310 243411 bp DNA linear HTG 13-NOV-2002

AC135310 243411 bp DNA linear HTG 13-NOV-2002

AC135310 243411 bp DNA linear HTG 13-NOV-2002

AC135310 243411 bp DNA linear HTG 13-NOV-2002

AC135310 243411 bp DNA linear HTG 13-NOV-2002

#### AUTHORS

Muzny, D. Marie, Metzger, M. Lee, Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Albrooks, S., Amin, A., Angiano, D., Anyalebechi, V., Ayegbi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benhammed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Butrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Casar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Ditya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Faves, K., Egan, A., Escoto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flaggs, N., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabbit, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebreyes, B., Geier, K., Gill, R., Grady, M., Guerra, M., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hernandez, J., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M., Hollins, B., Howell, S., Hu, Y. S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpach, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kover, C., Kowals, C., Kraft, C. L., Ledow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, D., Lorenshewa, L., Loulsegod, H., Lotado, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindaratne, M., Mahmood, M., Malloy, K., Mangum, A., Mangum, B., Mapus, P., Martin, K., McNeill, T. Z., Meenen, E., Mawhney, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Moore, S., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Murphy, M., Nair, L., Morgan, M., Morris, K., Morris, S., Mundasa, M., Murphy, M., Nair, L., Narkewicz, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwokilemech, O., Okunolu, G., Olarundasegun, A., Pal, S., Parks, K., Patel, N., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Polindexter, A., Popovic, D., Primus, B., Pu, L., L., Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C. D., Smajda, D., Sneed, A., Sodergren, E., Song, X. Z., Sorlie, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Swatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umami, K., Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Weczyk, R., Wenden, H., Worley, K., Williams, G., Wilson, R., Wiczyk, R., Woodson, H., Yoon, L., Yoon, V., Yu, P., Zhang, J., Zhou, J., Zhou, J., Zhou, S., Yen, J., Yoon, L., Yoon, V., Niederhausem, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G. and Gibbs, R. A.

#### TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

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TITLE

JOURNAL

genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

## ----- Genome Center

Center: Baylor College of Medicine  
Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu

## ----- Project Information

Center project name: GEMP  
Center clone name: CH230-11C16

## ----- Summary Statistics

Assembly program: Phrap; version 0.990329  
Consensus quality: 217795 bases at least Q40  
Consensus quality: 222117 bases at least Q30  
Consensus quality: 224860 bases at least Q20  
Estimated insert size: 223813; sum-of-contigs estimation  
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).

\* NOTE: This is a 'working draft' sequence. It currently  
consists of 5 contigs. The true order of the pieces  
is not known and their order in this sequence record is  
arbitrary. Gaps between the contigs are represented as  
runs of N, but the exact sizes of the gaps are unknown.  
This record will be updated with the finished sequence  
as soon as it is available and the accession number will  
be preserved.

1 24504: contig of 24504 bp in length  
\* 24505 24604: gap of unknown length  
\* 24605 97195: contig of 72591 bp in length  
\* 97196 97295: gap of unknown length  
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\* 210509 210608: gap of unknown length  
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2; Mismatches

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2; Mismatches

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Query Match

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Matches

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2; Mismatches

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## ORIGIN

gap

Query Match

Best Local Similarity

Matches

16; Conservative

2; Mismatches

0; Indels

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ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.

REFERENCE 1  
 AUTHORS Cross, S.H., Charlton, J.A., Nan, X. and Bird, A.P.  
 TITLE Purification of CpG islands using a methylated DNA binding column  
 JOURNAL Nat. Genet. 6 (3), 236-244 (1994)  
 PUBMED 8012384

REFERENCE 2 (bases 1 to 275)  
 AUTHORS MacDonald, M., Huckle, E., Wilkinson, P. and Micklem, G.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-Oct-1995) The Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1RQ, England. E-mail contact: humquery@sanger.ac.uk  
 VECT: pGEM-5Zf(-)  
 Clones are available from the UK MRC Human Genome Mapping Project  
 Resource Centre, Hinxton, Cambridgeshire CB10 1RQ, UK. See URL:  
 http://www.hgmp.mrc.ac.uk/ for details  
 or contact: biocentre@hmp.mrc.ac.uk.  
 Location/Qualifiers  
 1..275  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /clone="7095"  
 /sex="male"  
 /tissue\_type="Blood"  
 /clone\_lib="CGI-1"  
 /dev\_stage="adult"

ORIGIN

Query Match 87.0%; Score 17.4; DB 8; Length 275;  
 Best Local Similarity 84.2%; Pred. No. 1.3e+03;  
 Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 1 AGGACAGCCAGACGACG 19  
 |||:|||||:|||||:  
 54 AGGTACAGCCGAGACTACG 72

Db

RESULT 9  
 AC073834/c 172415 bp DNA linear PRI 16-APR-2005  
 LOCUS Homo sapiens BAC clone RP11-250N10 from 2, complete sequence.  
 DEFINITION AC073834  
 AC073834 GI:13677134  
 VERSION  
 KEYWORDS HTG  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 1 (bases 1 to 172415)  
 Cordum, H., Belter, E. and Mishra, S.  
 The sequence of Homo sapiens BAC clone RP11-250N10  
 Unpublished (2001)  
 2 (bases 1 to 172415)  
 Waterston, R.H.  
 Direct Submission  
 Submitted (29-JUN-2000) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 3 (bases 1 to 172415)  
 Waterston, R.H.  
 Direct Submission  
 Submitted (23-MAY-2001) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 4 (bases 1 to 172415)  
 Waterston, R.  
 Direct Submission  
 Submitted (07-NOV-2001) Department of Genetics, Washington  
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 5 (bases 1 to 172415)  
 AUTHORS Wilson, R.K.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-APR-2005) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 On Apr 19, 2001 this sequence version replaced gi:13491268.  
 ----- Genome Center  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: http://genome.wustl.edu  
 Contact: submissions@wustl.edu  
 ----- Summary Statistics  
 Center project name: H\_NH0250N10  
 -----

NOTICE:

This sequence was finished as follows unless otherwise noted:  
 all regions were double stranded, sequenced with an alternate  
 chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by sequence  
 from more than one subclone; and the assembly was confirmed by  
 restriction digest.

MAPPING INFORMATION:  
 Mapping information for this clone was provided by Dr. Wes Warren,  
 Department of Genetics, Washington University, St. Louis MO. For  
 additional information about the map position of this sequence, see  
 http://genome.wustl.edu

SOURCE INFORMATION:  
 The RP11-11 human BAC library was made from the blood of one male  
 donor, as described by Osogawa, K., Moon, P. Y., Zhao, B., Frenken, B.,  
 Teleno, M., Catanesa, J. J. and de Jong, P. J. (1998) An improved  
 approach for construction of bacterial artificial chromosome  
 libraries. Genomics 51:1-8. The clone may be obtained either from  
 Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong  
 and coworkers at http://www.chori.org  
 VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:  
 The clone sequenced to the left is RP11-540F24, the clone sequenced  
 to the right is RP11-91J18. Actual start of this clone is at base  
 position 1 of RP11-250N10; actual end is at base position 172415 of  
 RP11-250N10.

FEATURES  
 source  
 1..172415  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /chromosome="2"  
 /clone="RP11-250N10"  
 /clone\_lib="RP11-11"  
 1066..31373  
 /gene="AGPS"  
 join(1066..1127,6915..7004,14365..14464,16844..16901,  
 31170..31373)  
 /gene="AGPS"  
 join(1066..1127,6915..7004,14365..14464,16844..16901,  
 31170..31291)  
 /gene="AGPS"  
 /note="Homo sapiens alkyglycerone phosphate synthase  
 (AGPS), mRNA.; H\_NH0250N10.1  
 This gene was based on gi14501992)  
 Continued from H\_NH0540F24.1"  
 /codon\_start=1  
 /product="unknown"  
 /protein\_id="AAK93112.1"  
 /db\_xref="GI:62702186"  
 /translation="DIALEYVYLGSPFSPAPDRVVDLCRNKERTTBECKEKYQF  
 APSTCRVGTVDAGACIYFYFAFNTRGISDPLVPEQTEAARREIILANGGSLSHHH

```

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; Sw:,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-326K2 is
from the RPCT-23 Mouse PAC Library
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBAC3.6.

FEATURES
    source
        1..200966
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /db_xref="taxon:10090"
            /chromosome="11"
            /clone="RP23-326K2"
            /clone_1bp="RPCT-23"

ORIGIN
    Query Match      87.0%; Score 17.4; DB 9; Length 200966;
    Best Local Similarity 89.5%; Pred. No. 8,7e+02;
    Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy      1 AGTGAACGCCAGACGACG 19
        ||| ||||| ||||| |||
        166365 AGGAAACAGCAGCAGCTACG 166347

RESULT 11
LOCUS AY547816/c
DEFINITION Uncultured bacterium clone B42-25.04 16S ribosomal RNA gene.
VERSION AY547816
KEYWORDS partial sequence.
ACCESSION AY547816
VERSION AY547816.1 GI:45439624
ENV.
    uncultured bacterium
    uncultured bacterium
    Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 598)
AUTHORS van der Wielen, P.W.J.J.
TITLE Prokaryotic communities in the interface of the deep hypersaline
    anoxic Bannock basin, Eastern Mediterranean
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 598)
AUTHORS van der Wielen, P.W.J.J.
TITLE Direct Submmission
JOURNAL Submitted (13-FEB-2004) Microbial Ecology, University of Groningen,
    Kercklaan 30, Haren 9751 NN, The Netherlands
FEATURES
    source
        1..598
            /organism="uncultured bacterium"
            /mol_type="genomic DNA"
            /isolation_source="Drine interface of Bannock basin,
                Eastern Mediterranean"
            /db_xref="taxon:77133"
            /clone="B42-25.04"
            /environmental_sample
            /product="16S ribosomal RNA"
            <1..5598

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## ORIGIN

Query Match 85.0%; Score 17; DB 3; Length 598;  
 Best Local Similarity 88.2%; Pred. No. 2e+03;  
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 UACAGCCAGACUACGA 20  
 :|||||:|||||:  
 Db 57 TACAGCCAGACUACGA 41

RESULT 12  
 AY164354/c 700 bp DNA linear ENV 28-DEC-2004  
 LOCUS Uncultured Verrucomicrobia bacterium clone ALIB-68 16S ribosomal  
 DEFINITION RNA gene, partial sequence.

ACCESSION AY164354  
 VERSION AY164354.1 GI:27371648  
 KEYWORDS ENV.

SOURCE uncultured Verrucomicrobia bacterium  
 ORGANISM Bacteria; Verrucomicrobia; environmental samples.

REFERENCE 1 (bases 1 to 700)  
 AUTHORS van der Wielen, P.W.J.J., Brons, J.K. and Bolhuis, H.  
 TITLE Bacterial and Archaeal Communities of 4 Deep-Sea Hypersaline Anoxic Basins in the Mediterranean Sea

JOURNAL Unpublished  
 2 (bases 1 to 700)  
 REFERENCES van der Wielen, P.W.J.J., Brons, J.K. and Bolhuis, H.  
 AUTHORS Direct Submission  
 TITLE Submitted (14-OCT-2002) CEBS, University of Groningen, Laboratory  
 JOURNAL of Microbial Ecology, Kerklaan 30, Haren 9751 NN, The Netherlands

FEATURES  
 source  
 1..700  
 /organism="uncultured Verrucomicrobia bacterium"  
 /mol\_type="genomic DNA"  
 /isolation\_source="hypersaline anoxic basin; brine  
 interface of L'Atalante, Mediterranean Sea"  
 /db\_xref="taxon:156588"  
 /clone="ALIB-68"  
 /environmental\_sample  
 <1..>700  
 /product="16S ribosomal RNA"

ORIGIN  
 rRNA  
 <1..>700  
 /product="16S ribosomal RNA"

Query Match 85.0%; Score 17; DB 3; Length 700;  
 Best Local Similarity 88.2%; Pred. No. 1.9e+03;  
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 UACAGCCAGACUACGA 20  
 :|||||:|||||:  
 Db 129 TACAGCCAGACUACGA 113

RESULT 13  
 AY164380/c 700 bp DNA linear ENV 28-DEC-2004  
 LOCUS Uncultured Verrucomicrobia bacterium clone BLIB-55 16S ribosomal  
 DEFINITION RNA gene, partial sequence.

ACCESSION AY164380  
 VERSION AY164380.1 GI:27371674  
 KEYWORDS ENV.

SOURCE uncultured Verrucomicrobia bacterium  
 ORGANISM Bacteria; Verrucomicrobia; environmental samples.

REFERENCE 1 (bases 1 to 700)  
 AUTHORS van der Wielen, P.W.J.J., Brons, J.K. and Bolhuis, H.  
 TITLE Bacterial and Archaeal Communities of 4 Deep-Sea Hypersaline Anoxic Basins in the Mediterranean Sea

JOURNAL Unpublished  
 2 (bases 1 to 700)  
 REFERENCES van der Wielen, P.W.J.J., Brons, J.K. and Bolhuis, H.  
 AUTHORS Direct Submission  
 TITLE

JOURNAL Submitted (14-OCT-2002) CEBS, University of Groningen, Laboratory  
 of Microbial Ecology, Kerklaan 30, Haren 9751 NN, The Netherlands  
 Location/Qualifiers  
 1..700

## FEATURES

source  
 1..700  
 /organism="uncultured Verrucomicrobia bacterium"  
 /mol\_type="genomic DNA"  
 /isolation\_source="hypersaline anoxic basin; brine  
 interface of Bannock, Mediterranean Sea"  
 /db\_xref="taxon:156588"  
 /clone="BLIB-55"  
 /environmental\_sample  
 <1..>700  
 /product="16S ribosomal RNA"

## ORIGIN

Query Match 85.0%; Score 17; DB 3; Length 700;  
 Best Local Similarity 88.2%; Pred. No. 1.9e+03;  
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 UACAGCCAGACUACGA 20  
 :|||||:|||||:  
 Db 134 TACAGCCAGACUACGA 118

RESULT 14  
 AF011463/c 1908 bp rRNA linear INV 05-APR-2004  
 LOCUS Monopylocystis viresvarai small subunit ribosomal RNA, complete  
 DEFINITION sequence.

ACCESSION AF011463  
 VERSION AF011463  
 KEYWORDS AF011463.1 GI:4102252

SOURCE Monopylocystis viresvarai  
 ORGANISM Monopylocystis viresvarai  
 Eukaryota; Heterolobosea; Monopylocystis.

REFERENCE 1 (bases 1 to 1908)  
 AUTHORS O'Kelly, C.J., Silberman, J.D., Amaral Zettler, L.A., Nerd, T.A. and  
 Sogin, M.L.  
 TITLE Monopylocystis viresvarai N. Gen., N. Sp. and Sawyeria  
 marylandensis N. Gen., N. Sp.: Two New Amitochochondrial  
 Heterolobosean Amoebae From Anoxic Environments

JOURNAL Unpublished  
 2 (bases 1 to 1908)  
 REFERENCES Silberman, J.D., Roger, A.J., Nerd, T.A., Gunderson, J.H. and  
 Sogin, M.L.  
 AUTHORS Direct Submission

JOURNAL Submitted (30-JUN-1997) Bay Paul Center for Comparative Molecular  
 Biology and Evolution, Marine Biological Laboratory, 7 MBL St.,  
 Woods Hole, MA 02543, USA

FEATURES  
 source  
 1..1908  
 /organism="Monopylocystis viresvarai"  
 /mol\_type="rRNA"  
 /strain="ATCC 50576"  
 /db\_xref="ATCC:50576"  
 /db\_xref="taxon:63603"  
 1..1908  
 /product="small subunit ribosomal RNA"

## ORIGIN

Query Match 85.0%; Score 17; DB 2; Length 1908;  
 Best Local Similarity 88.2%; Pred. No. 1.8e+03;  
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 UACAGCCAGACUACGA 20  
 :|||||:|||||:  
 Db 1107 TACAGCCAGACUACGA 1091

RESULT 15  
 AC160912/c 177687 bp DNA linear HTG 04-MAY-2005  
 LOCUS Rhinolphus ferrugineum clone VWRCT-253D3, WORKING DRAFT  
 DEFINITION



SEQUENCE, 8 unordered pieces.  
AC160912  
HTG, HTGS, PHASE1; HTGS, DRAFT.  
Rhinolophus ferrumequinum (greater horseshoe bat)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureloostomi  
Mammalia; Eutheria; Laurasiatheria; Chiroptera; Microchiroptera;  
Rhinolophidae; Rhinolophinae; Rhinolophus.  
1 (bases 1 to 177687)  
Antonecilla, A., Ayele, K., Benjamin, B., Blakesley, R.W., Boake, A.,  
Bouffard, G.G., Brinley, C., Brooks, S., Chu, G., Coleman, H.,  
Engle, J., Fukeenko, T., Gestole, M., Greene, A., Guan, X., Gupta, J.,  
Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., Hunter, G.,  
Hutle, B., Idol, J.R., Kwong, P., Laitz, P., Larson, S., Lee-Lin, S.-Q.,  
Legaspi, R., Madden, M., Maduro, Q.L., Maduro, V.B., Margulies, E.H.,  
Masiello, C., Maekert, B., McDowell, J., Mojidi, H.A., Mullikin, J.C.,  
Oestreicher, J.S., Park, M., Portnoy, M.B., Prasad, A., Puri, O.,  
Reddi-Dugue, N., Schandler, K., Schueler, M.G., Slson, C.,  
Stanttipop, S., Stephen, B., Teye, A., Thomas, J.W., Thomas, P.J.,  
Tsipouris, V., Ung, L., Vogt, J.L., Wetherby, K.D., Young, A. and  
Green, E.D.  
NISC Comparative Sequencing Initiative  
Unpublished  
2 (bases 1 to 177687)  
Green, E.D.  
Direct Submission  
Submitted (04-MAY-2005) NIH Intramural Sequencing Center, 5625  
Fishers Lane, Rockville, MD 20852, USA  
----- Genome Center  
Center: NIH Intramural Sequencing Center  
Center code: NISC  
Web site: <http://www.nisc.nih.gov>  
Contact: nisc\_zoo@ngri.nih.gov  
----- Project Information  
Center project name: 11r  
Center clone name: 253D03  
----- Summary Statistics  
Sequencing vector: plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye, 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 174630 bases at least Q40  
Consensus quality: 175289 bases at least Q40  
Consensus quality: 175664 bases at least Q20  
Insert size: 192000; agarose-fp  
Insert size: 176987; sum-of-contigs  
Quality coverage: 9.86x in Q20 bases; agarose-fp  
Quality coverage: 10.69x in Q20 bases; sum-of-contigs  
-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 8 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1  
\* 9793: contig of 9793 bp in length  
\* 9893: gap of unknown length  
\* 9894 21264: contig of 11371 bp in length  
\* 21265 21364: gap of unknown length  
\* 21365 33884: contig of 12520 bp in length  
\* 33885 33984: gap of unknown length  
\* 33985 48903: contig of 14919 bp in length  
\* 48904 49003: gap of unknown length  
\* 49004 69905: contig of 20902 bp in length  
\* 69906 70005: gap of unknown length  
\* 70006 97843: contig of 27837 bp in length  
\* 97843 135962: gap of unknown length  
\* 135963 136062: contig of 38020 bp in length  
\* 136063 177687: gap of unknown length  
\* 177687: contig of 41625 bp in length.  
Location/Qualifiers

[illegible]

Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Diya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falle, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabis, A., Gante, R., Garcia, A., Garner, T., Garza, P., Gebregiorgis, B., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamli, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howell, S., Huliy, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpach, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovac, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenz, H., Louised, H., Lozada, R.J., Lu, X., Ma, J., Maneswar, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, R., Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, B., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Muddasa, M., Murphy, M., Nair, L., Narkervis, C., Neal, D., Newton, G., Olarnpungoon, A., Pal, S., Parke, K., Paoletti, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plapper, F., Poindexter, A., Popovic, D., Primus, B., Pu, L., Puzo, M., Quiroz, J., Rachin, R., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S., Sander, W., Saverly, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shivarebeyn, A., Sisson, I., Sitter, C.D., Smaj, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Soza, J., Steidle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Uemah, K., Valas, R., Vera, V., Villaseca, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, P., Williams, G., Willson, R., Wleczek, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, S., Zhao, S., Dunn, D., von Niederhausen, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submision  
Unpublished  
2 (bases 1 to 191592)

Worley, K.C.  
Direct Submision  
Submitted (13-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 191592)  
Rat Genome Sequencing Consortium.  
Direct Submision  
Submitted (11-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

## COMMENT

On Oct 11, 2002 this sequence version replaced gi:21746209. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with 'N's to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information

Center project name: GTYG  
Center clone name: CH230-377A5  
----- Summary Statistics  
Assembly program: Phrap; version 0.990329  
Consensus quality: 183102 bases at least Q40  
Consensus quality: 184856 bases at least Q30  
Consensus quality: 185893 bases at least Q20  
Estimated insert size: 190794; sum-of-contigs estimation  
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

-----  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 5 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of 'N' but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 145387: contig of 145387 bp in length  
\* 145388 145487: gap of unknown length  
\* 145488 146610: contig of 1123 bp in length  
\* 146611 146710: gap of unknown length  
\* 146711 148251: contig of 1541 bp in length  
\* 148252 148351: gap of unknown length  
\* 148352 151275: contig of 2924 bp in length  
\* 151276 151375: gap of unknown length  
\* 151376 151592: contig of 40217 bp in length.  
Location/Qualifiers  
1. 191592  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="CH230-377A5"  
1742  
855. 1742  
/note="clone boundary  
clone end:sp6  
site:Mbol  
end\_sequence:RXAMQ03rv"  
139424. 140309  
/note="clone boundary  
clone end:T7  
site:Mbol  
end\_sequence:RXAMQ03rv"  
141333. 142663  
/note="wgs\_end\_extension  
clone\_end:T7"  
144303. 145387  
/note="wgs\_end\_extension  
clone\_end:T7"  
145388. 145487  
/estimated\_length=unknown  
146611. 146710  
/estimated\_length=unknown  
148252. 148351  
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151276. 151375  
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ORIGIN  
Query Match 85.0%; Score 17; DB 14; Length 191592;  
Best Local Similarity 88.2%; Pred. No. 1.4e+03;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Gy 2 GGUACAGCCAGACGACUAC 18  
Db 71733 GGTACAGCCAGACGACTAC 71749

RESULT 17  
AC154620/c  
LOCUS 193801 bp DNA linear ROD 03-AUG-2005

DEFINITION Mus musculus BAC clone RP23-323M20 from chromosome 13, complete sequence.

ACCESSION AC154620 AC120857

VERSION AC154620.2 GI:71725589

KEYWORDS HTG.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE TITLE 1 (bases 1 to 193801)

JOURNAL The sequence of Mus musculus BAC clone RP23-323M20

REFERENCE AUTHORS 2 (bases 1 to 193801)

JOURNAL Unpublished (2001)

REFERENCE TITLE Wilson, R.K.

JOURNAL Direct Submission

REFERENCE Submitted (30-DEC-2004) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE TITLE 3 (bases 1 to 193801)

JOURNAL Wilson, R.K.

REFERENCE Direct Submission

REFERENCE Submitted (12-JAN-2005) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE TITLE 4 (bases 1 to 193801)

JOURNAL Wilson, R.K.

REFERENCE Direct Submission

REFERENCE Submitted (03-AUG-2005) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

COMMENT On Aug 3, 2005 this sequence version replaced gi:5690246.

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUSGC

Web site: <http://genome.wustl.edu>

Contact: [submissions@wustl.edu](mailto:submissions@wustl.edu)

----- Summary Statistics

Center project name: M\_BA0323M20

Drafting center: WTB

NOTICE:

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e. phred quality >30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone, fosmid clone or direct clone walk sequence. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to obtain the consensus sequence. The assembly was confirmed by restriction digest.

This finishing standard has slightly changed from the previous human standard. Specifically, standards for regions of low sequence complexity (such as dinucleotide repeats and small unit tandem repeats) have been relaxed. These regions are very prevalent in the mouse genome, and the return on extended finishing efforts is minimal.

If a sequence meets the criteria of the above statement, it needs no comments or tags. If the criteria are not met, such as ambiguous bases, then the region is duly annotated.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

SOURCE INFORMATION:

The BAC library has been constructed by Kazutoyo Oseegawa and Minako Tateo in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (<http://www.resgen.com>) or

Pieter de Jong and coworkers at <http://www.chori.org>

This sequence is the entire insert of the clone.

Location/Qualifiers

1..193801

/organism="Mus musculus"

/mol\_type="genomic DNA"

/db\_xref="taxon:10090"

/chromosome="13"

/clone="RP23-323M20"

/clone\_1id="RPC1-23"

125240..125409

/note="Unresolved simple sequence repeat."

125410..125453

/note="Sequence derived from one plasmid subclone."

168907..168928

/note="Unresolved homopolymeric repeat."

172159..172248

/note="Unresolved simple sequence repeat."

ORIGIN

Query Match 85.0%; Score 17; DB 9; Length 193801;

Best Local Similarity 88.2%; Pred. No. 1.4e+03;

Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GUACAGCCAGACGACG 19

Db 61853 GTACAGCCAGACGACG 61837

RESULT 18

CT025535

LOCUS 194439 bp DNA linear HTG 03-AUG-2005

DEFINITION Mus musculus chromosome 14 clone RP23-35905, \*\*\* SEQUENCING IN PROGRESS \*\*\*; 8 unordered pieces.

CT025535

ACCESSION CT025535.3 GI:71793992

VERSION HTG; HTGS PHASE1.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

1 (bases 1 to 194439)

Stm,S.

Direct Submission

Submitted (02-AUG-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgehire, CB10 1SA, UK. E-mail enquiries: [vegas@sanger.ac.uk](mailto:vegas@sanger.ac.uk)

Clone requests: [clonerequest@sanger.ac.uk](mailto:clonerequest@sanger.ac.uk)

On Aug 3, 2005 this sequence version replaced gi:71793983.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: [vegas@sanger.ac.uk](mailto:vegas@sanger.ac.uk)

----- Project Information

Center project name: BM35905

----- Summary Statistics

Assembly program: XGAP4; version 4.5

Chemistry: Dye-terminator; 100% of reads

Consensus quality: 192076 bases at least Q40

Consensus quality: 192699 bases at least Q30

Consensus quality: 193232 bases at least Q20

Insert size: 193739; sum-of-contigs

Insert size: 193745; 4.7% error; agarose-fp

Quality coverage: 7.84x in Q20 bases; sum-of-contigs Quality coverage: 7.84x in Q20 bases; agarose-fp

-----

\* NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as \* runs of N, but the exact sizes of the gaps are unknown.

## FEATURES

**ORIGIN**

## KEYWORDS

**Rattus norvegicus (Norway rat)**

*Rattus norvegicus* (Norway rat)  
Rattus norvegicus  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Rattus.  
1 (bases 1 to 25467)  
Nuzny,D.,Marie,,Metzker,M.Lee,,Abramson,S.,Adams,C.,Alder,J.,  
Brown,A.,Jouinon,D.,Jain,A.

TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	
Direct Submission	Unpublished	2 (bases 1 to 252467)	Worley, K.C.	Direct Submission	Submitted (27-JAN-2002)	Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	3 (bases 1 to 252467)	Rat Genome Sequencing Consortium.	Direct Submission	Submitted (13-MAY-2003)	Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
										On May 13, 2003 this sequence version replaced gi:23111072. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas ( <a href="http://www.hbrc.bcm.tmc.edu/projects/rel/">http://www.hbrc.bcm.tmc.edu/projects/rel/</a> ). Each contig described	

In the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

#### Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

Project Information

Center project name: GRP

Center clone name: CH230-29E2

Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 232152 bases at least Q40

Consensus quality: 234728 bases at least Q30

Consensus quality: 236632 bases at least Q20

Restricted insert size: 242175; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length

\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).

\* NOTE: This is a working draft sequence. It currently

\* consists of 4 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will

\* be preserved.

\* 1 247030: contig of 247030 bp in length

\* 247031 247130: gap of unknown length

\* 247131 248423: contig of 1293 bp in length

\* 248424 248523: gap of unknown length

\* 248524 250348: contig of 1825 bp in length

\* 250349 250448: gap of unknown length

\* 250449 252467: contig of 2019 bp in length.

\* Location/Qualifiers

1..252467

/organism="Rattus norvegicus"

/mol\_type="genomic DNA"

/db\_xref="taxon:10116"

/clone="CH230-29E2"

1..1489

/note="wgs contig"

247031..247130

/estimated\_length=unknown

248424..248523

/estimated\_length=unknown

250349..250448

/estimated\_length=unknown

ORIGIN

Query Match 85.0%; Score 17; DB 14; Length 252467;

Best Local Similarity 88.2%; Pred. No. 1.4e+03;

Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GUACAGCCAGACGACG 19

Db 69203 GTACAGCCAGACGACG 69219

RESULT 20

PSBLASRA1 720 bp DNA linear BCT 21-JAN-2003

DEFINITION Pseudomonas aeruginosa gene for laeR, complete cds.

ACCESSION D30812 GI:541656

VERSION D30812.1 GI:541656

#### KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

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REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

Pseudomonas aeruginosa

Pseudomonas aeruginosa

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

Pseudomonadaceae; Pseudomonas.

1

Gambello, M.J. and Iglewski, B.H.

Cloning and characterization of the Pseudomonas aeruginosa laeR

gene, a transcriptional activator of elastase expression.

J. Bacteriol. 173 (9), 3000-3009 (1991)

1902216

2 (bases 1 to 720)

Fukushima, J., Ishiwata, T., Kurata, M., You, Z. and Okuda, K.

Intracellular receptor-type transcription factor, laeR, contains a

highly conserved amphipathic region which precedes the putative

helix-turn-helix DNA binding motif

Nucleic Acids Res. 22 (18), 3706-3707 (1994)

7937080

3 (bases 1 to 720)

Fukushima, J.

Direct Submission

Submitted (25-MAY-1994) Jun Fukushima, Yokohama City University

School of Medicine, Department of Bacteriology, 3-9 Fukura,

Kanazawa-ku, Yokohama, Kanagawa 236, Japan

(E-mail: jfukushima@med.yokohama-cu.ac.jp, Tel: 81-45-787-2602,

Fax: 81-45-787-2509)

Location/Qualifiers

1..720

/organism="Pseudomonas aeruginosa"

/mol\_type="genomic DNA"

/strain="F03455"

/db\_xref="taxon:1287"

/clone="pTlac1aer3455"

1..720

/note="transcriptional activator"

/codon\_start=1

/transl\_table=11

/product="laeR"

/protein\_id="BAA06489.1"

/db\_xref="GI:541657"

/translation="MALVDGFLERSSGSLERSSALIKKASDLGFSKILPGLPKPOS

ODVENAFIVGNYPAAAREHYDRAGVADPTVCHQOSVLPFMBSIYGTROHPRP

ERASAGIYVGLTLPPLHARGELGALSISYRANRANRPFISVYPTLMMDYALQ

SGGLAPRHPVPSKPVVLSRKEVLCQWIKGKTSWISVYCNCSKANVNFHKNIRK

FGYTSRVAIVMNVNGLITL"

#### FEATURES

source

CDs

variation

gene

variation

ORIGIN

Query Match 84.0%; Score 16.8; DB 1; Length 720;

Best Local Similarity 85.0%; Pred. No. 2.4e+03;

Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGUACAGCCAGACGACG 20

Db 124 AAGACAGCCAGACGACG 143

RESULT 21

PSBLASRB 720 bp DNA linear BCT 21-JAN-2003

DEFINITION Pseudomonas aeruginosa gene for laeR, complete cds.

ACCESSION D30813 GI:541658

VERSION D30813.1 GI:541658

SOURCE

ORGANISM

Pseudomonas aeruginosa

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

Pseudomonadaceae; Pseudomonas.

1

Gambello, M.J. and Iglewski, B.H.

Cloning and characterization of the Pseudomonas aeruginosa laeR

gene, a transcriptional activator of elastase expression.

J. Bacteriol. 173 (9), 3000-3009 (1991)

1902216

2 (bases 1 to 720)

Fukushima, J., Ishiwata, T., Kurata, M., You, Z. and Okuda, K.

Intracellular receptor-type transcription factor, laeR, contains a

highly conserved amphipathic region which precedes the putative

helix-turn-helix DNA binding motif

Nucleic Acids Res. 22 (18), 3706-3707 (1994)

7937080

3 (bases 1 to 720)

Fukushima, J.

Direct Submission

Submitted (25-MAY-1994) Jun Fukushima, Yokohama City University

School of Medicine, Department of Bacteriology, 3-9 Fukura,

Kanazawa-ku, Yokohama, Kanagawa 236, Japan

(E-mail: jfukushima@med.yokohama-cu.ac.jp, Tel: 81-45-787-2602,

Fax: 81-45-787-2509)

Location/Qualifiers

1..720

/organism="Pseudomonas aeruginosa"

/mol\_type="genomic DNA"

/strain="F03455"

/db\_xref="taxon:1287"

/clone="pTlac1aer3455"

1..720

/note="transcriptional activator"

/codon\_start=1

/transl\_table=11

/product="laeR"

/protein\_id="BAA06489.1"

/db\_xref="GI:541657"

/translation="MALVDGFLERSSGSLERSSALIKKASDLGFSKILPGLPKPOS

ODVENAFIVGNYPAAAREHYDRAGVADPTVCHQOSVLPFMBSIYGTROHPRP

ERASAGIYVGLTLPPLHARGELGALSISYRANRANRPFISVYPTLMMDYALQ

SGGLAPRHPVPSKPVVLSRKEVLCQWIKGKTSWISVYCNCSKANVNFHKNIRK

FGYTSRVAIVMNVNGLITL"

REFERENCE 1 (bases 1 to 720)  
 AUTHORS Fukushima, J., Ishiwata, T., Kurata, M., You, Z. and Okuda, K.  
 TITLE Intracellular receptor-type transcription factor, LasR, contains a highly conserved amphipathic region which precedes the putative helix-turn-helix DNA binding motif  
 JOURNAL Nucleic Acids Res. 22 (18), 3706-3707 (1994)  
 PUBMED 7937080  
 REFERENCE 2 (bases 1 to 720)  
 AUTHORS Fukushima, J.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-MAY-1994) Jun Fukushima, Yokohama City University School of Medicine, Department of Bacteriology, 3-9 Fukuoka, Kanazawa-ku, Yokohama, Kanagawa 236, Japan  
 (E-mail: j.fukushima@med.yokohama-cu.ac.jp, Tel:81-45-787-2602, Fax:81-45-787-2503)  
 FEATURES  
 source Location/Qualifiers  
 1..720  
 /organism="Pseudomonas aeruginosa"  
 /mol\_type="genomic DNA"  
 /strain="PA103"  
 /db\_xref="taxon:287"  
 /clone="pBtaClaSR103"  
 1..720  
 /note="transcriptional activator"  
 /codon\_start=1  
 /transl\_table=11  
 /product="LasR"  
 /protein\_id="BA06490.1"  
 /db\_xref="GI:541659"  
 /translation="MALVDGFLERSSGKLEMSALIQKMSDYGFSKILFGLPKDS  
 ODYENAFIVGNVPALMRHRYAGYARDPVVSHCTOSVLIPIFEPSPYQTRKHFF  
 EASASAGLVGGLTPELHARGELGALISVBAENRABANRPIESTLPTLMLKYVALQ  
 SGAGIAFEPVSKPVLTSSKEVYLQWCAIGTISWEISVICNCSBANVPFMGNIRK  
 FGVTSSRVAAIMAVNLGLITL"  
 ORIGIN  
 Query Match 84.0%; Score 16.8; DB 1; Length 720;  
 Best Local Similarity 85.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 Oy 1 AGGACAGCCAGGACUACGA 20  
 |||||  
 124 AAGGACAGCCAGGACTACGA 143  
 RESULT 22  
 BD224017 720 bp DNA linear PAT 17-JUL-2003  
 LOCUS Gene switch.  
 BD224017  
 ACCESSION BD224017.1 GI:33033787  
 VERSION JP 2002522079-A/16.  
 KEYWORDS Pseudomonas aeruginosa  
 SOURCE Pseudomonas aeruginosa  
 ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 Pseudomonadaceae; Pseudomonas.  
 1 (bases 1 to 720)  
 Martinez, A., Jepsen, I. and Fray, R.G.  
 Gene switch  
 Patent: JP 2002522079-A 16 23-JUL-2002;  
 SYNGENTA LTD  
 OS Pseudomonas aeruginosa  
 PN JP 2002522079-A/16  
 PD 23-JUL-2002  
 PF 12-AUG-1999 JP 2000565139  
 PR 13-AUG-1998 GB 9817704.1  
 PI ALBERTO MARTINEZ, IAN JEPSEN, ROBERT GEORGE FRAY PC  
 C12N15/09, A01H5/00, C12N5/10, C12O1/02, C12N5/10, C12R1/91, PC  
 C12O1/02, C12R1/91, C12N15/00, C12N5/00, C12N5/00, C12R1/91 CC  
 Gene switch  
 FH Key Location/Qualifiers  
 FT source 1..720  
 /organism="Pseudomonas aeruginosa".

FEATURES  
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 /organism="Pseudomonas aeruginosa"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:287"  
 ORIGIN  
 Query Match 84.0%; Score 16.8; DB 6; Length 720;  
 Best Local Similarity 85.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 Oy 1 AGGACAGCCAGGACUACGA 20  
 |||||  
 124 AAGGACAGCCAGGACTACGA 143  
 RESULT 23  
 CO839858 720 bp DNA linear PAT 29-JUL-2004  
 LOCUS Sequence 4 from Patent WO2004058996.  
 CO839858  
 ACCESSION CO839858.1 GI:50837795  
 VERSION  
 KEYWORDS  
 SOURCE Pseudomonas aeruginosa  
 ORGANISM Pseudomonas aeruginosa  
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 Pseudomonadaceae; Pseudomonas.  
 1  
 Feesche, J., Stumpe, S., Maurer, K.H., Breves, R. and Hoven, N.  
 Method for controlling processes based on microbial interaction  
 Patent: WO 2004058996-A 4 15-JUL-2004;  
 Henkel Kommanditgesellschaft auf Aktien (DE)  
 Location/Qualifiers  
 1..720  
 /organism="Pseudomonas aeruginosa"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:287"  
 1..720  
 /note="unnamed protein product"  
 /codon\_start=1  
 /transl\_table=11  
 /protein\_id="CAH05768.1"  
 /db\_xref="GI:50837796"  
 /translation="MALVDGFLERSSGKLEMSALIQKMSDYGFSKILFGLPKDS  
 ODYENAFIVGNVPALMRHRYAGYARDPVVSHCTOSVLIPIFEPSPYQTRKHFF  
 EASASAGLVGGLTPELHARGELGALISVBAENRABANRPIESTLPTLMLKYVALQ  
 SGAGIAFEPVSKPVLTSSKEVYLQWCAIGTISWEISVICNCSBANVPFMGNIRK  
 FGVTSSRVAAIMAVNLGLITL"  
 ORIGIN  
 Query Match 84.0%; Score 16.8; DB 6; Length 720;  
 Best Local Similarity 85.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 Oy 1 AGGACAGCCAGGACUACGA 20  
 |||||  
 124 AAGGACAGCCAGGACTACGA 143  
 RESULT 24  
 CO839862 720 bp DNA linear PAT 29-JUL-2004  
 LOCUS Sequence 8 from Patent WO2004058996.  
 CO839862  
 ACCESSION CO839862.1 GI:50837799  
 VERSION  
 KEYWORDS  
 SOURCE Pseudomonas aeruginosa  
 ORGANISM Pseudomonas aeruginosa  
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 Pseudomonadaceae; Pseudomonas.  
 1  
 Feesche, J., Stumpe, S., Maurer, K.H., Breves, R. and Hoven, N.  
 Method for controlling processes based on microbial interaction



**CDS**

23, 021, 928 chimpanzee whole genome shotgun reads were aligned to the Human genome NCBI Build 34 (hg16, July 2003). Chimp WGS reads were from 9 donors, including Clint (Pan troglodytes verus), 3 other Pan troglodytes verus chimps (Donald, Karlien, Yvonne), 3 Pan (Noemie, Masuku, Clara) and 2 chimps of unknown origin (Gon, Unknown Chimp). Common names: Pan troglodytes verus is the western chimp and Pan troglodytes troglodytes is the central chimp. To be included in chimpanzee SNP discovery, a read must be at least 500bp in length, at least 50% of its base score >= 20, at least 30% of its base calls must satisfy SNOS(30,25) (single strand NOS, the base in question has phred score >= 30, the surrounding 10 bases in the read have phred score >= 25), and the read must have at least 200 bp SNOS(30,25) bases. Reads not uniquely



GEPVLRSGAMHIYSAIVIDNALDEPFNLTETKTIDIMASVYIFDATTETLAKALDATL  
 QAGGIMYDGSQVSNLFTNTSYRSKADYQEDENGDDGKSVYLHRIPIPYDGGMP  
 GSPGMYPIGTFRVRSBGHMSKPDLPVHNDPDLMDPVGGHCELTCTNNATYL  
 GTLIPATIIIRGGGLGYIKRAYEALDLSVWPKVETQTSERSTNSGFSKSKM  
 VLSAISVSNABKQOIPATITIGTKSTICAHVHKNHIDLTAAVTELTAKTRDREHND  
 ICPETGACIDRPHICILMHYCAKSLQDIMENDIKDMSFLASLIDLVGLYVLS  
 SEIKSHGLKSNKNCVDRNRYLQITDYLHFRKQKEDVDLGHAKLARLMTAPER  
 LREKSMHPGCTPKGDIYSFSLITEMSROEPHENDBLADIIARVSKGEPYRP  
 VLVNVEAPPCVLTARACWEDPMBEPNIIIVRTMAPLOKIKPVILLNMTAIE  
 RYTNNEIUNDERTELOKAKAKTRQHLRLPRLPSISQILKGISVLPETDMSITF  
 SDIYGLIFHSLSGCRFLCSQVPLPLVPMHLSLTLPLHLPLIMNPLISSFAQPSW  
 SALSHSCSALHSS"

sig\_peptide  
 /note="signal peptide (AA -21 to -1)"  
 mat\_peptide  
 /product="guanylate cyclase (AA 1 - 965)"

Query Match 84.0%; Score 16.8; DB 2; Length 3444;  
 Best Local Similarity 85.0%; Pred. No. 2.2e+03;  
 Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 1 AGGACAGCCGACGACUACGA 20  
 981 AGGACAGCCGACGACUACCA 1000

RESULT 29  
 AB004572  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

AB004572 10238 bp DNA linear BCT 19-FEB-2003  
 Pseudomonas aeruginosa PA01, section 133 of 529 of the complete  
 genome.  
 AB004572 AB004091  
 AB004572.1 GI:9947372

Pseudomonas aeruginosa PA01  
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 Pseudomonadaceae; Pseudomonas.

1 (bases 1 to 10238)  
 Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrenner, P.,  
 Hickey, M.J., Brinkman, F.S.L., Hutnagle, W.O., Kowalik, D.J.,  
 Lagrou, M., Garber, R.L., Goltry, L., Tolentino, B.,  
 Westbrock-Madman, S., Yuan, Y., Brody, L.L., Coulter, S.N.,  
 Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H.,  
 Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reiter, J., Saler, M.H.,  
 Complete genome sequence of Pseudomonas aeruginosa PA01, an  
 opportunistic pathogen  
 Nature 406 (6799), 959-964 (2000)

2 (bases 1 to 10238)  
 10984043  
 Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrenner, P.,  
 Hickey, M.J., Brinkman, F.S.L., Hutnagle, W.O., Kowalik, D.J.,  
 Lagrou, M., Garber, R.L., Goltry, L., Tolentino, B.,  
 Westbrock-Madman, S., Yuan, Y., Brody, L.L., Coulter, S.N.,  
 Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H.,  
 Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reiter, J., Saler, M.H.,  
 Hancock, R.B.W., Lory, S. and Olson, M.V.  
 Direct Submission  
 Submitted (16-MAY-2000) Department of Medicine and Genetics,  
 University of Washington Genome Center, University Of Washington,  
 Box 352145, Seattle, WA 98195, USA  
 3 (bases 1 to 10238)

TITLE  
 JOURNAL  
 REFERENCE  
 PUBMED  
 AUTHORS  
 COMMENT

Pseudomonas aeruginosa Community Annotation Project (PseudoCAP)  
 Direct Submission  
 Submitted (04-FEB-2003) Department of Molecular Biology and  
 Biochemistry, Simon Fraser University, 8888 University Dr.,  
 Burnaby, British Columbia V5A 1S6, Canada

This represents the February 3, 2003 version of the continually  
 updated, reviewed, Pseudomonas aeruginosa PA01 genome annotation,  
 from PseudocAP (see <http://www.pseudomonas.com> for latest updates)

and links to alternate annotations). PseudoCAP is coordinated by  
 Fiona S.L. Brinkman (Simon Fraser University, Canada) and Robert  
 E.W. Hancock (University of British Columbia, Canada). We welcome  
 submission through [www.pseudomonas.com](http://www.pseudomonas.com) of any proposed changes.

'Protein name confidence' is used to rate our confidence of the  
 accuracy of the protein name.

Class 1: Function experimentally demonstrated in *P. aeruginosa*.  
 Class 2: Function of highly similar gene experimentally  
 demonstrated in another organism (and gene context consistent  
 in terms of pathways its involved in, if known).  
 Class 3: Function proposed based on presence of conserved amino  
 acid motif, structural feature or limited sequence similarity  
 to an experimentally studied gene.  
 Class 4: Homologs of previously reported genes of unknown function,  
 or no similarity to any previously reported sequences.

Location/Qualifiers

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 CDS

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CDS  
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Best Local Similarity	85.0%;	Pred. No. 2.1e+03;		
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Db	8590	AAGCAGCGCCGACGACTACA	8609	
RESULT 30	ACO16208	Homo sapiens clone RPl1-251L1, WORKING DRAFT SEQUENCE, 5 unordered pieces.	36255 bp	DNA linear HTG 14-MAY-2000
LOCUS	ACO16208			
DEFINITION	ACO16208			
ACCESSION	ACO16208			
VERSION	ACO16208.3	GI:7801427		
KEYWORDS	HTG; HTGS PHASE1; HTGS_DRAFT.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	1 (bases 1 to 36255)			
JOURNAL	Bitren,B., Linton,L., Nhusbaum,C. and lander,E.			
TITLE	Unpublished			
REFERENCE	2 (bases 1 to 36255)			
AUTHORS	Bitren,B., Linton,L., Nhusbaum,C., Lander,E., Allen,N., Anderson,M., Baldwin,J., Barina,N., Beckely,R., Boguslavsky,I., Boukhsalter,B., Brown,A., Castle,A., Colangelo,M., Collins,S., Collimore,A., Cooke,P., Deatellano,K., Dewar,K., Domingo,M., Donelan,L., Doyle,M., Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heatford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Lehoczy,J., Lien,C., Locke,K., MacDonald,P., Marquis,N., McGowan,P., McGuirk,A., McKernan,K., McDonald,I.J., Meldrum,J., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Peterson,K., Pollara,V., Riley.R., Roy,A., Santos,R., Severy,P., Stange-Thomann,N., Stefanovic,N., Subramanian,A., Talamas,J., Testaye,S., Titrrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wymen,D., Ye,W.J., Zimmer,A. and Zody,M.			
TITLE	Direct Submession			
JOURNAL	Submitted (23-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA			
COMMENT	On May 14, 2000 this sequence version replaced gi:6910681. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) <a href="http://ftp.genome.washington.edu/RM/RepeatMasker.html">http://ftp.genome.washington.edu/RM/RepeatMasker.html</a>			
	Genome Center			
	Center: Whitehead Institute/ MIT Center for Genome Research			
	Center code: WtBR			
	Web site: <a href="http://www-seq.wi.mit.edu">http://www-seq.wi.mit.edu</a>			
	Contact: <a href="mailto:sequence_submissions@genome.wi.mit.edu">sequence_submissions@genome.wi.mit.edu</a>			
	Project Information			
	Center project name: L4594			
	Center clone name: 25.L11			
	Summary Statistics			
	Sequencing vector: M13; M77815, 100% of reads			
	Chemistry: Dye-terminator Big Dye; 100% of reads			
	Assembly program: Phrap; version 0.960731			
	Consensus quality: 34932 bases at least Q40			
	Consensus quality: 35561 bases at least Q30			

\* \* \* \* \*

\* NOTE: This is a "working draft" sequence. It currently

\* consists of 5 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will

\* be preserved.

\* \* \* \* \*

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Matches	16;	Conservative	2;	Mismatches	2;
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LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
RESULT 31 AL161661	AL161661	93714 bp	DNA	linear	HTG 13-JUN-2001	
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	AL161661					
	AL161661.1 GI:7263577					
	HTG; HTGS PHASE2; HTGS_CANCELLED.					
	Homo sapiens (human)					
	Homo sapiens					
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;					

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

**COMMENT**

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominoidea; Homo.  
 1  
 Burton, J.  
 Direct Submission  
 Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgehire  
 CB10 1SA, UK. E-mail enquiries: humberquerry@sanger.ac.uk  
 requests: clonerequests@sanger.ac.uk  
 ----- Genome Center -----

```

Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
-----
Project Information
Center project name: d1984f23
-----
Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: Plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 93681 bases at least Q40
Consensus quality: 93706 bases at least Q30
Consensus quality: 93713 bases at least Q20
Insert size: 93714; sum-of-contigs
Insert size: 109355; 1.0% error; agarose-fp
Quality coverage: 8.25x in Q20 bases; sum-of-contigs
Quality coverage: 7.07x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
Location/Qualifiers

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ORIGIN
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Qy      1 AGGUCACGACGAGACUACGA 20
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Query Match      85.0%; Score 16.8; DB 14; Length 93714;
Best Local Similarity      84.0%; Pred. No. 1.8e+03;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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RESULT 32	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
AC166715/c	AC166715	111051 bp	DNA	linear	HTG 10-AUG-2005	Bos taurus clone CH240-190K8, *** SEQUENCING IN PROGRESS ***	24
						unordered pieces.	
	AC166715						
	AC166715						
	AC166715.2	GI.72095138					
	HTG; HTGS_PHASE1.						
	Bos taurus (cow)						
	Bos taurus						

REFERENCE  
AUTHORS

1 (Baes 1to 11051)  
Munzy, D., Adams, C., Agbat, II, O., Allen, C., Aisbrook, S., Archer, P.,  
Arredondo, H., Bandanarake, D., Bangurs, L., Beltran, B., Beltran,  
Beraducci, A., Biswal, K., Blyth, P., Bonham, H., Buway, C., Butch, P.,  
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Chacko, J., Chahrouh, M., Chavez, D., Chen, A., Chen, G., Chen, R.,  
Chung, M.-T., Chu, J., Clerc, K., Cockrell, R., Coyle, M., Cree, A.,  
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Anda, C., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H.,  
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Dzinda, D., Egan, A., Escotto, M., Espinosa, V., Eugene, C., Fa, M.,  
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Primus, E., Pu, L., L., Puzo, M., Qin, X., Quinn, A., Quirroz, J.,  
Rabata, D., Rachlin, B., Reigh, R., Ren, Y., Reuter, M., Richards, S.,  
Rivers, C., Rodriguez, F., Rojas, A., Ruiz, S., J., Sana, M., Sanders, W.,  
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Svatek, A., Taylor, E., Taylor, T., Thomas, N., Thorn, R., Thornton, R.,  
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Zhang, Z., Zhou, J., Weinrock, G., and Gibbs, R.

**TITLE**  
Unpublished

**JOURNAL**  
2 (bases 1 to 111051)

**REFERENCE**  
Worley, K.C.

**AUTHORS**  
Direct Submission

**TITLE**  
Submitted (05-AUG-2005) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

**JOURNAL**  
3 (bases 1 to 111051)

**REFERENCE**  
Worley, K.C.

**AUTHORS**  
Direct Submission

**TITLE**  
Submitted (10-AUG-2005) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

**JOURNAL**  
On Aug 10, 2005 this sequence version replaced gi:71834693.

**COMMENT**  
----- Genome Center

Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help.tmc.edu

----- Project Information

Center project name: PKYL  
Center clone name: CH240-190K8

----- Summary Statistics

Sequencing vector: Plasmid,  
Chemistry: Dye-terminator Big Dye 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 12309 bases at least Q40  
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Estimated insert size: 143053; agarose-fp estimation  
Quality coverage: 2x in Q20 bases; agarose-fp estimation  
Quality coverage: 2x in Q20 bases; sum-of-contigs estimation

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\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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8717: gap of unknown length  
8816: contig of 4188 bp in length  
13005: gap of 3553 bp in length  
13105: contig of unknown length  
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16578: gap of 2336 bp in length  
16758: contig of unknown length  
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33231: gap of unknown length  
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43322: gap of unknown length  
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70332: contig of 3685 bp in length  
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106994: contig of 13283 bp in length  
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11051: contig of 3957 bp in length.  
107095: Location/Qualifiers

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ORIGIN
Query Match      84.0%; Score 16.8; DB 14; Length 111051;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

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Cy      1 AGGUAACGCCGACGACUACGA 20
      |||:|||||:|||||:
Db      66176 AGGTATAGCCGACGACTATGA 66157

```

```

RESULT 33
LOCUS      AC073138
DEFINITION Homo sapiens BAC clone RP11-708P17 from 7, complete sequence.
ACCESSION  AC073138
VERSION     AC073138.3 GI:14010936
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1 (bases 1 to 118396)
AUTHORS    Hillier,L.W., Fulton,R.S., Fulton,L.A., Graves,T.A., Pepin,K.H.,
            Wagner-McPherson,C., Layman,D., Maas,J., Jaeger,S., Walker,R.,
            Wyllie,K., Sekhon,M., Becker,M.C., O'Laughlin,M.D., Schaller,M.B.,
            Powell,G.A., Delehaunty,K.D., Miner,T.L., Nash,W.E., Cordes,M.,
            Du,H., Sun,H., Edwards,J., Bradshaw-Cordum,H., Ali,J., Andrews,S.,
            Iakki,A., Vanbrunt,A., Nguyen,C., Du,P., Lamar,B., Courtney,L.,
            Kalicki,J., Ozerik,P., Biellik,L., Scott,K., Holmes,A.,
            Harkins,R., Harris,A., Strong,C.M., Hou,S., Tomlinson,C.,
            Dauphin-Kohlberg,S., Kozlowski-Reilly,A., Leonard,S., Rohlfing,T.,
            Rock,S.M., Tin-Wollam,A.M., Abbott,A., Minx,P., Maupin,R.,
            Stromer,C., Latreille,P., Miller,N., Johnson,D., Murray,J.,
            Woessner,J.P., Wendt,M.C., Yang,S.P., Schultz,B.R., Wallis,J.W.,
            Spieth,J., Bieri,T.A., Nelson,J.O., Berkowicz,N., Wohlmann,P.B.,
            Cook,L.L., Hickenbotham,M.T., Eldred,J., Williams,D., Bedell,J.A.,
            Mardis,E.R., Clifton,S.W., Chissole,S.L., Marra,M.A., Raymond,C.,
            Haugen,E., Gillett,W., Zhou,Y., James,R., Phelps,K., Iadonato,S.,
            Babb,K., Sims,E., Levy,R., Clendenning,J., Kaul,R., Kent,W.J.,

```

```

Porey,T.S., Baertsch,R.A., Brent,M.R., Kehler,E., Rieck,P.,
Bork,P., Suyama,M., Bailey,U.A., Portnoy,M.B., Torrents,D.,
Chinwalla,A.T., Gish,W.R., Eddy,S.R., McPherson,D., Olson,M.V.,
Richler,E.E., Green,E.D., Waterston,R.H. and Wilson,R.K.
The DNA sequence of human chromosome 7
Nature 424 (6945), 157-164 (2003)
12853948
2 (bases 1 to 118396)
Du,P., Gibson,A. and Maupin,R.
The sequence of Homo sapiens BAC clone RP11-708P17
Unpublished (2001)
3 (bases 1 to 118396)
Waterston,R.H.
Direct Submission
Submitted (08-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 118396)
Waterston,R.
Direct Submission
Submitted (09-MAY-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
5 (bases 1 to 118396)
Wilson,R.
Direct Submission
Submitted (31-JUN-2004) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On May 9, 2001 this sequence version replaced gi:19838323.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUSC
Web site: http://genome.wustl.edu
Contact: saplens@wustl.wustl.edu
----- Summary Statistics
Center project name: H_NH0708P17
-----

```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:  
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/CTB/CH7>, send <mailto:egreen@nhgri.nih.gov>, or see <http://genome.wustl.edu>

SOURCE INFORMATION:  
The RP11-708P17 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,B., Tateo,M., Cataneese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pictet de Jong and coworkers at <http://www.chori.org>

NEIGHBORING SEQUENCE INFORMATION:  
The clone RP11-708P17 shows evidence of possibly several transposons in the growth of the clone, which is not part of the

submitted sequence. The exact base position for these insertion sites appear to change with each subsequent growth of the clone.

The clone sequenced to the left is RP4-778K6, 200 bp overlap the clone sequenced to the right is CTD-2305P9. Actual start of this clone is at base position 102929 of RP4-778K6 actual end is at base position 118396 of RP11-708P17.

# FEATURES

source  
1. 118396  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="7"  
/map="7"  
/clone="RP11-708P17"  
/clone\_lib="RPC1-11"  
1. .96  
/rpt\_family="Alu"  
103. .157  
/rpt\_family="MALR"  
201. .247  
/rpt\_family="MALR"  
352. .413  
/rpt\_family="MIR"  
428. .873  
/rpt\_family="MALR"  
880. .1178  
/rpt\_family="Alu"  
1331. .1414  
/rpt\_family="MIR"  
1440. .1571  
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1598. .1765  
/rpt\_family="Alu"  
1766. .1806  
/rpt\_family="(TTG)n"  
1807. .1907  
/rpt\_family="Alu"  
2980. .3448  
/rpt\_family="LA"  
3477. .3607  
/rpt\_family="Alu"  
3630. .3921  
/rpt\_family="Alu"  
4028. .4303  
/rpt\_family="Alu"  
4306. .4336  
/rpt\_family="(TAA)n"  
4715. .4810  
/rpt\_family="MIR"  
5300. .5600  
/rpt\_family="Alu"  
5789. .6046  
/rpt\_family="Alu"  
6133. .6204  
/rpt\_family="MER2\_type"  
6205. .6507  
/rpt\_family="Alu"  
6508. .6655  
/rpt\_family="MER2\_type"  
6666. .6971  
/rpt\_family="Alu"  
6972. .7001  
/rpt\_family="MER2\_type"  
7002. .7189  
/rpt\_family="MALR"  
7190. .7213  
/rpt\_family="(GA)n"  
7214. .7401  
/rpt\_family="MALR"  
7402. .7412  
/rpt\_family="MER2\_type"  
7413. .7719

repeat\_region /rpt\_family="Alu"  
7720. .7776  
repeat\_region /rpt\_family="MER2\_type"  
7782. .8067  
repeat\_region /rpt\_family="MER2\_type"  
8068. .9036  
repeat\_region /rpt\_family="L1"  
10589. .10792  
repeat\_region /rpt\_family="Alu"  
10793. .11458  
repeat\_region /rpt\_family="L1"  
11459. .11475  
repeat\_region /rpt\_family="Alu"  
11477. .12452  
repeat\_region /rpt\_family="L1"  
12453. .12473  
repeat\_region /rpt\_family="AT-rich"  
12474. .12667  
repeat\_region /rpt\_family="MER2\_type"  
12668. .12963  
repeat\_region /rpt\_family="Alu"  
12964. .13464  
repeat\_region /rpt\_family="MER2\_type"  
13465. .13771  
repeat\_region /rpt\_family="Alu"  
13772. .13792

Query Match 84.0%; Score 16.8; DB 8; Length 118396;  
Best Local Similarly 80.0%; Pred. No. 1.8e+03;  
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Cy 1 AGGACAGCCAGACACGCA 20  
Db 103784 AGGTACAGACGACACTCA 103803

## RESULT 34

LOCUS AC008794 131972 bp DNA linear PRI 03-OCT-2001  
DEFINITION Homo sapiens chromosome 19 clone CTD-2050118, complete sequence.  
ACCESSION AC008794  
VERSION AC008794.8 GI:15887256  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

1 (bases 1 to 131972)  
DOE Joint Genome Institute and Stanford Human Genome Center.

REFERENCE  
TITLES Direct Submission  
JOURNAL Unpublished

2 (bases 1 to 131972)  
DOE Joint Genome Institute.

REFERENCE  
TITLES Direct Submission  
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
3 (bases 1 to 131972)  
DOE Joint Genome Institute and Stanford Human Genome Center.

REFERENCE  
TITLES Direct Submission  
JOURNAL Submitted (28-JUL-2000) DOE Joint Genome Institute, 2800 Mitchell

Drive, Walnut Creek, CA 94598, USA  
4 (bases 1 to 131972)  
DOE Joint Genome Institute and Stanford Human Genome Center.

REFERENCE  
TITLES Direct Submission  
JOURNAL Submitted (03-OCT-2001) DOE Joint Genome Institute, 2800 Mitchell

Drive, Walnut Creek, CA 94598, USA  
On Oct 3, 2001 this sequence version replaced gi:9558576.

Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www-ehgc.stanford.edu

Quality: Phrap Quality >=40 99.5% of Sequence;

Estimated Total Number of Errors is 0.7.

# FEATURES

Location/Qualifiers

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/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="19"  
/clone="CTD-2050118"

## ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 131972;  
Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 AGGACAGCCAGGACGACGCA 20  
102831 AGGACAGCCAGGACGACGCA 102850

## RESULT 35

AC142244/c  
LOCUS  
DEFINITION Mus musculus chromosome 1 clone RP23-79H24 map 1, \*\*\* SEQUENCING IN PROGRESS \*\*\*  
AC142244  
AC142244.10 GI:68989342  
HTG; HTGS PHASE2; HTGS\_FULLTOP; HTGS\_ACTIVEFIN.  
MUS musculus (house mouse)  
ORGANISM Mus musculus

## REFERENCE

1 (bases 1 to 132063)  
Britten, B., Nussbaum, C. and Lander, B.  
Mus musculus chromosome 1, clone RP23-79H24  
Unpublished  
2 (bases 1 to 132063)  
Britten, B., Nussbaum, C., Lander, B., Abouneillel, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Haefz, N., Hagopian, D., Hago, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Madditt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunhthang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Reta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., Zody, M.,

Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 132063)  
Britten, B., Nussbaum, C., Lander, B., Abouneillel, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Haefz, N., Hagopian, D., Hago, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Madditt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, V., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mleng, V.,

## TITLE

Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunhthang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Reta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., and Zody, M.  
Direct Submission  
Submitted (06-JUL-2005) Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02141, USA  
On Jul 6, 2005 this sequence version replaced gi:66351892.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
Genome Center  
Center: Broad Institute of MIT and Harvard  
Center code: W1BR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@broad.mit.edu  
Project Information  
Center project name: L14737  
Center clone name: 79\_H\_24

## COMMENT

## FEATURES

NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.  
This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.  
1 132063: contig of 132063 bp in length.  
Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/chromosome="1"  
/map="1"  
/clone="RP23-79H24"  
/clone\_1db="RP23-79H24"  
/clone\_1db="RP23-79H24" Female Mouse BAC

## ORIGIN

Query Match 84.0%; Score 16.8; DB 14; Length 132063;  
Best Local Similarity 85.0%; Pred. No. 1.8e+03;  
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 AGGACAGCCAGGACGACGCA 20  
28025 AGGACAGCCAGGACGACGCA 28006

Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, UK  
147815 bp DNA linear PRI 18-MAY-2005  
Human DNA sequence from clone RP5-99846 on chromosome 20q13.1  
Contains the CDH22 gene for cadherin-11-like 22, a novel gene and two Cpg islands, complete sequence.  
AL031687  
AL031687.17 GI:13366276  
HTG; C20orf25; cadherin; CDH22; Cpg island; D20S17; PB-Cadherin.  
Homo sapiens (human)  
Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.  
Laird, G.  
1 (bases 1 to 147815)  
Direct Submission  
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, UK

## TITLE

Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, UK

## REFERENCE

Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, UK

## COMMENT

Cambridgehire, CB10 1SA, UK. E-mail enquiries: [vega@sanger.ac.uk](mailto:vega@sanger.ac.uk)  
 Clone requests: [clonerequest@sanger.ac.uk](mailto:clonerequest@sanger.ac.uk)  
 On Mar 16, 2001 this sequence version replaced gi:10198608.  
 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:  
 Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at  
[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at  
<http://www.sanger.ac.uk/Map/Chr20>  
 RP5-998H6 is from the library RPCT-5 constructed by the group of Pieter de Jong. For further details see  
<http://www.chori.org/bacpac/home.htm>  
 VECTOR: pCYPAC2

----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: <http://www.sanger.ac.uk>  
 Contact: [vega@sanger.ac.uk](mailto:vega@sanger.ac.uk)  
 -----

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

## FEATURES

## SOURCE

Location/Qualifiers

1..147815

/organism="Homo sapiens"

/mol\_type="Genomic DNA"

/db\_xref="RZPD:RPCIP704H06998"

/db\_xref="taxon:9606"

/chromosome="20"

/map="q13.1"

/clone="RP5-998H6"

/clone\_1fb="RPC1-5"

## misc\_feature

1 /note="Clone left end: RP5-998H6"

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/locus\_tag="RP5-998H6.2-001"

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/locus\_tag="RP5-998H6.2-001"

/note="match: cDNAs: AK057411.1"

complement(join(114275..15619,18488..18739,27130..27247,

27368..27489,39965..40101,50849..51102,53537..53730,

57368..57535,68050..68169,81505..81799,91582..92237))

/gene="CDH22"

/locus\_tag="RP5-998H6.3-001"

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27368..27489,39965..40101,50849..51102,53537..53730,

57368..57535,68050..68169,81505..81799,91582..92237))

/gene="CDH22"

/locus\_tag="RP5-998H6.3-001"

complement(join(14275..15619,18488..18739,27130..27247,

27368..27489,39965..40101,50849..51102,53537..53730,

57368..57535,68050..68169,81505..81799,91582..92237))

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/locus\_tag="RP5-998H6.3-001"

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27368..27489,39965..40101,50849..51102,53537..53730,

57368..57535,68050..68169,81505..81799,91582..92237))

/gene="CDH22"

/locus\_tag="RP5-998H6.3-001"

/standard name="OTTHUMP0000031774"  
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/codon\_start=1

/protein\_id="CBAS1587.2"

/db\_xref="GI:13366277"

/db\_xref="Gene:13251"

/db\_xref="GOA:Q9U99"

/db\_xref="HSP:INCU"

/db\_xref="InterPro:IPR00223"

/db\_xref="InterPro:IPR002126"

/db\_xref="UniProt/Swiss-Prot:Q9U99"

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SAPGADQDGLAGRVKRGVWVQFVVEYETELVYKHSDDSDGAKYITIS

INSGRFLPLDELTCGDIHMERLDRKQKFTYTRARARATRLLEPSEFTIKQD

GNAGRTPLHPLTIGSVASLSPGTSMQVMAADPTTGSARLVYSLDGHHT

VDKRTGVTIRAVPDLDRESGREYVIAQDMAGQGLSGSTTVITVVDNDPR

FPKQWTFSTIGESAPITGTVAGRVKASDSDVDMDMTYHLKSSSGGVFKYTDSD

TOBAITVQKRLDPSQPHVTILBALNKFVDRPADLGTFRPOAIVRVAVTVDESP

EFPPSGQLLEVOBDAQVSLVGVTAADPDAARPVRAIDRSDLDQITDIDADCA

IVYKGLDRETAGHNIITVAMEADNHAOLSRSLRLRLVDNDPELATPYBAVC

EDAKPGQLITGTVSDRDEPOGGRFFFLVPAAPSHPFLSLDIDQNTAVTAHVAG

PNQRODVFPLPLIVVDSGSPPTLSNGTFLTRICGDSGSLTIOSTATAVMAASLP

GALIALIVCVLILVTVLTLTRRHHSKLSLSDSDMDMDVYIKYVDEGGSDTGA

YDMSALSLYDFELKGGDGGSAAGGAGGGSGGAGSPQAHLPSEHGLPGSPSP

EPDFSVPRDTSRKVALADGLDLPVPDAQTVAFGADSPASLSLSHSGSGSD

PATVSWGPRFRPLAALYAGRGDDDEAQA"

29571

/note="Clone right end: RP4-599F21"

complement(join(50363..51102,53537..53730,57368..57535,

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/gene="CDH22"

/locus\_tag="RP5-998H6.3-002"

complement(join(50363..51102,53537..53730,57368..57535,

60340..60455,60970..61391))

/gene="CDH22"

/locus\_tag="RP5-998H6.3-002"

/note="match: ESTs: BG717973.1

match: cDNAs: BC031232.1"

complement(50363)

/gene="CDH22"

/locus\_tag="RP5-998H6.3-002"

147815

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/note="Clone right end: RP5-998H6"

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/note="Clone right end: RP5-998H6"

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147815

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/note="Clone right end: RP5-998H6"

147815

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147815

/note="Clone right end: RP5-998H6"

147815

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147815

Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacho, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Day-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Evans, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, T., Garza, M., Gebregorgis, R., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Haylak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jollivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowals, C., Kraft, C.L., Lebow, H., Levay, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshew, L., Louised, H., Lozano, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindarcne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, B., Mawliny, S., McLeod, M.P., McNeill, T.Z., Meenen, B., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundaasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwokedi, O., Okwou, G., Olarundagbon, A., Pal, S., Parke, K., Paternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Polindexter, A., Popovic, D., Primus, B., Pu, L., Puzo, M., Quiroz, J., Rachlin, R., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajic, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Swatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Uemari, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wiczek, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, S., Zhao, S., Dunn, D., von Weinstock, G., and Gibbs, R.A.

Unpublished  
Direct Submission  
2 (bases 1 to 149208)  
Worley, K.C.  
Direct Submission  
Submitted (17-JUN-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 149208)  
Cow Genome Sequencing Consortium.  
Direct Submission  
Submitted (01-JUL-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Jun 29, 2005 this sequence version replaced gi:67906226.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

Genome Center  
Center: Baylor College of Medicine

Center code: BCM  
Web site: http://www.hgsc.bcm.tmc.edu/  
Contact: hgsc.help@bcm.tmc.edu  
----- Project Information -----  
Center project name: F1JF  
Center clone name: CH240-14909  
----- Summary Statistics -----  
Assembly program: Atlas 3.0;  
Consensus quality: 145336 bases at least Q40  
Consensus quality: 146024 bases at least Q30  
Consensus quality: 146570 bases at least Q20  
Estimated insert size: 147769; sum-of-contigs estimation  
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation  
-----  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 8 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\*  
\* 1 23708: contig of 23708 bp in length  
\* 23709: gap of 447 bp  
\* 24156: contig of 30362 bp in length  
\* 24158: gap of 50 bp  
\* 54568: contig of 33483 bp in length  
\* 88051: gap of 622 bp  
\* 88672: contig of 3677 bp in length  
\* 92350: gap of 50 bp  
\* 92399: contig of 21974 bp in length  
\* 114373: gap of 283 bp  
\* 114374: contig of 32269 bp in length  
\* 114657: gap of 171 bp  
\* 146926: contig of 996 bp in length  
\* 147097: gap of unknown length  
\* 148093: contig of 1016 bp in length.  
\* 148193: Location/Qualifiers  
\* 1.149208  
\* /organism="Bos taurus"  
\* /mol\_type="genomic DNA"  
\* /db\_xref="taxon:9913"  
\* /clone="CH240-14909"  
\* 23709.24155  
\* /estimated\_length=447  
\* 54518.54567  
\* /estimated\_length=50  
\* 88051.88672  
\* /estimated\_length=622  
\* 92350.92399  
\* /estimated\_length=50  
\* 114374.114656  
\* /estimated\_length=283  
\* 146926.147096  
\* /estimated\_length=171  
\* 148093.148192  
\* /estimated\_length=unknown  
\*  
ORIGIN  
Query Match 84.0%; Score 16.8; DB 14; Length 149208;  
Best Local Similarity 80.0%; Pred. No. 1.7e+03;  
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Oy 1 AGGUACAGCGACGACUACGA 20  
||:|||||:|||||:|||||:  
Db 20553 AGCTACGCTCGATCGATCGA 20672  
-----  
RESULT 38  
AC148601/c  
LOCUS 160241 bp DNA linear HTG 17-MAY-2005

DEFINITION Gaesterosteus aculeatus clone ch213-199b3, WORKING DRAFT SEQUENCE, 6 ordered pieces.

ACCESSION AC148601

VERSION AC148601.21 GI:65812358

KEYWORDS HTG, HTGS, PHASE2, HTGS\_DRAFT.

SOURCE Gaesterosteus aculeatus (three spined stickleback)

ORGANISM Gaesterosteus aculeatus (three spined stickleback)

REFERENCE 1 (bases 1 to 160241)

AUTHORS Qin,B., Lin,S., Postlethwait,J. and Roe,B.A.

TITLE Gaesterosteus aculeatus BAC Clone ch213-199b3

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 160241)

AUTHORS Qin,B., Lin,S., Postlethwait,J. and Roe,B.A.

TITLE Direct Submission

JOURNAL Submitted (20-MAR-2004) Department of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA

REFERENCE 3 (bases 1 to 160241)

AUTHORS Qin,B., Lin,S., Postlethwait,J. and Roe,B.A.

TITLE Direct Submission

JOURNAL Submitted (17-MAY-2005) Department of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA

COMMENT On May 17, 2005 this sequence version replaced gi:62734771.

----- Genome Center

Center: Department of Chemistry and Biochemistry

The University of Oklahoma

Center code:UOKMOR

-----

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 6 contigs. Gaps between the contigs

\* are represented as runs of N. The order of the pieces

\* is believed to be correct as given, however the sizes

\* of the gaps between them are based on estimates that have

\* provided by the submitter.

\* This sequence will be replaced

\* by the finished sequence as soon as it is available and

\* the accession number will be preserved.

1 14138: contig of 14138 bp in length

1 14139 14238: gap of unknown length

1 14239 30871: contig of 16533 bp in length

1 30872 30872: gap of unknown length

1 30872 105980: contig of 75109 bp in length

1 105981 106080: gap of unknown length

1 106081 119781: contig of 13701 bp in length

1 119782 119881: gap of unknown length

1 119882 132445: contig of 12564 bp in length

1 132446 132545: gap of unknown length

1 132546 160241: contig of 27696 bp in length.

Location/Qualifiers

1. 160241

/organism="Gaesterosteus aculeatus"

/mol\_type="genomic DNA"

/db\_xref="taxon:69293"

/clone="ch213-199b3"

/clone\_1lb="Gaesterosteus aculeatus BAC library chori-213"

14139. 14238

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30772. 30871

/estimated\_length=unknown

105981. 106080

/estimated\_length=unknown

119782. 119881

/estimated\_length=unknown

132446. 132545

/estimated\_length=unknown

ORIGIN

Query Match 84.0%; Score 16.8; DB 14; Length 160241;

Best Local Similarity 80.0%; Pred. No. 1.7e+03;

Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGTACAGCCAGCACTACCA 20

Db 37690 AAGTACAGCCAGCACTACCA 37671

RESULT 39

AC104460/c 162514 bp DNA linear PRI 29-APR-2002

LOCUS Homo sapiens chromosome 1 clone RP11-438011, complete sequence.

DEFINITION AC104460 AL358195

ACCESSION AC104460

VERSION AC104460.2 GI:20336796

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 162514)

AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Phelps,K.A., Buckley,D., Raymond,C. and Haugen,B.D.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 162514)

AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,B.D.

TITLE Direct Submission

JOURNAL Submitted (11-DEC-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA

REFERENCE 3 (bases 1 to 162514)

AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Phelps,K.A., Buckley,D., Raymond,C. and Haugen,B.D.

TITLE Direct Submission

JOURNAL Submitted (29-APR-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA

COMMENT On Apr 29, 2002 this sequence version replaced gi:17488642.

----- Genome Center

Center: University of Washington Genome Center

Center Code: UWGC

Web site: <http://www.genome.washington.edu>

Contact: [uwgchgs@u.washington.edu](mailto:uwgchgs@u.washington.edu)

Drafting Center: SC

----- Project Information

Center project name: chr-1

Center clone name: RP11-438011 (sc0707)

----- Summary Statistics

Sequencing vector: plasmid; 44% of reads

Chemistry: Dye-terminator RT; 50% of reads

Chemistry: Dye-terminator Big Dye; 50% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 162405 bases at least Q40

Consensus quality: 162506 bases at least Q30

Consensus quality: 162514 bases at least Q20

Insert size: 162514; sum-of-contigs

Quality coverage: 8.5x in Q20 bases; sum-of-contigs

-----

Overlapping Sequences:

5': RP11-351A7 AL356361

3': RP11-343J24 AL513543, 2079-bp overlap

-----

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.





RESULT 40  
 AC073317/c 162701 bp DNA linear HTG 17-NOV-2000  
 LOCUS Homo sapiens chromosome UNK clone RP11-195N21, WORKING DRAFT  
 DEFINITION  
 ACCESSION AC073317  
 VERSION AC073317.5 GI:11079593  
 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
 SOURCE  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.  
 1 (bases 1 to 162701)  
 Waterston, R.H.  
 The sequence of Homo sapiens clone  
 Unpublished  
 2 (bases 1 to 162701)  
 Waterston, R.H.  
 Direct Submission  
 Submitted (14-JUN-2000) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 On Nov 3, 2000 this sequence version replaced gi:10337669.

COMMENT  
 ----- Genome Center -----  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: http://genome.wustl.edu/gsc/index.shtml  
 ----- Project Information -----  
 Project name: H\_NH0195N21  
 Center project name: H\_NH0195N21  
 ----- Summary Statistics -----  
 Sequencing vector: M13; 60%  
 Chemistry: Dye-terminator Big Dye; 36% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 149699 bases at least Q40  
 Consensus quality: 153330 bases at least Q30  
 Consensus quality: 155040 bases at least Q20  
 Insert size: 168; agarose-fp  
 Insert size: 161702; sum-of-contigs  
 Quality coverage: 4.94 in Q20 bases; sum-of-contigs  
 Quality coverage: 5.26 in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 23 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 1167: contig of 1167 bp in length  
 \* 1168 1267: gap of unknown length  
 \* 1268 3212: contig of 1945 bp in length  
 \* 3213 3312: gap of unknown length  
 \* 3313 5058: contig of 1746 bp in length  
 \* 5059 5158: gap of unknown length  
 \* 5159 7422: contig of 2264 bp in length  
 \* 7423 7522: gap of unknown length  
 \* 7523 9790: contig of 2268 bp in length  
 \* 9791 9891: gap of unknown length  
 \* 9891 13294: contig of 3404 bp in length  
 \* 13295 13394: gap of unknown length  
 \* 13395 16584: gap of 3190 bp in length  
 \* 16585 16684: gap of unknown length  
 \* 16685 20753: contig of 4069 bp in length  
 \* 20754 20854: gap of unknown length  
 \* 20855 24326: contig of 3473 bp in length  
 \* 24327 24427: gap of unknown length  
 \* 24428 28594: contig of 4168 bp in length

FEATURES  
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 1. 162701  
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 /db\_xref="taxon:9606"  
 /chromosome="UNK"  
 /clone="RP11-195N21"  
 Location/Qualifiers  
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 1168..1267  
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 1268..3212  
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 3213..3312  
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 3313..5058  
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 7423..7522  
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 7523..9790  
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 9891..13294  
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 /note="assembly\_name:Contig32"  
 16585..16684  
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 16685..20753  
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 20754..20853  
 /estimated\_length=unknown  
 20854..24326  
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 /estimated\_length=unknown  
 24427..28594  
 /note="assembly\_name:Contig35"  
 clone\_end:17  
 vector\_side:right

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misc_feature	28695. .32625	/note="assembly_name:Contig36"
gap	32626. .32725	/estimated_length=unknown
misc_feature	32726. .39439	/note="assembly_name:Contig37"
gap	39440. .39539	/estimated_length=unknown
misc_feature	39540. .44814	/note="assembly_name:Contig38"
gap	44815. .44914	/estimated_length=unknown
misc_feature	44915. .52189	/note="assembly_name:Contig39"
gap	52190. .52289	/estimated_length=unknown
misc_feature	52290. .58734	/note="assembly_name:Contig40"
gap	58735. .58834	/estimated_length=unknown
misc_feature	58835. .66484	/note="assembly_name:Contig41"
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misc_feature	66585. .74428	/note="assembly_name:Contig42"
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misc_feature	74529. .84369	/note="assembly_name:Contig43"
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misc_feature	84470. .91569	/note="assembly_name:Contig44"
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misc_feature	101548. .119545	/note="assembly_name:Contig46
gap	clone_end:SP6	vector_side:right"
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misc_feature	119646. .137645	/note="assembly_name:Contig47"
gap	137646. .137745	/estimated_length=unknown
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Query Match Similarity	84.0%	Score 16.8	DB 14	Length 162701
Best Local Similarity	80.0%	Pred. No. 1.7e+03		
Matches 16	Conservative 2	Mismatches 2	Indels 0	Gaps 0
QY	1 AGUACAGCCAGAGACTUACGA 20			
Db	131778 AGTACAGACAGAGACTACTA 131759			
RESULT 41				
AC015723/c				
LOCUS	AC015723	163386 bp	DNA	linear PRI 01-APR-2001
DEFINITION	Homo sapiens chromosome, clone RP11-168G16, complete sequence.			
ACCESSION	AC015723			
VERSION	AC015723.8	GI:13357369		
KEYWORDS	HTG.			
SOURCE	Homo sapiens (human)			

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 163386)  
Birtren,B., Linton,L., Nuebaum,C. and Lander,E.  
Homo sapiens chromosome, clone RP11-168G16  
Unpublished

TITLE 2 (bases 1 to 163386)  
Birtren,B., Linton,L., Nuebaum,C., Lander,E., Allen,N., Anderson,M., Baldwin,J., Barua,N., Beckerly,R., Boguslavsky,L., Bouthgalter,B., Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Deatellano,K., Dewar,K., Donlo,M., Donelan,L., Doyle,M., Ferreira,P., Fitzhugh,W., Forret,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagoes,B., Heatford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Lebeck,J.J., Lien,C., Locke,K., Macdonald,P., Marquis,N., McSwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J., Morow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Titrrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

REFERENCE 3 (bases 1 to 163386)  
Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

TITLE 3 (bases 1 to 163386)  
Birtren,B., Linton,L., Nuebaum,C., Lander,E., Allen,N., Anderson,S., Barua,N., Bastien,V., Boguslavsky,L., Bouthgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chopeal,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Deatellano,K., Dewar,K., Diaz,J.S., Dodge,S., Fato,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagoes,B., Heatford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Karatas,A., LaRoque,K., Lamazere,R., Landers,T., Lebeck,J., Levine,R., Liu,G., Maclean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M., McSwan,P., McKernan,K., McPheeters,R., Meldrum,J., Menue,L., Mhova,T., Mlenka,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Plunkhang,P., Pterre,N., Pollara,V., Raymond,C., Retta,R., Riebeck,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schnuppach,R., Seaman,S., Severy,P., Soungue,C., Spender,B., Stange-Thomann,N., Stojanovic,N., Straus,M., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Travers,M., Travis,N., Trigillo,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zaitoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE Direct Submission  
Submitted (01-APR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 16, 2001 this sequence version replaced g1:13194369.  
All repeats were identified using RepeatMasker:  
Smit, A.P.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RV/RepeatMasker.html>

TITLE --- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Contact: WtBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: sequence\_submissions@genome.wi.mit.edu  
--- Project Information  
Center project name: L1410  
Center clone name: 168\_G16

FEATURES  
source  
location/Qualifiers  
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/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
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complement(88..1207)  
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repeat\_region

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repeat_region complement(1220, .2064)
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repeat_region complement(2043, .2076)
/rpt_family="L1MA4A"
repeat_region complement(2077, .2371)
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RESULT 42
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DEFINITION
AL139378 Human DNA sequence from clone RP11-271B5 on chromosome 13 contains
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factor (GAF, HBRG-9)), a ribosomal protein S7 (40S ribosomal
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ACCESSION AL139378
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SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

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REFERENCE 1 (bases 1 to 166703)  
 AUTHORS Pelan S.  
 TITLE Direct Submission  
 JOURNAL Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk  
 On Jun 4, 2000 this sequence version replaced gi:8246895.  
 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:  
 Bm: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at  
 http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at  
 http://www.sanger.ac.uk/HGP/Chr13  
 ----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: vegas@sanger.ac.uk  
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 RP11-271B5 is from the library RPCT-11.1 constructed by the group of Pieber de Jong. For further details see  
 http://www.chori.org/bacpac/home.htm  
 VECTOR: pBAC3.6  
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.  
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 1  
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 mRNA

misc\_feature 166703  
/note="Clone\_right\_end: RP11-271B5"

ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 166703;  
Best Local Similarity 80.0%; Pred. No. 1.7e+03;  
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGTACAGCCAGGACUACGA 20  
|||||  
Db 30829 AGGTACAGCCAGGACUACGA 30848

RESULT 43  
AC157818 168087 bp DNA linear HTG 01-JUN-2005  
LOCUS Mus musculus chromosome 3 clone RP24-268H11 map 3, \*\*\* SEQUENCING  
DEFINITION IN PROGRESS \*\*\*, 5 unordered pieces.

AC157818  
AC157818.4 GI:66841572  
HTG: HTGS\_PHASE1; HTGS\_FUULTOP; HTGS\_ACTIVEPIN.  
MUS musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 168087)  
Birren, B., Nuebaum, C., and Lander, B.  
Mus musculus chromosome 3, clone RP24-268H11  
Unpublished

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS

2 (bases 1 to 168087)  
Birren, B., Nuebaum, C., Lander, B., Abouelleil, A., Allen, N.,  
Anderson, M., Anderson, S., Archchi, H.M., Barna, N., Bastien, V.,  
Bloom, T., Boguslavsky, L., Boukhalter, B., Camarate, J., Chang, J.,  
Chapel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B.,  
Deatellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L.,  
Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D.,  
Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N.,  
Hagopian, D., Hagoos, B., Hall, J., Horton, L., Hulme, W., Iliev, I.,  
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T.,  
Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R.,  
Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C.,  
McCarthy, M., Meldrim, J., Menus, J., Mihova, T., Mlenga, V.,  
Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C.,  
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,  
Phunhthang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C.,  
Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schnapack, R.,  
Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N.,  
Stojanovic, N., Stubbs, M., Talamas, J., Testafaye, S., Theodore, J.,  
Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R.,  
Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L.,  
Zimmer, A., and Zody, M.  
Direct Submission  
Submitted (01-MAR-2005) Broad Institute of MIT and Harvard, 320  
Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 168087)  
Birren, B., Nuebaum, C., Lander, B., Abouelleil, A., Allen, N.,  
Anderson, M., Anderson, S., Archchi, H.M., Barna, N., Bastien, V.,  
Bloom, T., Boguslavsky, L., Boukhalter, B., Camarate, J., Chang, J.,  
Chapel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B.,  
Deatellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L.,  
Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D.,  
Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N.,  
Hagopian, D., Hagoos, B., Hall, J., Horton, L., Hulme, W., Iliev, I.,  
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T.,  
Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R.,  
Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C.,  
McCarthy, M., Meldrim, J., Menus, J., Mihova, T., Mlenga, V.,  
Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C.,  
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,  
Phunhthang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C.,  
Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schnapack, R.,  
Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N.,

TITLE  
JOURNAL  
COMMENT

Stojanovic, N., Stubbs, M., Talamas, J., Testafaye, S., Theodore, J.,  
Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R.,  
Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L.,  
Zimmer, A., and Zody, M.  
Direct Submission  
Submitted (01-JUN-2005) Broad Institute of MIT and Harvard, 320  
Charles Street, Cambridge, MA 02141, USA  
On Jun 1, 2005 this sequence version replaced gi:62629962.  
All repeats were identified using RepeatMasker:  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
Smit, A.F.A. & Green, P. (1996-1997)  
----- Genome Center  
Center: Broad Institute of MIT and Harvard  
Center code: W1BR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@broad.mit.edu  
----- Project Information  
Center project name: L31870  
Center clone name: 268\_H\_11

\*\*\*\*\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 5 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 18596: contig of 18596 bp in length  
\* 18597 18696: gap of unknown length  
\* 18697 22311: contig of 3615 bp in length  
\* 22312 22411: gap of unknown length  
\* 22412 58665: contig of 36254 bp in length  
\* 58666 58765: gap of unknown length  
\* 58766 74058: contig of 15293 bp in length  
\* 74059 74158: gap of unknown length  
\* 74159 168087: contig of 93929 bp in length.

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/clone\_11b="RPCT-24 Male Mouse BAC"  
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gap 22312..22411  
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ORIGIN

Query Match 84.0%; Score 16.8; DB 14; Length 168087;  
Best Local Similarity 85.0%; Pred. No. 1.7e+03;  
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGTACAGCCAGGACUACGA 20  
|||||  
Db 42939 AGGTACAGCCAGGACUACGA 42958

RESULT 44  
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LOCUS Mus musculus clone RP24-115M17, WORKING DRAFT SEQUENCE, 8 unordered  
DEFINITION pieces.  
AC131061  
AC131061.3 GI:289313177  
HTG: HTGS\_PHASE1; HTGS\_DRAFT.



**SOURCE**  
Mus musculus (house mouse)

**ORGANISM**  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae; Mus.

**REFERENCE**  
1 (bases 1 to 187700)  
Birren, B., Nusbaum, C. and Lander, E.  
Mus musculus, clone RP24-115M17  
Unpublished  
2 (bases 1 to 187700)

**AUTHORS**  
Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,  
Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouckwalter, B.,  
Cammarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,  
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,  
Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,  
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,  
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,  
Karatas, A., Kells, C., Lander, E., Levine, R., Lindblad-Toh, K.,  
Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C.,  
McCarthy, M., Meldrum, J., Menus, L., Mihova, T., Mienga, V.,  
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Notbu, C., Norman, C.H.,  
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,  
Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,  
Roman, J., Roy, A., Schauer, S., Schuback, R., Seaman, S., Severy, P.,  
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,  
Teafaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,  
Zembek, L., Zimmer, A. and Zody, M.

**TITLE**  
Direct Submission

**JOURNAL**  
Submitted (16-AUG-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 187700)

**REFERENCE**  
3 (bases 1 to 187700)  
Birren, B., Nusbaum, C., Lander, E., Aboueleil, A., Allen, N.,  
Anderson, S., Archchell, H.M., Barna, N., Bastien, V., Bloom, T.,  
Boguslavsky, L., Bouckwalter, B., Cammarata, J., Chang, J., Choepel, Y.,  
Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K.,  
Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,  
Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S.,  
Graham, L., Grand-Pierre, N., Hater, N., Hagopian, D., Hagos, B.,  
Hall, U., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,  
Kamat, A., Karatas, A., Kells, C., Lander, E., Levine, R.,  
Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., Maclean, C.,  
Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,  
Meldrum, J., Menus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J.,  
Nguyen, C., Nicol, R., Notbu, C., O'Connor, T., O'Donnell, P.,  
O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,  
Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,  
Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C.,  
Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,  
Talamas, J., Teafaye, S., Theodore, J., Topham, K., Travers, M.,  
Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,  
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

**TITLE**  
Direct Submission

**JOURNAL**  
Submitted (11-MAR-2003) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 11, 2003 this sequence version replaced gi:28394870.  
All repeats were identified using RepeatMasker:  
Smt, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

**COMMENT**  
Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WTR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
Project Information  
Center project name: L27077  
Center clone name: 115 M.17  
Sequencing vector: Plasmid, n/a, 100% of reads  
Chemistry: Dye-terminator Big Dye, 100% of reads  
Assembly program: Phrap, version 0.960731  
Consensus quality: 185316 bases at least Q40  
Consensus quality: 186310 bases at least Q30

Consensus quality: 186759 bases at least Q20  
Insert size: 184000; agarose-fp  
Insert size: 187000; sum-of-contigs  
Quality coverage: 9.4 in Q20 bases; agarose-fp  
Quality coverage: 9.3 in Q20 bases; sum-of-contigs

\*\*\*\*\*  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 8 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preceeded.  
\*\*\*\*\*

1 65220: contig of 65220 bp in length  
\* 65320: gap of 100 bp  
\* 65321 66009: contig of 689 bp in length  
\* 66010 66109: gap of 100 bp  
\* 66110 73823: contig of 7714 bp in length  
\* 73824 73923: gap of 100 bp  
\* 73924 85287: contig of 1164 bp in length  
\* 85288 85387: gap of 100 bp  
\* 85388 99141: contig of 13754 bp in length  
\* 99142 99241: gap of 100 bp  
\* 99242 134109: contig of 3486 bp in length  
\* 134110 134209: gap of 100 bp  
\* 134210 165462: contig of 31253 bp in length  
\* 165463 165562: gap of 100 bp  
\* 165563 187700: contig of 22138 bp in length.  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/clone="RP24-115M17"  
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vector\_side:left"  
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65321..66009  
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66010..66109  
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73824..73923  
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73924..85287  
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85288..85387  
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85388..99141  
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99142..99241  
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99242..134109  
/note="assembly\_fragment"  
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/estimated\_length=100  
134210..165462  
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165563..187700  
/note="assembly\_fragment  
clone\_end:T7  
vector\_side:right"

ORIGIN  
Query Match 84.0%, Score 16.8; DB 14; Length 187700;

Best Local Similarity 85.0%; Pred. No. 1.7e+03;  
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0

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QY      1 AGGACAGCCAGGACTUACGA 20
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Db 40699 AGGACAGCCAGGACTUACA 40718

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	RESULT	45
AC011141		
LOCUS	192104 bp	DNA linear HTG 26-MAY-2000
DEFINITION	Hom sapiens clone RP11-1J10, WORKING DRAFT SEQUENCE, 27 unordered clones	

VERSION AC011141.3 GI:8072508  
 HTG: HTGS\_PHASE1; HTGS\_DRAFT.  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Vertebrata; Chordata; Craniata; Vertebrata; Euteleostomi

[illegible]

2 (Cases 1 to 1923/04)

Birtren, B., Linton, L., Nusbäum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukhaller, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dextrallano, K., Dewar, K., Domino, M., Donegan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, B., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Hearford, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatsas, A., Klein, J., Lemocksky, J., Lien, C., Locke, K., MacDonald, P., Margolis, N., McMan, P., McGurt, A., McKernan, K., McLaughlin, J., Meldrum, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thoman, N., Stojanovic, N., Subramanian, A., Talamas, J., Teefaye, S., Tittell, A., Vasilevic, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A., and Cody, M.

**TITLE** Direct Submission  
**JOURNAL** Submitted (01-Oct-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
**COMMENT** On May 25, 2000 this sequence version replaced gi:6479099.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
Faster

-----  
Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
-----  
Project Information

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-- Summary Statistics
Sequencing vector: M13, M77815, 100% of reads
Chemistry: Dye-terminator Big Dye, 100% of reads
Assembly program: Phrap, version 0.960731
Consensus quality: 14793 bases at least Q40
Consensus quality: 171774 bases at least Q30
Consensus quality: 16219 bases at least Q20
Insert size: 170000; agarose-fp
Insert size: 189504; sum-of-contigs
Quality coverage: 3.5 in Q20 bases; agarose-fp
Quality coverage: 3.2 in Q20 bases; sum-of-contigs

```

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 27 configs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the configs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will  
\* be preserved. 1106. cont'd of 1106 bp in length

1	1106:	contig of 1106 bp in length
1107	1206:	gap of 100 bp
1207	2306:	contig of 1100 bp in length
2307	2406:	gap of 100 bp
2407	4512:	contig of 2106 bp in length
4513	4612:	gap of 100 bp
4613	6348:	contig of 1736 bp in length
6349	6448:	gap of 100 bp
6449	8688:	contig of 2240 bp in length
8689	8788:	gap of 100 bp
8789	11301:	contig of 2513 bp in length
11302	11401:	gap of 100 bp
11402	15966:	contig of 4585 bp in length
15967	16086:	gap of 100 bp
16087	18414:	contig of 2338 bp in length
18415	18514:	gap of 100 bp
18515	22441:	contig of 3927 bp in length
22442	22541:	gap of 100 bp
22542	27370:	contig of 4828 bp in length
27371	27470:	gap of 100 bp
27471	33405:	contig of 5935 bp in length
33406	33505:	gap of 100 bp
33506	40793:	contig of 7288 bp in length
40794	40894:	gap of 100 bp
40894	46513:	contig of 5620 bp in length
46514	46613:	gap of 100 bp
46614	52704:	contig of 6091 bp in length
52705	52804:	gap of 100 bp
52805	59694:	contig of 6890 bp in length
59695	59794:	gap of 100 bp
59795	67016:	contig of 7222 bp in length
67017	67116:	gap of 100 bp
67117	73668:	contig of 6552 bp in length
73669	73768:	gap of 100 bp
73769	80994:	contig of 7226 bp in length
80995	81094:	gap of 100 bp
81095	88180:	contig of 6986 bp in length
88081	88180:	gap of 100 bp
88181	97941:	contig of 9761 bp in length
97942	98041:	gap of 100 bp
98042	104558:	contig of 6517 bp in length
104559	104558:	gap of 100 bp
104560	114543:	contig of 9985 bp in length
114544	114643:	gap of 100 bp
114644	123467:	contig of 8824 bp in length
123468	123567:	gap of 100 bp
123568	136898:	contig of 13331 bp in length
136899	136998:	gap of 100 bp
136999	151693:	contig of 14695 bp in length
151694	151793:	gap of 100 bp
151794	169813:	contig of 18020 bp in length
169814	169913:	gap of 100 bp
169914	192104:	contig of 22191 bp in length

## FEATURES

**Source**

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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="RPI1-1J10"
/clone_1fb="RPCI-11 Human Male BAC

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2307. 2406

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Query Match 84.0%; Score 16.8; DB 14; Length 192104;  
Best Local Similarity 80.0%; Pred. No.1.7e+03;  
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

LOCUS	AC135809	195041 bp	DNA	linear	ROD 29-MAY-200
DEFINITION	Mus musculus BAC clone RP23-353F16 from chromosome 7, complete sequence.				
ACCESSION	AC135809				
VERSION	AC135809.4	GI:47777610			
KEYWORDS	HTG.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Bukacinska, J.; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 195041) Vanbrunt, A., Van Brunt, A., Kozlowicz, A., Bielicki, L., Haglund, K. and Meyer, R.				
TITLE	The sequence of Mus musculus BAC clone RP23-353F16				
JOURNAL	Unpublished (2001)				
REFERENCE	2 (bases 1 to 195041)				
AUTHORS	McPherson, J. D. and Waterston, R. H.				
TITLE	Direct Submission				
JOURNAL	Submitted (22-OCT-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA				
REFERENCE	3 (bases 1 to 195041)				
AUTHORS	Wilson, R. K.				
TITLE	Direct Submission				
JOURNAL	Submitted (08-MAY-2004) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA				
REFERENCE	4 (bases 1 to 195041)				
AUTHORS	Wilson, R. K.				
TITLE	Direct Submission				
JOURNAL	Submitted (28-MAY-2004) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA				
REFERENCE	5 (bases 1 to 195041)				
AUTHORS	Wilson, R. K.				
TITLE	Direct Submission				
JOURNAL	Submitted (29-MAY-2004) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA				
COMMENT	On May 28, 2004 this sequence version replaced gi:47084674.				

**NOTICE:**

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

### MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see: <http://genome.wucl.edu>

**SOURCE INFORMATION**

The RPCT-23Bac Library has been constructed by Kazutoyo Oseagawa and Minako Tateno in the laboratory of Pieter de Jong (<http://www.chori.org>) from female C57BL/6 mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

# NEIGHBORING SEQUENCE INFORMATION: This sequence is the entire insert of the clone.

FEATURES  
source

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545..660  
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720..907  
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908..974  
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Query Match 84.0%; Score 16.8; DB 9; Length 195041;  
Best Local Similarity 85.0%; Pred. No. 1.7e+03;  
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGUAACGCCAGACUACGA 20  
DB 63581 AGGTACTGCGACGACCA 63600

RESULT 47  
AC127377/c 195767 bp DNA linear ROD 01-JAN-2004  
LOCUS Mus musculus BAC clone RP23-51N3 from chromosome 3, complete  
DEFINITION sequence.  
AC127377

VERSION AC127377.4 GI:40363333  
KEYWORDS HTG.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 195767)

Courtney, L., Kozlowski, A., Bielicki, L. and Haakenson, W.

The sequence of Mus musculus BAC clone RP23-51N3

JOURNAL 2 (bases 1 to 195767)

REFERENCE 2 (bases 1 to 195767)

Wilson, R.

Sequencing of Mus musculus

JOURNAL 3 (bases 1 to 195767)

REFERENCE 3 (bases 1 to 195767)

McPherson, J.D. and Waterston, R.H.

Direct Submision

JOURNAL Submitted (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park

REFERENCE 4 (bases 1 to 195767)

Wilson, R.K.

Direct Submision

JOURNAL Submitted (07-NOV-2003) Genome Sequencing Center, 4444 Forest Park

REFERENCE 5 (bases 1 to 195767)

Wilson, R.K.

Direct Submision

JOURNAL Submitted (25-DEC-2003) Genome Sequencing Center, 4444 Forest Park

REFERENCE 6 (bases 1 to 195767)

Wilson, R.

Direct Submision

JOURNAL Submitted (01-JAN-2004) Department of Genetics, Washington

REFERENCE 7 (bases 1 to 195767)

University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

On Dec 25, 2003 this sequence version replaced gi:38198744.

Center: Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: http://genome.wustl.edu

Contact: submissions@wustl.edu

Center project name: M\_BA0051N03

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NOTICE: This sequence may not represent the entire insert of this

clone. It may be shorter because we only sequence overlapping

clone sections once, or longer because we provide a small overlap

between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:

all regions were double stranded, sequenced with an alternate

chemistry, or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by sequence

from more than one subclone; and the assembly was confirmed by

restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren,

Department of Genetics, Washington University, St. Louis MO, For

additional information about the map position of this sequence, see

http://genome.wustl.edu

SOURCE INFORMATION:

The RPI-23 BAC Library has been constructed by Kazuhiro Oseigawa

and Minako Tateo in the laboratory of Pter de Jong

(http://www.chori.org) from female C57BL/6J mouse kidney and/or

brain genomic DNA. The clone and detailed information can be

obtained from Research Genetics, Inc. (http://www.resgen.com) or

# FEATURES

## SOURCE

### location/Qualifiers

#### 1.195767

##### /organism="Mus musculus"

##### /mol\_type="genomic DNA"

##### /db\_xref="taxon:10090"

##### /chromosome="3"

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##### /clone\_1kb="RPI-23"

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##### /product="tRNA-Ser"

##### /note="Likely pseudogene (HMM Sc=31.87 / Sec struct Sc=9.21)"

##### 46960..47032

##### /product="tRNA-Ser"

##### /note="Likely pseudogene (HMM Sc=36.43 / Sec struct Sc=9.72)"

##### 66101..66174

##### /product="tRNA-Ser"

##### /note="Likely pseudogene (HMM Sc=37.15 / Sec struct Sc=11.71)"

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##### /product="tRNA-Ser"

##### /note="Likely pseudogene (HMM Sc=30.31 / Sec struct Sc=9.30)"

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##### /product="tRNA-Ser"

##### /note="Likely pseudogene (HMM Sc=45.36 / Sec struct Sc=12.35)"

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##### /product="tRNA-Ser"

##### 167203..168307

##### /note="CpG island (4GC=73.3, o/e=0.93, #CpGs=140)"

##### complement(187130..187201)

##### /product="tRNA-Ser"

##### /note="Likely pseudogene (HMM Sc=32.62 / Sec struct Sc=5.57)"

## ORIGIN

### Query Match

#### Best Local Similarity 85.0%; Score 16.8; DB 9; Length 195767;

#### Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

#### Db 56269 AGGAACAGCGACGACTACGA 56250

#### OR 1 AGTACGCCAGACGACGACA 20

#### ACT104205/c 201745 bp DNA linear ROD 15-JUN-2005

#### LOCUS Mus musculus chromosome 3, clone RP23-250M22, complete sequence.

#### DEFINITION ACT104205

#### ACCESSION ACT104205.15 GI:70887890

#### VERSION HTG.

#### KEYWORDS Mus musculus (house mouse)

#### SOURCE Mus musculus

#### ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

#### Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

#### Sciurognathi; Muridae; Murinae; Mus.

#### 1 (bases 1 to 201745)

#### Sectiura, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,

#### Gande, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,

#### Anderson, S., Barina, N., Bastien, V., Boguslavsky, L., Boughalter, B.,

#### Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,

#### Choepel, Y., Colangelo, M., Collins, S., Collimore, A., Cook, A.,

#### Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fero, S.,

#### Perreira, P., Plitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,

#### Gande, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,

#### Barren, B., Linton, L., Nusbaum, C., Lander, B., Ali, A., Allen, N.,

#### Anderson, S., Barina, N., Bastien, V., Boguslavsky, L., Boughalter, B.,

#### Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,

#### Choepel, Y., Colangelo, M., Collins, S., Collimore, A., Cook, A.,

#### Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fero, S.,

#### Perreira, P., Plitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,

This sequence is the entire insert of the clone.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lacroque, K., Llanazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., Maclean, C., Macdonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheters, R., Meldrum, J., Menus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhkanh, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Straus, N., Subramanian, A., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigglio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (06-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 201745)

TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Birren, B., Nusbaum, C., Lander, E., Abouelella, A., Allen, N., Bloom, T., Boguslavsky, L., Bouckhalter, B., Camarata, J., Chang, J., Choquet, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Deaellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Mlenga, V., McCarthy, M., Meldrum, J., Menus, L., Mihova, T., Niocoli, N., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhkanh, P., Pierre, N., Rachupka, A., Rasmussen, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schnupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (26-MAY-2005) Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02141, USA  
4 (bases 1 to 201745)

REFERENCE  
AUTHORS

Birren, B., Nusbaum, C., Lander, E., Abouelella, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouckhalter, B., Camarata, J., Chang, J., Choquet, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Deaellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Mlenga, V., McCarthy, M., Meldrum, J., Menus, L., Mihova, T., Niocoli, N., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhkanh, P., Pierre, N., Rachupka, A., Rasmussen, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schnupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE  
JOURNAL

Submitted (15-JUL-2005) Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT  
On Jul 15, 2005 this sequence version replaced gi:66730823.

All repeats were identified using RepeatMasker:

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center

Center: Broad Institute of MIT and Harvard  
Center code: W1BR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@broad.mit.edu  
Project Information  
Center project name: L19628  
Center clone name: 250\_M\_22

FEATURES  
Source

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28510..28698  
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repeat_region /rpt_family="ORR1A3"
repeat_region 29101..29243
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repeat_region 29246..31097
repeat_region /rpt_family="ORR1A-Int"
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 Best Local Similarity 85.0%; Pred. No. 1.7e+03;  
 Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 AGGUAAGCAGCAGACUACGA 20  
 Db 78233 AGGAAAGCCAGCAGACTACGA 78214

RESULT 49  
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 LOCUS  
 DEFINITION Pan troglodytes chromosome UNK clone RPa3-16604, \*\*\* SEQUENCING IN  
 AC145989  
 VERSION AC145989.1 GI:33386940  
 KEYWORDS HTG; HTGS; PHASE1  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Pan.  
 1 (bases 1 to 204393)  
 Wilson,R.K.  
 The sequence of Pan troglodytes clone  
 Unpublished  
 2 (bases 1 to 204393)  
 Wilson,R.K.  
 Direct Submission  
 Submitted (01-AUG-2003) Genetics, Genome Sequencing Center, 4444  
 Forest Park Parkway, St. Louis, MO 63108, USA  
 COMMENT  
 AUTHORS  
 TITLE  
 JOURNAL  
 REFERENCE  
 JOURNAL  
 AUTHORS  
 TITLE  
 JOURNAL

----- Genome Center -----  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: http://genome.wustl.edu/gsc/index.shtml  
 ----- Project Information -----  
 Center project name: C\_PT166004  
 ----- Summary Statistics -----

Sequencing vector: M13; 0%  
 Sequencing vector: plasmid; 100%  
 Chemistry: Dye-primer RT; 0% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 189315 bases at least Q40  
 Consensus quality: 192131 bases at least Q30  
 Consensus quality: 194979 bases at least Q20  
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 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 27 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

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1 1302: contig of 1302 bp in length
* 1303 1402: gap of unknown length
* 1403 2811: contig of 1409 bp in length
* 2812 2911: gap of unknown length
* 2912 4488: contig of 1577 bp in length
* 4489 4589: gap of unknown length
* 4590 5802: contig of 1214 bp in length
* 5803 5902: gap of unknown length
* 5903 7459: contig of 1557 bp in length
* 7460 7559: gap of unknown length
* 7560 9074: contig of 1515 bp in length
* 9075 9174: gap of unknown length
* 9175 10338: contig of 1164 bp in length
* 10339 10438: gap of unknown length
* 10439 11928: contig of 1490 bp in length
* 11929 12028: gap of unknown length
* 12029 13086: contig of 1058 bp in length
* 13087 13186: gap of unknown length
* 13187 14590: contig of 1404 bp in length
* 14591 14690: gap of unknown length
* 14691 15988: contig of 1298 bp in length
* 15989 16088: gap of unknown length
* 16089 17273: contig of 1185 bp in length
* 17274 17373: gap of unknown length
* 17374 18705: contig of 1332 bp in length
* 18706 18805: gap of unknown length
* 18806 20080: contig of 1275 bp in length
* 20081 20180: gap of unknown length
* 20181 21588: contig of 1408 bp in length
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* 23907 24006: gap of unknown length
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* 27786 31199: contig of 3414 bp in length
* 31200 31299: gap of unknown length
* 31300 37408: contig of 6109 bp in length
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* 37509 43246: contig of 5738 bp in length
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* 43347 53109: contig of 9763 bp in length
* 53110 53209: gap of unknown length
* 53210 62904: contig of 9695 bp in length
* 62905 63004: gap of unknown length
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LOCUS Mus musculus chromosome 3, clone RP23-187N22, complete sequence.
DEFINITION AC158309
ACCESSION AC158309 GI:71044080
VERSION AC158309.6
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Graniata; Vertebrata; Euteleostomi;
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Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 206775)
Birren, B., Nuebaum, C., and Lander, E.
Mus musculus chromosome 3, clone RP23-187N22
Unpublished
2 (bases 1 to 206775)
Birren, B., Nuebaum, C., Lander, E., Abouelleil, A., Allen, N.,
Anderson, M., Anderson, S., Arachchi, H.M., Barina, N., Baetien, V.,
Blom, T., Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, J.,
Chopel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B.,
DeArillano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L.,
Erickson, J., Fairo, S., Ferreira, P., FitzGerald, M., Gage, D.,
Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N.,
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Johnson, R., Jones, C., Kamat, A., Karatas, A., Kelle, C., Landers, T.,
Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R.,
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Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norby, C.,
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
Phunhphang, P., Pierre, N., Rachupka, A., Ramasamy, D., Raymond, C.,
Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupbach, R.,
Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Stubbs, M., Talama, S., Testaye, S., Theodore, J.,
Topham, K., Travers, M., Vassiliev, H., Venkatakrishnan, V.S., Viel, R.,
Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zaitoun, J., Zemdek, L.,
Zimmer, A. and Zody, M.

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TITLE	JOURNAL	REFERENCE	AUTHORS
Direct Submission	Submitted (10-MAR-2005) Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02141, USA	3 (bases 1 to 206775)	Birren, B., Nusbaum, C., Lander, E., Abouelell, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H. M., Barina, N., Baetjen, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karacas, A., Kelleys, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramsamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Strange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission	Submitted (25-MAY-2005) Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02141, USA	4 (bases 1 to 206775)	Birren, B., Nusbaum, C., Lander, E., Abouelell, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H. M., Barina, N., Baetjen, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karacas, A., Kelleys, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramsamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Strange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission	Submitted (21-JUL-2005) Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02141, USA	On Jul 21, 2005 this sequence version replaced g166571527.	All repeats were identified using RepeatMasker: http://ftp.genome.washington.edu/RM/RepeatMasker.html
Genome Center	Broad Institute of MIT and Harvard	Center code: WDR	Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@broad.mit.edu	Project Information	Center project name: L31503	Center clone name: 187_N_22
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 18:35:00 ; Search time 914.538 Seconds  
(without alignments)  
1118.796 Million cell updates/sec

Title: US-10-800-926-1

Perfect score: 18

Sequence: 1 agagggucgcagcgsgua 18

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 1000 summaries

Database :

GenBml:\*  
1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
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5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_ro:\*  
11: gb\_sy:\*  
12: gb\_un:\*  
13: gb\_vl:\*  
14: gb\_hng:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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C 2	18	100.0	18	6	AR154731 Sequence
C 3	18	100.0	18	6	BD069939 Use of nu
C 4	18	100.0	18	6	BD205570 Method of
C 5	18	100.0	18	6	BD261112 Methods a
C 6	18	100.0	18	6	BD267877 Methods f
C 7	18	100.0	18	6	AR222220 Sequence
C 8	18	100.0	18	6	AR432481 Sequence
C 9	18	100.0	18	6	AX103812 Sequence
C 10	18	100.0	18	6	AX103864 Sequence
C 11	18	100.0	18	6	AX355457 Sequence
C 12	18	100.0	18	6	AX455590 Sequence
C 13	18	100.0	18	6	AX546865 Sequence
C 14	18	100.0	18	6	AX546917 Sequence
C 15	18	100.0	18	6	BD009122 Immunob
C 16	17	94.4	17	6	AR052611 Sequence
C 17	17	94.4	17	6	BD187524 REGULATOR
C 18	17	94.4	17	6	AR630675 Sequence

C 19	16.4	91.1	289	1	AY207027	AY207027 Acinetoba
C 20	16	88.9	32	6	AX513690	AX513690 Sequence
C 21	16	88.9	32	6	AX513691	AX513691 Sequence
C 22	16	88.9	101451	14	AC138105	AC138105 Mus muscu
C 23	16	88.9	191504	14	AC021215	AC021215 Homo sapi
C 24	16	88.9	191504	14	AC021215	AC021215 Homo sapi
C 25	15.4	85.6	544	3	AF432629	AF432629 Unculture
C 26	15.4	85.6	625	3	AY988985	AY988985 Unculture
C 27	15.4	85.6	849	3	DO123679	DO123679 Unculture
C 28	15.4	85.6	855	3	DO123747	DO123747 Unculture
C 29	15.4	85.6	1029	3	R5025692	R5025692 Rhizospha
C 30	15.4	85.6	1330	3	AY102340	AY102340 Unculture
C 31	15.4	85.6	1330	3	AY102345	AY102345 Unculture
C 32	15.4	85.6	1871	5	BC082645	BC082645 Xenopus 1
C 33	15.4	85.6	2394	5	BC073203	BC073203 Xenopus 1
C 34	15.4	85.6	132418	2	AC159431	AC159431 Trypanoso
C 35	15.4	85.6	142479	2	AC159420	AC159420 Trypanoso
C 36	15.4	85.6	144820	14	AC099556	AC099556 Trypanoso
C 37	15.4	85.6	150671	2	AC007862	AC007862 Trypanoso
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C 39	15.4	85.6	344249	1	BX842654	BX842654 Bdellovib
C 40	15.4	85.6	347625	1	BX248356	BX248356 Corynebac
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C 43	15	83.3	17	6	BD192460	BD192460 Compositi
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C 49	15	83.3	1936	6	AX333656	AX333656 Sequence
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C 54	15	83.3	84158	15	AC067754	AC067754 Arabidops
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C 58	14.8	82.2	447	1	MSF516039	MSF516039 Micrococ
C 59	14.8	82.2	534	3	AY712503	AY712503 Unculture
C 60	14.8	82.2	551	10	BV379519	BV379519 S245P6190
C 61	14.8	82.2	553	10	BV278497	BV278497 S232P6271
C 62	14.8	82.2	654	10	BV256945	BV256945 S235P6167
C 63	14.8	82.2	916	1	PSRG1	PSRG1 Pseudomonas
C 64	14.8	82.2	1381	3	AY222091	AY222091 Unculture
C 65	14.8	82.2	2938	5	BC072817	BC072817 Xenopus 1
C 66	14.8	82.2	12248	1	AB001929	AB001929 Deinococc
C 67	14.8	82.2	14340	1	AB010345	AB010345 Methanopy
C 68	14.8	82.2	14878	15	AF440398	AF440398 Mycosphae
C 69	14.8	82.2	29255	5	AL627162	AL627162 Zebraphish
C 70	14.8	82.2	35159	1	AY943952	AY943952 Streptomy
C 71	14.8	82.2	98945	8	AC016961	AC016961 Homo sapi
C 72	14.8	82.2	110000	1	CP000075	CP000075 Homo sapi
C 73	14.8	82.2	110000	14	CP000075	CP000075 Homo sapi
C 74	14.8	82.2	110000	14	AP006491	AP006491 Continuation (16 o
C 75	14.8	82.2	110000	14	AP006491	AP006491 Continuation (16 o
C 76	14.8	82.2	110000	15	AP006491	AP006491 Continuation (16 o
C 77	14.8	82.2	121515	14	AP008218	AP008218 Continuation (16 o
C 78	14.8	82.2	122493	14	AL161737	AL161737 Homo sapi
C 79	14.8	82.2	125750	14	AC092011	AC092011 Fells cat
C 80	14.8	82.2	129841	14	AC140102	AC140102 Fells cat
C 81	14.8	82.2	133073	14	AC154475	AC154475 Daerypus n
C 82	14.8	82.2	146845	14	CR847989	CR847989 Bos tauru
C 83	14.8	82.2	149982	14	AC148745	AC148745 Bos tauru
C 84	14.8	82.2	150221	14	AC144676	AC144676 Rattus no
C 85	14.8	82.2	162820	8	AL138765	AL138765 Human DNA
C 86	14.8	82.2	167712	14	AC023809	AC023809 Mus muscu
C 87	14.8	82.2	173244	5	AL292952	AL292952 Zebraphish
C 88	14.8	82.2	178009	7	AC115549	AC115549 Rattus no
C 89	14.8	82.2	180500	14	AY967407	AY967407 Enterobac
C 90	14.8	82.2	183056	5	BX927369	BX927369 Zebraphish
C 91	14.8	82.2	187325	14	AC142432	AC142432 Rattus no

92	14.8	82.2	194222	9	AC154368	AC154368 Mus muscu	c 165	14.4	80.0	110000	14	CT005265_05
c 93	14.8	82.2	194316	9	AC108844	AC108844 Mus muscu	166	14.4	80.0	110000	14	LMFLCHR26_4
c 94	14.8	82.2	204106	9	AL591113	AL591113 Mouse DNA	167	14.4	80.0	110000	14	LMFLCHR26_5
c 95	14.8	82.2	208273	14	AC134942	AC134942 Homo sapi	168	14.4	80.0	123255	8	AC006003
c 96	14.8	82.2	210476	14	AC164045	AC164045 Bos tauru	169	14.4	80.0	123073	3	AF210726
c 97	14.8	82.2	218320	14	AC128946	AC128946 Rattus no	170	14.4	80.0	130910	14	AC141688
c 98	14.8	82.2	223076	14	AC133526	AC133526 Rattus no	171	14.4	80.0	131217	13	AF528864
c 99	14.8	82.2	243210	14	AC136831	AC136831 Rattus no	172	14.4	80.0	133719	13	AF083501
c 100	14.8	82.2	244843	14	AC107162	AC107162 Rattus no	173	14.4	80.0	134426	13	IH1CG
c 101	14.8	82.2	246890	14	AC117302	AC117302 Rattus no	174	14.4	80.0	160855	14	AC011579
c 102	14.8	82.2	246979	14	AC094480	AC094480 Rattus no	175	14.4	80.0	161090	8	AC117415
c 103	14.8	82.2	254671	14	AC103573	AC103573 Rattus no	176	14.4	80.0	164270	13	AB049735
c 104	14.8	82.2	261992	14	AC119481	AC119481 Rattus no	177	14.4	80.0	164270	13	AB049735
c 105	14.8	82.2	283619	14	CR753821	CR753821 Danio rer	178	14.4	80.0	164681	9	AC101996
c 106	14.8	82.2	295712	14	AC120456	AC120456 Rattus no	179	14.4	80.0	167610	14	CR974453
c 107	14.8	82.2	299050	1	SC0939119	AL939119 Streptomy	180	14.4	80.0	168201	8	AC087675
c 108	14.8	82.2	306050	1	BX321858	BX321858 Nitrosomo	181	14.4	80.0	169824	14	AP001854
c 109	14.8	82.2	326653	8	AF011889	AF011889 Human Xq2	182	14.4	80.0	170880	14	AC145870
c 110	14.4	80.0	378	6	AX070757	AX070757 Sequence	183	14.4	80.0	170943	14	AC166591
c 111	14.4	80.0	386	10	BV394357	BV394357 S243P6109	184	14.4	80.0	184026	1	AP006619
c 112	14.4	80.0	655	15	AF162080	AF162080 Harpochyt	185	14.4	80.0	190669	9	AL590429
c 113	14.4	80.0	1748	5	BC090363	BC090363 Xenopus t	186	14.4	80.0	194319	14	AC161082
c 114	14.4	80.0	2000	6	AX509069	AX509069 Sequence	187	14.4	80.0	194520	14	AC148837
c 115	14.4	80.0	2000	6	HSX0280RF	X99270 H.sepiens X	188	14.4	80.0	204209	14	AC160523
c 116	14.4	80.0	2193	6	CQ868596	CQ868596 Sequence	189	14.4	80.0	204658	14	AC106579
c 117	14.4	80.0	2193	6	AX695681	AX695681 Sequence	190	14.4	80.0	205732	9	AC108439
c 118	14.4	80.0	2193	6	MM06140	AJ006140 Mus muscu	191	14.4	80.0	206543	14	AC164931
c 119	14.4	80.0	2238	4	RABNANCOT	M84020 Oryctolagus	192	14.4	80.0	208503	9	AC116730
c 120	14.4	80.0	2238	6	111726	111726 Sequence 1	193	14.4	80.0	211493	14	CR956635
c 121	14.4	80.0	2259	9	BC036558	BC036558 Mus muscu	194	14.4	80.0	211611	14	AC163008
c 122	14.4	80.0	2580	2	OCTBETUB	LI0111 Octopus dof	195	14.4	80.0	219065	14	AC137014
c 123	14.4	80.0	4028	4	OCATG1	X04751 Rabbit alph	196	14.4	80.0	237992	14	AC129733
c 124	14.4	80.0	4031	4	RABHABPT	M1113 Rabbit alph	197	14.4	80.0	252215	14	AC123125
c 125	14.4	80.0	6287	1	AF042281	AF042281 Ralstonia	198	14.4	80.0	273131	14	AC157235
c 126	14.4	80.0	10621	4	RABGLOBIN	M74142 Rabbit zeta	199	14.4	80.0	301443	1	AB012560
c 127	14.4	80.0	10845	1	AE003918	AE003918 Xylella f	200	14.4	80.0	312640	14	AC132785
c 128	14.4	80.0	12032	1	AE003956	AE003956 Xylella f	201	14.4	80.0	320050	1	BX248336
c 129	14.4	80.0	14506	1	AE005730	AE005730 Caulobact	202	14.4	80.0	327650	1	BX248337
c 130	14.4	80.0	27846	6	AX695680	AX695680 Sequence	203	14.4	80.0	339650	1	SC093108
c 131	14.4	80.0	35961	1	MLU15181	U15181 Mycobacteri	204	14.4	80.0	348450	1	MLBPRN4
c 132	14.4	80.0	35961	6	AR345370	AR345370 Sequence	205	14.4	80.0	349564	1	BX842574
c 133	14.4	80.0	36526	1	MSGY42	AD000005 Mycobacte	206	14.4	80.0	349564	1	BX842574
c 134	14.4	80.0	36620	6	AR534338	AR534338 Sequence	207	14.4	80.0	349640	1	BX572600
c 135	14.4	80.0	37474	6	AR534333	AR534333 Sequence	208	14.4	77.8	16	6	CS124146
c 136	14.4	80.0	37781	6	CQ868595	CQ868595 Sequence	209	14.4	77.8	17	6	AR052612
c 137	14.4	80.0	38519	6	AR534336	AR534336 Sequence	210	14.4	77.8	17	6	BD187525
c 138	14.4	80.0	44273	2	AY028171	AY028171 Leishmani	211	14.4	77.8	17	6	BD192461
c 139	14.4	80.0	44273	2	AY028171	AY028171 Leishmani	212	14.4	77.8	17	6	BD192462
c 140	14.4	80.0	79043	8	HSJAU9614	AJ009614 Homo sapi	213	14.4	77.8	17	6	AR630676
c 141	14.4	80.0	93754	14	AC138754	AC138754 Homo sapi	214	14.4	77.8	17	6	AR653969
c 142	14.4	80.0	97299	5	BX649451	BX649451 Zebrafish	215	14.4	77.8	17	6	AR653970
c 143	14.4	80.0	102212	14	CT005258	CT005258 (7 of	216	14.4	77.8	397	6	AR500612
c 144	14.4	80.0	102212	14	CT005258	CT005258 (7 of	217	14.4	77.8	397	6	AR500612
c 145	14.4	80.0	104016	15	AC004138	AC004138 Arabidops	218	14.4	77.8	481	8	HSX338552
c 146	14.4	80.0	104729	8	HS118B18	AL034344 Human DNA	219	14.4	77.8	575	6	AX150704
c 147	14.4	80.0	110000	1	AE000516	AE000516 (8 of	220	14.4	77.8	575	6	AX150704
c 148	14.4	80.0	110000	1	AE000516	AE000516 (10 o	221	14.4	77.8	660	1	PSHRBGAA
c 149	14.4	80.0	110000	1	AP006618	AP006618 (33 o	222	14.4	77.8	1269	1	AY220299
c 150	14.4	80.0	110000	1	AY596297	AY596297 Haloracul	223	14.4	77.8	1661	1	PAREGA
c 151	14.4	80.0	110000	1	AY596297	AY596297 (9 of	224	14.4	77.8	4317	6	CO802951
c 152	14.4	80.0	110000	1	CP000076	CP000076 (12 o	225	14.4	77.8	6276	6	CO614312
c 153	14.4	80.0	110000	2	AP006486	AP006486 (5 of	226	14.4	77.8	6658	1	AF932616
c 154	14.4	80.0	110000	14	CR954199	CR954199 (5 of	227	14.4	77.8	8997	2	AY485268
c 155	14.4	80.0	110000	14	CR954199	CR954199 (6 of	228	14.4	77.8	18105	14	AC017203
c 156	14.4	80.0	110000	14	CR954199	CR954199 (8 of	229	14.4	77.8	43081	7	AP001553
c 157	14.4	80.0	110000	14	CR954199	CR954199 (9 of	230	14.4	77.8	43155	7	AY954961
c 158	14.4	80.0	110000	14	CR954200	CR954200 (9 of	231	14.4	77.8	43576	6	AR540874
c 159	14.4	80.0	110000	14	CR954201	CR954201 (6 of	232	14.4	77.8	43594	6	BD245634
c 160	14.4	80.0	110000	14	CR954201	CR954201 (8 of	233	14.4	77.8	43594	6	BD245634
c 161	14.4	80.0	110000	14	CR954202	CR954202 (9 of	234	14.4	77.8	65851	14	AC124280
c 162	14.4	80.0	110000	14	CR954202	CR954202 (9 of	235	14.4	77.8	110000	1	CR955306_30
c 163	14.4	80.0	110000	14	CR954216	CR954216 Ostrycoc	236	14.4	77.8	110000	1	CR955306_31
c 164	14.4	80.0	110000	14	CT005258	CT005258 (6 of	237	14.4	77.8	110000	1	AE016853_30
							c 165	14.4	80.0	110000	14	CT005265_05
							c 166	14.4	80.0	110000	14	LMFLCHR26_4
							c 167	14.4	80.0	110000	14	LMFLCHR26_5
							c 168	14.4	80.0	123255	8	AC006003
							c 169	14.4	80.0	123073	3	AF210726
							c 170	14.4	80.0	130910	14	AC141688
							c 171	14.4	80.0	131217	13	AF528864
							c 172	14.4	80.0	133719	13	AF083501
							c 173	14.4	80.0	134426	13	IH1CG
							c 174	14.4	80.0	160855	14	AC011579
							c 175	14.4	80.0	161090	8	AC117415
							c 176	14.4	80.0	164270	13	AB049735
							c 177	14.4	80.0	164270	13	AB049735
							c 178	14.4	80.0	164681	9	AC101996
							c 179	14.4	80.0	167610	14	CR974453
							c 180	14.4	80.0	168201	8	AC087675
							c 181	14.4	80.0	169824	14	AP001854
							c 182	14.4	80.0	170880	14	AC145870
							c 183	14.4	80.0	170943	14	AC166591
							c 184	14.4	80.0	184026	1	AP006619
							c 185	14.4	80.0	190669	9	AL590429
							c 186	14.4	80.0	194319	14	AC161082
							c 187	14.4	80.0	194520	14	AC148837
							c 188	14.4	80.0	204209	14	AC160523
							c 189	14.4	80.0	204658	14	AC106579
							c 190	14.4	80.0	205732	9	AC108439
							c 191	14.4	80.0	206543	14	AC164931
							c 192	14.4	80.0	208503	9	AC116730
							c 193	14.4	80.0	211493	14	CR956635
							c 194	14.4	80.0	211611	14	AC163008
							c 195	14.4	80.0	219065	14	AC137014
							c 196	14.4	80.0	237992	14	AC129733
							c 197	14.4	80.0	252215	14	AC123125
							c 198	14.4	80.0	273131	14	AC157235
							c 199	14.4	80.0	301443	1	AB012560
							c 200	14.4	80.0	312640	14	AC132785
							c 201	14.4	80.0	320050	1	BX248336
							c 202	14.4	80.0	327650	1	BX248337
							c 203	14.4	80.0	339650	1	SC093108
							c 204	14.4	80.0	348450	1	MLBPRN4
							c 205	14.4	80.0	349564	1	BX842574
							c 206	14.4	80.0	349564	1	BX842574
							c 207	14.4	80.0	349640	1	BX572600
							c 208	14.4	77.8	16	6	CS124146
</												



C 238	14	77.8	110000	1	CP000030 10	Continuation (11 o	311	13.8	76.7	259	2	AY572592
C 239	14	77.8	110000	1	CP000075_02	Continuation (3 of	312	13.8	76.7	259	2	AY572593
C 240	14	77.8	110000	1	CP000075_70	Continuation (21 o	313	13.8	76.7	259	2	AY572597
C 241	14	77.8	110000	15	AP008209_230	Continuation (231	314	13.8	76.7	259	2	AY572599
C 242	14	77.8	113685	15	AC135557	AC135557 Oryza sat	315	13.8	76.7	259	2	AY572600
C 243	14	77.8	119773	14	AC155464	AC155464 Zea mays	316	13.8	76.7	259	2	AY572601
C 244	14	77.8	129014	8	AC004916	AC004916 Homo sapi	317	13.8	76.7	259	2	AY572602
C 245	14	77.8	131995	13	OP075930	UTS930 Oryza puen	318	13.8	76.7	259	2	AY502798
C 246	14	77.8	137304	8	AC005627	AC005627 Homo sapi	319	13.8	76.7	335	6	AB518080
C 247	14	77.8	141703	8	AL360269	AL360269 Human DNA	320	13.8	76.7	353	6	AB583985
C 248	14	77.8	142538	15	AC135227	AC135227 Oryza sat	321	13.8	76.7	364	6	BD026494
C 249	14	77.8	156251	14	AC107325	AC107325 Drosophila	322	13.8	76.7	364	6	AX886884
C 250	14	77.8	161371	14	AC096972	AC096972 Homo sapi	323	13.8	76.7	417	1	KX041962
C 251	14	77.8	168103	14	AC149635	AC149635 Pan trogl	324	13.8	76.7	426	1	AF214552
C 252	14	77.8	168959	14	AC141841	AC141841 Apis mell	325	13.8	76.7	435	15	AF349712
C 253	14	77.8	169818	14	AC155502	AC155502 Zea mays	326	13.8	76.7	466	3	AF432646
C 254	14	77.8	170523	8	AP002387	AP002387 Homo sapi	327	13.8	76.7	491	3	AY144235
C 255	14	77.8	171415	14	AP002771	AP002771 Homo sapi	328	13.8	76.7	491	3	AY144251
C 256	14	77.8	171976	8	AC150278	AC150278 Pan trogl	329	13.8	76.7	491	3	AY144257
C 257	14	77.8	174133	8	AC093183	AC093183 Homo sapi	330	13.8	76.7	491	3	AY144259
C 258	14	77.8	176875	8	AC018638	AC018638 Homo sapi	331	13.8	76.7	491	3	AY144263
C 259	14	77.8	183541	8	AL606534	AL606534 Human DNA	332	13.8	76.7	494	3	AY144264
C 260	14	77.8	183948	8	AC009376	AC009376 Drosophila	333	13.8	76.7	494	3	DO080950
C 261	14	77.8	188138	8	AC147478	AC147478 Pan trogl	334	13.8	76.7	505	3	AF432645
C 262	14	77.8	203635	8	AC148310	AC148310 Pan trogl	335	13.8	76.7	505	3	AY145578
C 263	14	77.8	235814	14	AC106156	AC106156 Rattus no	336	13.8	76.7	523	6	AB520752
C 264	14	77.8	240438	14	AC152285	AC152285 Bos tauru	337	13.8	76.7	540	15	AF629423
C 265	14	77.8	244139	14	AC162214	AC162214 Bos tauru	338	13.8	76.7	555	6	CQ731328
C 266	14	77.8	305312	1	AB003516	AB003516 Drosophila	339	13.8	76.7	574	15	AF230899
C 267	14	77.8	349970	1	BX571659	BX571659 Wolinella	340	13.8	76.7	576	15	RCR277911
C 268	13.8	76.7	24	6	BD093109	BD093109 Novel pol	341	13.8	76.7	590	3	AY596155
C 269	13.8	76.7	24	6	AB584503	AB584503 Sequence	342	13.8	76.7	597	3	AY187599
C 270	13.8	76.7	24	6	BD010808	BD010808 Novel pol	343	13.8	76.7	600	6	AB505374
C 271	13.8	76.7	100	6	AX992565	AX992565 Sequence	344	13.8	76.7	633	10	BV3341081
C 272	13.8	76.7	147	9	MUSIGHOP	M30556 Mouse Ig re	345	13.8	76.7	636	3	AY988976
C 273	13.8	76.7	184	10	AB165303	AB165303 Bos tauru	346	13.8	76.7	637	10	BV079092
C 274	13.8	76.7	255	2	AY572579	AY572579 Toxoplasma	347	13.8	76.7	654	10	BV043921
C 275	13.8	76.7	255	2	AY572594	AY572594 Toxoplasma	348	13.8	76.7	672	3	AY534199
C 276	13.8	76.7	257	2	AY572562	AY572562 Toxoplasma	349	13.8	76.7	684	15	AY061657
C 277	13.8	76.7	257	2	AY572565	AY572565 Toxoplasma	350	13.8	76.7	686	3	AY988952
C 278	13.8	76.7	257	2	AY572566	AY572566 Toxoplasma	351	13.8	76.7	688	15	AY750161
C 279	13.8	76.7	257	2	AY572567	AY572567 Toxoplasma	352	13.8	76.7	696	8	HSN323652
C 280	13.8	76.7	257	2	AY572568	AY572568 Toxoplasma	353	13.8	76.7	698	3	AY988969
C 281	13.8	76.7	257	2	AY572569	AY572569 Toxoplasma	354	13.8	76.7	699	15	AF418620
C 282	13.8	76.7	257	2	AY572571	AY572571 Toxoplasma	355	13.8	76.7	701	15	AF418619
C 283	13.8	76.7	257	2	AY572572	AY572572 Toxoplasma	356	13.8	76.7	708	15	AY061712
C 284	13.8	76.7	257	2	AY572573	AY572573 Toxoplasma	357	13.8	76.7	721	15	AY061673
C 285	13.8	76.7	257	2	AY572574	AY572574 Toxoplasma	358	13.8	76.7	726	6	AX100248
C 286	13.8	76.7	257	2	AY572575	AY572575 Toxoplasma	359	13.8	76.7	730	8	HSN32965
C 287	13.8	76.7	257	2	AY572576	AY572576 Toxoplasma	360	13.8	76.7	733	10	BV603787
C 288	13.8	76.7	257	2	AY572577	AY572577 Toxoplasma	361	13.8	76.7	733	15	RCR277910
C 289	13.8	76.7	257	2	AY572578	AY572578 Toxoplasma	362	13.8	76.7	742	3	AY989140
C 290	13.8	76.7	257	2	AY572580	AY572580 Toxoplasma	363	13.8	76.7	743	3	BC002873
C 291	13.8	76.7	257	2	AY572581	AY572581 Toxoplasma	364	13.8	76.7	744	15	AY061717
C 292	13.8	76.7	257	2	AY572582	AY572582 Toxoplasma	365	13.8	76.7	762	3	AY917642
C 293	13.8	76.7	257	2	AY572583	AY572583 Toxoplasma	366	13.8	76.7	762	10	BV018264
C 294	13.8	76.7	257	2	AY572585	AY572585 Toxoplasma	367	13.8	76.7	832	3	AT795718
C 295	13.8	76.7	257	2	AY572588	AY572588 Toxoplasma	368	13.8	76.7	875	4	SHPLZM3A
C 296	13.8	76.7	257	2	AY572590	AY572590 Toxoplasma	369	13.8	76.7	875	4	SHPLZM4A
C 297	13.8	76.7	257	2	AY572591	AY572591 Toxoplasma	370	13.8	76.7	875	4	SHPLZM4B
C 298	13.8	76.7	257	2	AY572595	AY572595 Toxoplasma	371	13.8	76.7	881	4	SHPLZM2A
C 299	13.8	76.7	257	2	AY572596	AY572596 Toxoplasma	372	13.8	76.7	891	4	BOVLSZ1B
C 300	13.8	76.7	257	2	AY572598	AY572598 Toxoplasma	373	13.8	76.7	906	4	BOVLSZ1A
C 301	13.8	76.7	257	2	AY572603	AY572603 Toxoplasma	374	13.8	76.7	981	5	AF161603
C 302	13.8	76.7	257	2	AY572604	AY572604 Toxoplasma	375	13.8	76.7	991	8	AF263921
C 303	13.8	76.7	257	2	DO009075	DO009075 Toxoplasma	376	13.8	76.7	1006	1	BRSODB
C 304	13.8	76.7	259	2	AY572563	AY572563 Toxoplasma	377	13.8	76.7	1006	11	AF339037
C 305	13.8	76.7	259	2	AY572564	AY572564 Toxoplasma	378	13.8	76.7	1066	15	AF346915
C 306	13.8	76.7	259	2	AY572570	AY572570 Toxoplasma	379	13.8	76.7	1087	5	BX933774
C 307	13.8	76.7	259	2	AY572584	AY572584 Toxoplasma	380	13.8	76.7	1087	5	AY228360
C 308	13.8	76.7	259	2	AY572586	AY572586 Toxoplasma	381	13.8	76.7	1090	15	FMO252962
C 309	13.8	76.7	259	2	AY572587	AY572587 Toxoplasma	382	13.8	76.7	1115	2	BD252095
C 310	13.8	76.7	259	2	AY572589	AY572589 Toxoplasma	383	13.8	76.7	1118	6	BD252095

C 384	13.8	76.7	1236	6	AR628236	Sequence	C 457	13.8	76.7	14384	1	D90705	D90705 Bactericla
C 385	13.8	76.7	1242	4	OP24672	Ochotona	C 458	13.8	76.7	15116	14	AC009579_4	Continuation (5 of
C 386	13.8	76.7	1248	1	AF127006	Becherich	C 459	13.8	76.7	15782	6	AR619699	AR619699 Sequence
C 387	13.8	76.7	1248	1	AF127007	Becherich	C 460	13.8	76.7	16325	14	AC015144	AC015144 Drosophila
C 388	13.8	76.7	1259	15	AR335443	Russula	C 461	13.8	76.7	17062	6	CO590729	CO590729 Sequence
C 389	13.8	76.7	1278	3	AM072427	Uncultured	C 462	13.8	76.7	18657	1	D90704	D90704 Bactericla
C 390	13.8	76.7	1283	3	MABRRM	Marine Buba	C 463	13.8	76.7	20334	8	AE001764	AE001764 Thermotog
C 391	13.8	76.7	1289	6	AX040114	Sequence	C 464	13.8	76.7	20704	1	CR383702	CR383702 Human DNA
C 392	13.8	76.7	1291	2	PS125260	Polysiph	C 465	13.8	76.7	21846	1	AB079515	AB079515 Agrobacteri
C 393	13.8	76.7	1298	15	AY228350	Rusnelli	C 466	13.8	76.7	24045	1	AB070941	AB070941 Streptomy
C 394	13.8	76.7	1322	1	AY515123	Bartonell	C 467	13.8	76.7	25617	1	AF170880	AF170880 Streptomy
C 395	13.8	76.7	1338	6	CO614079	Sequence	C 468	13.8	76.7	25617	6	AY027812	AY027812 Sequence
C 396	13.8	76.7	1370	2	AY973624	Caudospo	C 469	13.8	76.7	29000	8	AY027838	AY027838 Homo sapi
C 397	13.8	76.7	1374	2	AF132544	Wetleeria	C 470	13.8	76.7	33443	14	AC014332	AC014332 Drosophila
C 398	13.8	76.7	1375	2	AY090069	Polysiph	C 471	13.8	76.7	35984	8	AC153806	AC153806 Homo sapi
C 399	13.8	76.7	1414	6	AR520687	Sequence	C 472	13.8	76.7	36123	2	AC093553	AC093553 Leishman
C 400	13.8	76.7	1451	1	AF328417	Seccarot	C 473	13.8	76.7	37941	1	ADPC2361	ADPC2361 Amycolato
C 401	13.8	76.7	1457	1	AF328417	Seccarot	C 474	13.8	76.7	39261	14	AC020271	AC020271 Drosophila
C 402	13.8	76.7	1450	3	AY555803	Uncultured	C 475	13.8	76.7	41924	14	AC087403	AC087403 Homo sapi
C 403	13.8	76.7	1505	3	AY955088	Uncultured	C 476	13.8	76.7	42569	8	HS305C8	HS305C8 Homo sapi
C 404	13.8	76.7	1521	5	BX935504	Gallus ga	C 477	13.8	76.7	50000	6	AX081173	AX081173 Sequence
C 405	13.8	76.7	1705	5	CR942584	Xenopus t	C 478	13.8	76.7	53178	6	CO363755	CO363755 Sequence
C 406	13.8	76.7	1753	6	CO412938	Sequence	C 479	13.8	76.7	60298	8	AL359508	AL359508 Homo sapi
C 407	13.8	76.7	1808	5	BC063354	Xenopus t	C 480	13.8	76.7	63934	8	AL359618	AL359618 Homo sapi
C 408	13.8	76.7	1937	6	CO595464	Sequence	C 481	13.8	76.7	65978	14	AL596184	AL596184 Homo sapi
C 409	13.8	76.7	1949	2	AF322044	Malawimon	C 482	13.8	76.7	66669	14	AME16952	AME16952 Homo sapi
C 410	13.8	76.7	2001	5	AF322044	Gallus ga	C 483	13.8	76.7	68842	14	AC026915	AC026915 Homo sapi
C 411	13.8	76.7	2019	6	AR627784	Sequence	C 484	13.8	76.7	71496	14	AC090722	AC090722 Homo sapi
C 412	13.8	76.7	2098	6	AR183233	Sequence	C 485	13.8	76.7	71639	14	AC162785	AC162785 Homo sapi
C 413	13.8	76.7	2170	8	AB168562	Macaca fa	C 486	13.8	76.7	71507	14	AC014585	AC014585 Drosophila
C 414	13.8	76.7	2283	4	DQ119288	Bos tauru	C 487	13.8	76.7	76297	15	CR954201_10	CR954201_10 Continuation (11 o
C 415	13.8	76.7	2323	1	AF329831	Haemophil	C 488	13.8	76.7	79575	15	AP006357	AP006357 Locus cor
C 416	13.8	76.7	2354	2	AF025768	Erwinia c	C 489	13.8	76.7	80530	14	AC165498	AC165498 Homo sapi
C 417	13.8	76.7	2524	2	TOXUTBBA	M20025 T. gondii	C 490	13.8	76.7	82383	8	AL591623	AL591623 Homo sapi
C 418	13.8	76.7	3291	6	CO590720	Sequence	C 491	13.8	76.7	84392	14	AC013393	AC013393 Homo sapi
C 419	13.8	76.7	3295	2	AF125444	Cenornath	C 492	13.8	76.7	87286	14	AC014436	AC014436 Drosophila
C 420	13.8	76.7	3297	2	AY210836	Peripatus	C 493	13.8	76.7	87790	14	AL359498	AL359498 Homo sapi
C 421	13.8	76.7	3506	2	AY310313	Erlichia	C 494	13.8	76.7	91840	8	AC112254	AC112254 Homo sapi
C 422	13.8	76.7	4140	6	AR505330	Sequence	C 495	13.8	76.7	92375	15	AP003905	AP003905 Oryza sat
C 423	13.8	76.7	4347	15	AF015276	Volvox ca	C 496	13.8	76.7	92509	8	AL646086	AL646086 Ralstonia
C 424	13.8	76.7	4625	2	AY278365	Giardia i	C 497	13.8	76.7	94212	8	AP000246	AP000246 Homo sapi
C 425	13.8	76.7	5973	6	CO595463	Sequence	C 498	13.8	76.7	97477	15	AC148965	AC148965 Homo sapi
C 426	13.8	76.7	6497	6	CO614078	Sequence	C 499	13.8	76.7	100000	8	AP000207	AP000207 Homo sapi
C 427	13.8	76.7	6816	6	AR175747	Sequence	C 500	13.8	76.7	101027	8	AC023160	AC023160 Homo sapi
C 428	13.8	76.7	6816	6	AR352550	Sequence	C 501	13.8	76.7	101509	14	AC027353	AC027353 Homo sapi
C 429	13.8	76.7	6816	6	AR656259	Sequence	C 502	13.8	76.7	101586	14	AP007489	AP007489 Locus cor
C 430	13.8	76.7	6855	6	AR175748	Sequence	C 503	13.8	76.7	105956	8	AC074136	AC074136 Homo sapi
C 431	13.8	76.7	6855	6	AR352551	Sequence	C 504	13.8	76.7	106707	14	AC013314	AC013314 Homo sapi
C 432	13.8	76.7	6855	6	AR656260	Sequence	C 505	13.8	76.7	107356	8	AC113606	AC113606 Homo sapi
C 433	13.8	76.7	6866	6	AR453043	Sequence	C 506	13.8	76.7	109766	14	AC117712	AC117712 Mus muscu
C 434	13.8	76.7	6866	6	AX281155	Sequence	C 507	13.8	76.7	110000	1	AE005174_07	AE005174_07 Continuation (8 of
C 435	13.8	76.7	6866	6	AX345569	Sequence	C 508	13.8	76.7	110000	1	AE005674_06	AE005674_06 Continuation (7 of
C 436	13.8	76.7	7382	9	MUSACGRCA	Mus musculu	C 509	13.8	76.7	110000	1	CR555306_19	CR555306_19 Continuation (20 o
C 437	13.8	76.7	7382	15	AF176575	Emeticell	C 510	13.8	76.7	110000	1	CR555306_20	CR555306_20 Continuation (21 o
C 438	13.8	76.7	7919	13	HPV10	Human papill	C 511	13.8	76.7	110000	1	U00096_06	U00096_06 Continuation (7 of
C 439	13.8	76.7	8346	6	AX323713	Sequence	C 512	13.8	76.7	110000	1	AE013598_29	AE013598_29 Continuation (30 o
C 440	13.8	76.7	9336	15	AF178850	Aspergill	C 513	13.8	76.7	110000	1	AE013598_30	AE013598_30 Continuation (31 o
C 441	13.8	76.7	9336	15	AF546148	Streptomy	C 514	13.8	76.7	110000	1	AE016822_21	AE016822_21 Continuation (22 o
C 442	13.8	76.7	9556	6	AR619587	Sequence	C 515	13.8	76.7	110000	1	AE016853_16	AE016853_16 Continuation (17 o
C 443	13.8	76.7	9626	6	AR619587	Sequence	C 516	13.8	76.7	110000	1	AE016853_17	AE016853_17 Continuation (18 o
C 444	13.8	76.7	10016	6	CO595466	Sequence	C 517	13.8	76.7	110000	1	AE017283_16	AE017283_16 Continuation (17 o
C 445	13.8	76.7	10464	1	AE004634	Pseudomon	C 518	13.8	76.7	110000	1	AP008231_16	AP008231_16 Continuation (18 of
C 446	13.8	76.7	10557	8	HUMIMP	Sequence	C 519	13.8	76.7	110000	1	BA000007_07	BA000007_07 Continuation (9 of
C 447	13.8	76.7	11033	1	AE007311	Sinorhizo	C 520	13.8	76.7	110000	1	BA000012_08	BA000012_08 Continuation (9 of
C 448	13.8	76.7	11853	1	AF110737	Sequence	C 521	13.8	76.7	110000	1	BA000030_26	BA000030_26 Continuation (27 o
C 449	13.8	76.7	11857	1	AE009025	Agrobacte	C 522	13.8	76.7	110000	1	BA000030_32	BA000030_32 Continuation (53 o
C 450	13.8	76.7	11953	8	AL646019	Human DNA	C 523	13.8	76.7	110000	1	BA000030_72	BA000030_72 Continuation (73 o
C 451	13.8	76.7	12092	4	BOVLYSOZMA	Sequence	C 524	13.8	76.7	110000	1	BA000030_87	BA000030_87 Continuation (88 o
C 452	13.8	76.7	12222	4	BOVLYSOZMA	Sequence	C 525	13.8	76.7	110000	1	BA000045_30	BA000045_30 Continuation (31 o
C 453	13.8	76.7	13319	1	AE010317	Methanopy	C 526	13.8	76.7	110000	1	BX571965_01	BX571965_01 Continuation (23 o
C 454	13.8	76.7	13428	1	AE010315	Sequence	C 527	13.8	76.7	110000	1	BX50851_22	Continuation (23 o
C 455	13.8	76.7	14180	6	CO595469	Sequence	C 528	13.8	76.7	110000	1	CP000026_11	Continuation (12 o
C 456	13.8	76.7	14359	1	AE001221	Trepinema	C 529	13.8	76.7	110000	1	CP000031_00	Continuation (12 o

530	13.8	76.7	110000	CP000050	Xanthomon	603	13.8	76.7	130226	9	AC162239	AC162239	Homo sapi
531	13.8	76.7	110000	Continuation	(16 o	604	13.8	76.7	134151	8	AC104336	AC104336	Homo sapi
532	13.8	76.7	110000	Continuation	(2 of	605	13.8	76.7	134431	13	AY186265	AY186265	Bovine pa
533	13.8	76.7	110000	CP000079	Leishmani	606	13.8	76.7	136742	1	EC082598	EC082598	Escherichia
534	13.8	76.7	110000	CP000080	03	607	13.8	76.7	137029	15	AC099040	AC099040	Oryza sat
535	13.8	76.7	110000	CP000080	03	608	13.8	76.7	138533	8	AC011357	AC011357	Homo sapi
536	13.8	76.7	110000	Continuation	(4 of	609	13.8	76.7	138716	15	AC091234	AC091234	Oryza sat
537	13.8	76.7	110000	Continuation	(16 o	610	13.8	76.7	140551	15	AC137822	AC137822	Medicago
538	13.8	76.7	110000	Continuation	(4 of	611	13.8	76.7	141925	15	AC139870	AC139870	Felis cat
539	13.8	76.7	110000	Continuation	(2 of	612	13.8	76.7	142248	15	AC107315	AC107315	Genomic s
540	13.8	76.7	110000	AC115542	1	613	13.8	76.7	142696	14	AC143051	AC143051	Human DNA
541	13.8	76.7	110000	AC020850	0	614	13.8	76.7	143060	8	AL129247	AL129247	Human DNA
542	13.8	76.7	110000	AL137126	0	615	13.8	76.7	143093	15	OS200026	OS200026	Oryza sat
543	13.8	76.7	110000	AL137126	1	616	13.8	76.7	144644	15	AP006155	AP006155	Oryza sat
544	13.8	76.7	110000	AP006499	00	617	13.8	76.7	145709	8	AP069288	AP069288	Homo sapi
545	13.8	76.7	110000	CR954199	08	618	13.8	76.7	146548	14	AC120336	AC120336	Homo sapi
546	13.8	76.7	110000	CR954200	07	619	13.8	76.7	147075	14	AC139166	AC139166	Rattus no
547	13.8	76.7	110000	CR954201	09	620	13.8	76.7	148055	14	AC128178	AC128178	Rattus no
548	13.8	76.7	110000	CR954202	06	621	13.8	76.7	148120	14	AC141805	AC141805	Apis mell
549	13.8	76.7	110000	CR954204	07	622	13.8	76.7	148373	15	AC134348	AC134348	Oryza sat
550	13.8	76.7	110000	CR954210	0	623	13.8	76.7	148845	8	HS111441	HS111441	Oryza sat
551	13.8	76.7	110000	CR954212	0	624	13.8	76.7	149118	9	AC116520	AC116520	Equine he
552	13.8	76.7	110000	CR954216	2	625	13.8	76.7	149430	13	AY646052	AY646052	Equine he
553	13.8	76.7	110000	CT005244	0	626	13.8	76.7	149854	9	AC117225	AC117225	Mus muscu
554	13.8	76.7	110000	CT005252	0	627	13.8	76.7	150224	13	AY665713	AY665713	Mus muscu
555	13.8	76.7	110000	CT005253	0	628	13.8	76.7	150228	14	AC091994	AC091994	Equine he
556	13.8	76.7	110000	CT005253	2	629	13.8	76.7	150299	14	AC157251	AC157251	Equine he
557	13.8	76.7	110000	CT005255	1	630	13.8	76.7	150317	15	AP005739	AP005739	Oryza sat
558	13.8	76.7	110000	CT005262	6	631	13.8	76.7	150849	15	AC141935	AC141935	Rattus no
559	13.8	76.7	110000	CT005266	05	632	13.8	76.7	151182	8	AL611942	AL611942	Homo sapi
560	13.8	76.7	110000	CT005270	01	633	13.8	76.7	151262	9	AL192868	AL192868	Mouse DNA
561	13.8	76.7	110000	CT005272	10	634	13.8	76.7	151684	14	AC146305	AC146305	Homo sapi
562	13.8	76.7	110000	LMF1CHR32	17	635	13.8	76.7	151796	14	AC096695	AC096695	Homo sapi
563	13.8	76.7	110000	AP008214	032	636	13.8	76.7	151806	15	AP002093	AP002093	Oryza sat
564	13.8	76.7	110000	AP008215	052	637	13.8	76.7	151933	14	AC016118	AC016118	Homo sapi
565	13.8	76.7	110000	AP008216	065	638	13.8	76.7	152681	2	AC099008	AC099008	Drosophil
566	13.8	76.7	110000	AP008216	220	639	13.8	76.7	154986	14	AC141766	AC141766	Apis mell
567	13.8	76.7	110000	CR382129	19	640	13.8	76.7	155030	14	AC141807	AC141807	Apis mell
568	13.8	76.7	110000	AE017341	05	641	13.8	76.7	155942	14	AC136691	AC136691	Homo sapi
569	13.8	76.7	110000	AE017345	03	642	13.8	76.7	156411	14	AC141335	AC141335	Rattus no
570	13.8	76.7	110000	AP008207	060	643	13.8	76.7	157686	8	BS000110	BS000110	Pan trogl
571	13.8	76.7	110000	AP008208	061	644	13.8	76.7	157974	14	AC121070	AC121070	Sus scrofa
572	13.8	76.7	110000	AP008209	092	645	13.8	76.7	158033	8	AC018926	AC018926	Homo sapi
573	13.8	76.7	110000	AP008209	195	646	13.8	76.7	158508	14	AC063934	AC063934	Homo sapi
574	13.8	76.7	110000	AP008209	246	647	13.8	76.7	158740	2	AC159452	AC159452	Trypanoso
575	13.8	76.7	110000	AP008210	066	648	13.8	76.7	159122	14	AC025556	AC025556	Homo sapi
576	13.8	76.7	110000	AP008210	238	649	13.8	76.7	159857	8	AC018767	AC018767	Homo sapi
577	13.8	76.7	110000	AP008210	289	650	13.8	76.7	159893	8	AC0116903	AC0116903	Homo sapi
578	13.8	76.7	110000	AP008211	157	651	13.8	76.7	160129	15	OS0000082	OS0000082	Oryza sat
579	13.8	76.7	110000	AP008211	170	652	13.8	76.7	160298	14	AC067818	AC067818	Homo sapi
580	13.8	76.7	111590	HSJ08L15		653	13.8	76.7	160718	14	AC067839	AC067839	Homo sapi
581	13.8	76.7	1115643	HS1104B15		654	13.8	76.7	160813	14	AC155412	AC155412	Zea mays
582	13.8	76.7	1115643	AL663070	Human DNA	655	13.8	76.7	160817	2	AC008316	AC008316	Drosophil
583	13.8	76.7	1115767	AC012310	Homo sapi	656	13.8	76.7	161139	8	AC132812	AC132812	Homo sapi
584	13.8	76.7	1116326	BX323467	Zebrafish	657	13.8	76.7	161150	9	AC133503	AC133503	Mus muscu
585	13.8	76.7	1117951	AL1931803	Human DNA	658	13.8	76.7	161598	14	AC127513	AC127513	Homo sapi
586	13.8	76.7	1118158	AL607028	Homo sapi	659	13.8	76.7	164396	14	AC024651	AC024651	Homo sapi
587	13.8	76.7	111827	AC148516	Human DNA	660	13.8	76.7	164793	14	AC165143	AC165143	Mus muscu
588	13.8	76.7	1118741	AC005319	Human chr	661	13.8	76.7	164971	2	AC016792	AC016792	Drosophil
589	13.8	76.7	1118935	AC005368	Homo sapi	662	13.8	76.7	165510	14	AC022677	AC022677	Homo sapi
590	13.8	76.7	1119573	AC104706	Oryza sat	663	13.8	76.7	165768	14	AC023517	AC023517	Homo sapi
591	13.8	76.7	1119923	AC013943	Drosophil	664	13.8	76.7	165878	14	AC133153	AC133153	Mus muscu
592	13.8	76.7	120173	AC137630	Homo sapi	665	13.8	76.7	167886	14	AC166031	AC166031	Sus scrofa
593	13.8	76.7	121515	AC155380	Zea mays	666	13.8	76.7	168153	14	AC131519	AC131519	Rattus no
594	13.8	76.7	121774	AC084059	Mus muscu	667	13.8	76.7	168208	9	AC153550	AC153550	Mus muscu
595	13.8	76.7	122288	AL1539384	Human DNA	668	13.8	76.7	168613	8	AC091133	AC091133	Homo sapi
596	13.8	76.7	123795	AP007824	Lotus cor	669	13.8	76.7	168659	14	AL1539883	AL1539883	Homo sapi
597	13.8	76.7	124025	AL160169	Human DNA	670	13.8	76.7	168668	14	AC152918	AC152918	Zea mays
598	13.8	76.7	124571	AL450384	Human DNA	671	13.8	76.7	168731	8	AC007012	AC007012	Homo sapi
599	13.8	76.7	124666	AC155390	Zea mays	672	13.8	76.7	169770	14	AC141443	AC141443	Apis mell
600	13.8	76.7	125032	AC115286	Homo sapi	673	13.8	76.7	169985	8	CNS05T50	CNS05T50	Human chr
601	13.8	76.7	126945	AC162433	Atelerix	674	13.8	76.7	170914	2	AC010843	AC010843	Drosophil
602	13.8	76.7	127374	AC107675	Mus muscu	675	13.8	76.7	171062	14	AC022066	AC022066	Homo sapi

676	13.8	76.7	171289	8	AC096887	Homo sapi	AC096887 Homo sapi	c 749	13.8	76.7	201229	9	AC114578	AC114578 Mus muscu
677	13.8	76.7	172474	14	AC146950	Zea mays	AC146950 Zea mays	c 750	13.8	76.7	201309	14	AC159518	AC159518 Bos tauru
678	13.8	76.7	172481	1	AC102240	Mus muscu	AC102240 Mus muscu	c 751	13.8	76.7	201673	1	AL591544	AL591544 Mouse DNA
c 679	13.8	76.7	173071	14	AC166012	Oryctolag	AC166012 Oryctolag	c 752	13.8	76.7	203450	14	AP002009	AP002009 Homo sapi
680	13.8	76.7	173509	2	AC010031	Drosophi1	AC010031 Drosophi1	c 753	13.8	76.7	204855	9	AC133100	AC133100 Mus muscu
681	13.8	76.7	173608	8	AC107993	Homo sapi	AC107993 Homo sapi	c 754	13.8	76.7	204915	14	AC163150	AC163150 Bos tauru
682	13.8	76.7	173708	15	AC022251	Homo sapi	AC022251 Homo sapi	c 755	13.8	76.7	205516	8	AC008781	AC008781 Homo sapi
c 683	13.8	76.7	175153	15	AP003977	Oryza sat	AP003977 Oryza sat	c 756	13.8	76.7	205600	14	AC166865	AC166865 Oryctolag
c 684	13.8	76.7	175630	14	AC150234	Papio anu	AC150234 Papio anu	c 757	13.8	76.7	205642	14	AC007898	AC007898 Homo sapi
685	13.8	76.7	175896	2	AC150407	Branchios	AC150407 Branchios	c 758	13.8	76.7	206182	9	AC107720	AC107720 Mus muscu
c 686	13.8	76.7	175986	8	AC150407	Branchios	AC150407 Branchios	c 759	13.8	76.7	206624	14	AC109838	AC109838 Rattus no
687	13.8	76.7	175946	8	AC110000	Homo sapi	AC110000 Homo sapi	c 760	13.8	76.7	207439	13	AT509253	AT509253 Ostrfeld h
c 688	13.8	76.7	176349	15	AP002092	Oryza sat	AP002092 Oryza sat	c 761	13.8	76.7	210972	14	AC090288	AC090288 Mus muscu
c 689	13.8	76.7	176479	14	AC135631	Homo sapi	AC135631 Homo sapi	c 762	13.8	76.7	211115	9	AC147568	AC147568 Homo sapi
c 690	13.8	76.7	176526	14	AP001192	Homo sapi	AP001192 Homo sapi	c 763	13.8	76.7	211335	8	AC112640	AC112640 Homo sapi
691	13.8	76.7	176615	15	OS0000035	Al66595	AL66595 Oryza sat	c 764	13.8	76.7	211680	9	AL603682	AL603682 Mouse DNA
c 692	13.8	76.7	177028	2	AC008315	Drosophi1	AC008315 Drosophi1	c 765	13.8	76.7	212973	9	AL683847	AL683847 Mouse DNA
c 693	13.8	76.7	177364	9	AC156274	Mus muscu	AC156274 Mus muscu	c 766	13.8	76.7	214031	14	AC134141	AC134141 Rattus no
694	13.8	76.7	177883	14	AC046159	Homo sapi	AC046159 Homo sapi	c 767	13.8	76.7	214343	14	AC151563	AC151563 Mus muscu
695	13.8	76.7	178292	14	AC120830	Rattus no	AC120830 Rattus no	c 768	13.8	76.7	214445	9	AC110556	AC110556 Mus muscu
696	13.8	76.7	178315	8	AC122688	Homo sapi	AC122688 Homo sapi	c 769	13.8	76.7	214893	14	AC151972	AC151972 Mus muscu
697	13.8	76.7	178488	14	AC151856	Papio ham	AC151856 Papio ham	c 770	13.8	76.7	215050	1	AL646057	AL646057 Ralstonia
698	13.8	76.7	180426	15	AC134342	Oryza sat	AC134342 Oryza sat	c 771	13.8	76.7	215441	8	AP002800	AP002800 Homo sapi
c 699	13.8	76.7	180888	8	AC007491	Homo sapi	AC007491 Homo sapi	c 772	13.8	76.7	215647	14	AC068591	AC068591 Homo sapi
c 700	13.8	76.7	182213	14	AC136685	Homo sapi	AC136685 Homo sapi	c 773	13.8	76.7	215955	14	AC133815	AC133815 Rattus no
c 701	13.8	76.7	182452	14	AC120832	Rattus no	AC120832 Rattus no	c 774	13.8	76.7	216041	14	AC112524	AC112524 Drosophi1
c 702	13.8	76.7	182660	2	AC159404	Trypanoso	AC159404 Trypanoso	c 775	13.8	76.7	216266	9	AC073797	AC073797 Mus muscu
c 703	13.8	76.7	182847	14	AC126229	Papio anu	AC126229 Papio anu	c 776	13.8	76.7	216807	9	AC079681	AC079681 Mus muscu
c 704	13.8	76.7	183039	14	AC025288	Homo sapi	AC025288 Homo sapi	c 777	13.8	76.7	217265	9	AC145294	AC145294 Mus muscu
c 705	13.8	76.7	183151	2	AC007851	Drosophi1	AC007851 Drosophi1	c 778	13.8	76.7	218631	14	AC109532	AC109532 Rattus no
706	13.8	76.7	183347	15	CN8077P7	AL713930	AL713930 Oryza sat	c 779	13.8	76.7	218747	9	AC093339	AC093339 Mus muscu
707	13.8	76.7	183607	14	AC121176	Rattus no	AC121176 Rattus no	c 780	13.8	76.7	218880	14	AC150974	AC150974 Bos tauru
708	13.8	76.7	184010	14	AC150025	Papio anu	AC150025 Papio anu	c 781	13.8	76.7	220193	14	AC135719	AC135719 Homo sapi
709	13.8	76.7	184140	8	AC090630	Homo sapi	AC090630 Homo sapi	c 782	13.8	76.7	220679	2	AB003704	AB003704 Drosophi1
710	13.8	76.7	184855	9	AC124713	Mus muscu	AC124713 Mus muscu	c 783	13.8	76.7	221217	14	CR388081	CR388081 Datto rer
c 711	13.8	76.7	185655	9	MM0296304	Mus muscu	AJ296304 Mus muscu	c 784	13.8	76.7	221668	14	AC160265	AC160265 Bos tauru
c 712	13.8	76.7	185810	2	AC010995	Drosophi1	AC010995 Drosophi1	c 785	13.8	76.7	221873	14	AC128173	AC128173 Rattus no
713	13.8	76.7	186000	8	AC023892	Homo sapi	AC023892 Homo sapi	c 786	13.8	76.7	222853	14	AC160699	AC160699 Bos tauru
c 714	13.8	76.7	186000	14	AC153265	Bos tauru	AC153265 Bos tauru	c 787	13.8	76.7	223528	14	CR769780	CR769780 Datto rer
715	13.8	76.7	186217	9	AC122310	Mus muscu	AC122310 Mus muscu	c 788	13.8	76.7	223726	9	AL626807	AL626807 Mouse DNA
c 716	13.8	76.7	186350	14	AC022688	Homo sapi	AC022688 Homo sapi	c 789	13.8	76.7	223872	9	AC147221	AC147221 Mus muscu
c 717	13.8	76.7	186848	14	AC145556	Mus muscu	AC145556 Mus muscu	c 790	13.8	76.7	223854	9	AL606962	AL606962 Mouse DNA
c 718	13.8	76.7	187347	14	AC025880	Homo sapi	AC025880 Homo sapi	c 791	13.8	76.7	223987	14	AC147800	AC147800 Mus muscu
c 719	13.8	76.7	187707	15	AC077693	Oryza sat	AC077693 Oryza sat	c 792	13.8	76.7	224445	14	AC098492	AC098492 Rattus no
720	13.8	76.7	187958	14	AC135578	Rattus no	AC135578 Rattus no	c 793	13.8	76.7	225233	14	AC127530	AC127530 Homo sapi
721	13.8	76.7	188679	14	AC023121	Homo sapi	AC023121 Homo sapi	c 794	13.8	76.7	225534	14	AC114529	AC114529 Rattus no
c 722	13.8	76.7	188834	9	AC098642	Genomic B	AC098642 Genomic B	c 795	13.8	76.7	227313	14	AC161389	AC161389 Bos tauru
c 723	13.8	76.7	189055	14	AC073716	Mus muscu	AC073716 Mus muscu	c 796	13.8	76.7	228458	9	AC158782	AC158782 Mus muscu
c 724	13.8	76.7	190000	14	AC004479	Homo sapi	AC004479 Homo sapi	c 797	13.8	76.7	228718	14	AC103423	AC103423 Rattus no
725	13.8	76.7	190310	14	AC023225	Homo sapi	AC023225 Homo sapi	c 798	13.8	76.7	229092	14	AC160332	AC160332 Bos tauru
c 726	13.8	76.7	190390	2	AC005720	Drosophi1	AC005720 Drosophi1	c 799	13.8	76.7	229231	14	AC115211	AC115211 Rattus no
c 727	13.8	76.7	191557	8	AC008506	Homo sapi	AC008506 Homo sapi	c 800	13.8	76.7	229899	14	AC141728	AC141728 Rattus no
c 728	13.8	76.7	192735	14	AC150719	Callithr1	AC150719 Callithr1	c 801	13.8	76.7	230138	13	AP232689	AP232689 Rat cycom
c 729	13.8	76.7	193083	9	AC124584	Mus muscu	AC124584 Mus muscu	c 802	13.8	76.7	230854	14	AC165155	AC165155 Mus muscu
730	13.8	76.7	193953	14	AC149623	Papio anu	AC149623 Papio anu	c 803	13.8	76.7	231435	14	AC130519	AC130519 Rattus no
c 731	13.8	76.7	194024	14	AC166992	Mus muscu	AC166992 Mus muscu	c 804	13.8	76.7	231716	9	AC135409	AC135409 Rattus no
c 732	13.8	76.7	194474	14	AC137536	Bos scroff	AC137536 Bos scroff	c 805	13.8	76.7	236685	14	AC084744	AC084744 Mus muscu
c 733	13.8	76.7	194810	14	AC150924	Sus tauru	AC150924 Sus tauru	c 806	13.8	76.7	236838	9	AC125451	AC125451 Mus muscu
734	13.8	76.7	194905	8	AC068896	Homo sapi	AC068896 Homo sapi	c 807	13.8	76.7	237341	14	AC094780	AC094780 Rattus no
735	13.8	76.7	194986	14	AC152015	Callithr1	AC152015 Callithr1	c 808	13.8	76.7	237877	14	AC095587	AC095587 Rattus no
736	13.8	76.7	195204	9	AC132956	Mus muscu	AC132956 Mus muscu	c 809	13.8	76.7	238323	2	AB003684	AB003684 Drosophi1
c 737	13.8	76.7	195904	9	AC125525	Mus muscu	AC125525 Mus muscu	c 810	13.8	76.7	238608	14	AC095637	AC095637 Rattus no
c 738	13.8	76.7	196315	5	AC149502	Xenopus t	AC149502 Xenopus t	c 811	13.8	76.7	239057	14	AC116637	AC116637 Rattus no
c 739	13.8	76.7	198050	1	AL646061	Ralstonia	AL646061 Ralstonia	c 812	13.8	76.7	239467	9	AC113395	AC113395 Mus muscu
740	13.8	76.7	198224	14	AC161090	Callithr1	AC161090 Callithr1	c 813	13.8	76.7	239625	14	AC111384	AC111384 Rattus no
741	13.8	76.7	198254	14	AC016049	Homo sapi	AC016049 Homo sapi	c 814	13.8	76.7	240325	14	AC120246	AC120246 Rattus no
c 742	13.8	76.7	199182	8	AC005562	Homo sapi	AC005562 Homo sapi	c 815	13.8	76.7	242112	9	AC122923	AC122923 Mus muscu
c 743	13.8	76.7	199583	9	AC110206	Mus muscu	AC110206 Mus muscu	c 816	13.8	76.7	242159	14	AC091567	AC091567 Homo sapi
744	13.8	76.7	199893	14	AC025529	Mus muscu	AC025529 Mus muscu	c 817	13.8	76.7	242322	8	AC099668	AC099668 Homo sapi
c 745	13.8	76.7	200452	8	AC015804	Homo sapi	AC015804 Homo sapi	c 818	13.8	76.7	243369	14	AC115514	AC115514 Rattus no
c 746	13.8	76.7	200503	9	AC123724	Mus muscu	AC123724 Mus muscu	c 819	13.8	76.7	244008	14	AC136692	AC136692 Homo sapi
747	13.8	76.7	200791	14	AC125507	Papio anu	AC125507 Papio anu	c 820	13.8	76.7	245651	14	AC125537	AC125537 Rattus no
c 748	13.8	76.7	200875	9	AC144942	Mus muscu	AC144942 Mus muscu	c 821	13.8	76.7	246779	14	AC095254	AC095254 Rattus no

822	13.8	76.7	250010	14	AC074027	AC074027 Mus muscu	C 895	13.4	74.4	525	2	AF509342	AF509342 Anopheles
823	13.8	76.7	250029	2	AE003559	AE003559 Drosophill	C 896	13.4	74.4	526	2	AF509349	AF509349 Anopheles
824	13.8	76.7	252427	14	AC111287	AC111287 Rattus no	C 897	13.4	74.4	526	2	AF172564	AF172564 Anopheles
825	13.8	76.7	253887	14	AC135126	AC135126 Rattus no	C 898	13.4	74.4	527	2	AF509350	AF509350 Anopheles
826	13.8	76.7	255578	14	AC099432	AC099432 Rattus no	C 899	13.4	74.4	527	2	AF365051	AF365051 Anopheles
827	13.8	76.7	255952	14	AL513473	AL513473 Homo sapi	C 900	13.4	74.4	530	2	AF509348	AF509348 Anopheles
828	13.8	76.7	256393	14	AC020870	AC020870 Mus muscu	C 901	13.4	74.4	530	2	AF172565	AF172565 Anopheles
829	13.8	76.7	256938	14	AC097368	AC097368 Rattus no	C 902	13.4	74.4	534	10	G44735	G44735 unc1079 CA
830	13.8	76.7	259210	14	AC073368	AC073368 Homo sapi	C 903	13.4	74.4	540	2	AF172566	AF172566 Anopheles
831	13.8	76.7	261024	1	AE017256	AE017256 Wolbachia	C 904	13.4	74.4	540	2	AF172567	AF172567 Anopheles
832	13.8	76.7	264964	14	AC152738	AC152738 Bos tauru	C 905	13.4	74.4	544	8	HEA342035	HEA342035 Homo sapi
833	13.8	76.7	265118	1	CNSPAX06	AX248288 Pyrococcu	C 906	13.4	74.4	563	6	AF617360	AF617360 Sequence
834	13.8	76.7	265118	6	AX041922	AX041922 Sequence	C 907	13.4	74.4	578	2	AF768540	AF768540 Anopheles
835	13.8	76.7	266114	14	AC103150	AC103150 Rattus no	C 908	13.4	74.4	578	2	AF768542	AF768542 Anopheles
836	13.8	76.7	268984	2	AE001274	AE001274 Leishmani	C 909	13.4	74.4	589	9	MMU23100	MMU23100 Mus musculu
837	13.8	76.7	279011	8	AE006467	AE006467 Homo sapi	C 910	13.4	74.4	597	2	AF691517	AF691517 Anopheles
838	13.8	76.7	282207	14	AC163583	AC163583 Bos tauru	C 911	13.4	74.4	597	2	AF691518	AF691518 Anopheles
839	13.8	76.7	286712	14	AC157079	AC157079 Bos tauru	C 912	13.4	74.4	597	2	AF691519	AF691519 Anopheles
840	13.8	76.7	287287	2	AE003816	AE003816 Drosophill	C 913	13.4	74.4	597	2	AF691520	AF691520 Anopheles
841	13.8	76.7	290029	1	AE016980	AE016980 Shigella	C 914	13.4	74.4	597	2	AF691521	AF691521 Anopheles
842	13.8	76.7	291262	14	AC156198	AC156198 Bos tauru	C 915	13.4	74.4	608	15	HCO492626	HCO492626 Haldina c
843	13.8	76.7	292409	5	BX530407	BX530407 Zebrafish	C 916	13.4	74.4	608	15	HCO492631	HCO492631 Haldina c
844	13.8	76.7	296756	2	AE003492	AE003492 Drosophill	C 917	13.4	74.4	618	2	AV049004	AV049004 Anopheles
845	13.8	76.7	300029	15	AE017121	AE017121 Oryza sat	C 918	13.4	74.4	652	10	BV353697	BV353697 Anopheles
846	13.8	76.7	300540	1	AE017154	AE017154 Haemophil	C 919	13.4	74.4	662	2	AF406615	AF406615 Anopheles
847	13.8	76.7	300883	14	AE016809	AE016809 Vibrio vu	C 920	13.4	74.4	663	2	AF469855	AF469855 Anopheles
848	13.8	76.7	302214	14	AC117305	AC117305 Rattus no	C 921	13.4	74.4	663	2	AF469856	AF469856 Anopheles
849	13.8	76.7	302228	15	AE017070	AE017070 Oryza sat	C 922	13.4	74.4	663	2	AF469857	AF469857 Anopheles
850	13.8	76.7	305584	1	AE016920	AE016920 Chromobac	C 923	13.4	74.4	663	2	AF469858	AF469858 Anopheles
851	13.8	76.7	306050	14	AC123202	AC123202 Rattus no	C 924	13.4	74.4	663	2	AF469859	AF469859 Anopheles
852	13.8	76.7	310059	14	AC152075	AC152075 Mus muscu	C 925	13.4	74.4	663	2	AF469860	AF469860 Anopheles
853	13.8	76.7	310550	9	SC0939113	AL939113 Streptomy	C 926	13.4	74.4	663	2	AF469861	AF469861 Anopheles
854	13.8	76.7	312488	9	AC139934	AC139934 Mus muscu	C 927	13.4	74.4	663	2	AF469862	AF469862 Anopheles
855	13.8	76.7	324250	1	BX251410	BX251410 Tropherym	C 928	13.4	74.4	663	2	AF469863	AF469863 Anopheles
856	13.8	76.7	324227	1	AE016852	AE016852 Tropherym	C 929	13.4	74.4	663	2	AF469864	AF469864 Anopheles
857	13.8	76.7	330026	14	AC160694	AC160694 Bos tauru	C 930	13.4	74.4	663	2	AF469865	AF469865 Anopheles
858	13.8	76.7	332252	14	AC130121	AC130121 Rattus no	C 931	13.4	74.4	663	2	AF469866	AF469866 Anopheles
859	13.8	76.7	337344	6	CQ869859	CQ869859 Sequence	C 932	13.4	74.4	663	2	AF469867	AF469867 Anopheles
860	13.8	76.7	340000	8	AP001710	AP001710 Homo sapi	C 933	13.4	74.4	663	2	AF469868	AF469868 Anopheles
861	13.8	76.7	340968	14	AC115312	AC115312 Rattus no	C 934	13.4	74.4	663	2	AF469869	AF469869 Anopheles
862	13.8	76.7	342833	14	AC142817	AC142817 Macaca mu	C 935	13.4	74.4	663	2	AF469870	AF469870 Anopheles
863	13.8	76.7	346274	1	BX640443	BX640443 Bordetell	C 936	13.4	74.4	663	2	AF469871	AF469871 Anopheles
864	13.8	76.7	348014	1	BX640430	BX640430 Bordetell	C 937	13.4	74.4	663	2	AF469872	AF469872 Anopheles
865	13.8	76.7	349672	1	BX640419	BX640419 Bordetell	C 938	13.4	74.4	663	2	AF469873	AF469873 Anopheles
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873	13.4	74.4	382	6	AR618448	AR618448 Sequence	C 946	13.4	74.4	663	2	AF469881	AF469881 Anopheles
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883	13.4	74.4	475	2	AY953515	AY953515 Anopheles	C 956	13.4	74.4	663	2	AF469891	AF469891 Anopheles
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c 997 13.4 74.4 663 2 AY662441
c 998 13.4 74.4 663 2 AY662442
c 999 13.4 74.4 663 2 AY662443
c1000 13.4 74.4 663 2 AY662444

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## ALIGNMENTS

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RESULT 1
LOCUS AR146348 18 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 60 from patent US 6218371.
ACCESSION AR146348
VERSION AR146348.1 GI:15109537
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kriegl,A.M. and Weiner,G.
TITLES Methods and products for stimulating the immune system using
JOURNAL immunotherapeutic oligonucleotides and cytokines
FEATURES
source Location/Qualifiers
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Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.8e+02;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
LOCUS AR154731 18 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 60 from patent US 6239116.
ACCESSION AR154731

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VERSION AR154731.1 GI:15122784
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kriegl,A.M. and Kline,J.N.
TITLES Immunostimulatory nucleic acid molecules
JOURNAL Patent: US 6239116-A 60 29-MAY-2001;
FEATURES
source Location/Qualifiers
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RESULT 3
LOCUS BD069939 18 bp DNA linear PAT 27-AUG-2002
DEFINITION Use of nucleic acids containing unmethylated CpG dinucleotide in
ACCESSION BD069939
VERSION BD069939.1 GI:22615542
KEYWORDS JP 2001513776-A/28.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schwartz,D.A. and Kriegl,A.M.
TITLES Use of nucleic acids containing unmethylated CpG dinucleotide in
JOURNAL the treatment of LPS-associated disorders
COMMENT Patent: JP 2001513776-A 28 04-SEP-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION
OS Artificial Sequence
PN JP 2001513776-A/28
PD 04-SEP-2001
PR 25-FEB-1998 JP 1998537810
PR 28-FEB-1997 US 60/039405
PI DAVID A SCHWARTZ,ARTHUR M KRIEG
PC A61K49/00,C07H21/02,C07H21/04,A01N43/04
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LOCUS BD205570 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Method of controlling hematopoiesis by using CpG oligonucleotide.
ACCESSION BD205570

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VERSION BD20570.1 GI:33015340  
KEYWORDS JP 2002514397-A/60.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Wagner, H. and Lipford, G.  
TITLE Method of controlling hematopoiesis by using CpG oligonucleotide  
JOURNAL Patent: JP 2002514397-A 60 21-MAY-2002;  
CORY PHARMACEUTICALS GMBH, CORY PHARMACEUTICALS GROUP INC

COMMENT  
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PD 21-MAY-2002  
PR 14-MAY-1999 JP 2000547969  
PI 60/085516, 02-FEB-1999 US 09/241653 PI  
PC C12N15/09, A61K31/70, A61K39/39, C07H21/04//A61K45/00, C12N15/00  
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Db 18 AGAGGGTCCGACGCGGTA 1

RESULT 5  
BD261112/c 18 bp DNA linear PAT 17-JUL-2003  
LOCUS Methods and products for stimulating the immune system using  
DEFINITION immunotherapeutic oligonucleotides and cytokines.  
ACCESSION BD261112.1 GI:33070882  
VERSION BD261112  
KEYWORDS JP 2002510644-A/60.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Kriegl, A.M. and Weiner, G.  
TITLE Methods and products for stimulating the immune system using  
JOURNAL immunotherapeutic oligonucleotides and cytokines  
PATENT: JP 2002510644-A 60 09-APR-2002;  
UNIVERSITY OF IOWA RESEARCH FOUNDATION  
OS Artificial Sequence  
PN JP 2002510644-A/60  
PD 09-APR-2002  
PR 02-APR-1999 JP 2000542030  
PI 60/080729  
PC ARTHUR M KRIEGL, GEORGE WEINER  
PC A61K38/00, A61K31/7088, A61K39/00, A61P15/00, A61P35/00, A61P37/04,  
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Db 18 AGAGGGTCCGACGCGGTA 1

RESULT 6  
BD267877/c 18 bp DNA linear PAT 17-JUL-2003  
LOCUS Methods for the prevention and treatment of parasitic infections  
DEFINITION and related diseases using CpG oligonucleotides.  
ACCESSION BD267877.1 GI:33077645  
VERSION BD267877  
KEYWORDS JP 2002513763-A/50.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Gramzinski, R.A., Kriegl, A.M., Davis, H.L. and Hoffman, S.L.  
TITLE Methods for the prevention and treatment of parasitic infections  
JOURNAL and related diseases using CpG oligonucleotides  
PATENT: JP 2002513763-A 50 14-MAY-2002;  
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INSTITUTE, UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY  
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PN JP 2002513763-A/50  
PD 14-MAY-2002  
PR 06-MAY-1999 JP 2000546780  
PI 60/084512  
PC ROBERT A GRAMZINSKI, ARTHUR M KRIEGL, HEATHER L DAVIS, STEPHEN L  
PI HOFFMAN  
PC A61K31/711, A61K9/127, A61K38/00, A61K38/22, A61K45/00, A61P31/00,  
PC A61P33/00//  
PC C12N15/09, A61K37/02, A61K37/24, C12N15/00  
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Db 18 AGAGGGTCCGACGCGGTA 1

RESULT 7  
AR222220/c 18 bp DNA linear PAT 26-SEP-2002  
LOCUS Sequence 54 from patent US 6429199.  
DEFINITION AR222220  
ACCESSION AR222220.1 GI:23329685  
VERSION AR222220.1  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Kriegl, A.M. and Hartmann, G.  
TITLE Immunostimulatory nucleic acid molecules for activating dendritic  
JOURNAL cells  
PATENT: US 6429199-A 54 06-AUG-2002;



FEATURES University of Iowa Research Foundation; Iowa City, IA  
 source Location/Qualifiers  
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 DEFINITION AR432481  
 ACCESSION AR432481.1 GI:40194816  
 VERSION  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 18)  
 AUTHORS Kriegl,A.M. and Wehner,G.  
 TITLE Method of treating cancer using immunostimulatory oligonucleotides  
 JOURNAL Patent: US 6653292-A 60 25-NOV-2003;  
 University of Iowa Research Foundation; Iowa City, IA  
 FEATURES source  
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RESULT 9  
 AX103812/c 18 bp DNA linear PAT 30-APR-2001  
 LOCUS Sequence 4 from Patent WO0122972.  
 DEFINITION AX103812  
 ACCESSION AX103812  
 VERSION AX103812.1 GI:13920009  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Kriegl,A.M., Schetter,C. and Vollmer,J.C.  
 TITLE Immunostimulatory nucleic acids  
 JOURNAL Patent: WO 0122972-A 4 05-APR-2001;  
 UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical  
 GmbH (DE)  
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RESULT 10  
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 LOCUS Sequence 56 from Patent WO0122972.  
 DEFINITION AX103864  
 ACCESSION AX103864  
 VERSION AX103864.1 GI:13920061  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Kriegl,A.M., Schetter,C. and Vollmer,J.C.  
 TITLE Immunostimulatory nucleic acids  
 JOURNAL Patent: WO 0122972-A 56 05-APR-2001;  
 UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical  
 GmbH (DE)  
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 LOCUS Sequence 485 from Patent WO0197843.  
 DEFINITION AX355457  
 ACCESSION AX355457  
 VERSION AX355457.1 GI:18620125  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.  
 REFERENCE 1  
 AUTHORS Wehner,G. and Hartmann,G.  
 TITLE Method for enhancing antibody-induced cell lysis and treating  
 JOURNAL Cancer  
 Patent: WO 0197843-A 485 27-DEC-2001;  
 UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)  
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RESULT 12  
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LOCUS AX455590 18 bp DNA linear PAT 06-JUL-2002  
DEFINITION Sequence 67 from Patent WO0222809.  
ACCESSION AX455590  
VERSION AX455590.1 GI:21714658  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
REFERENCE 1  
AUTHORS Bauer, S., Lipford, G. and Wagner, H.  
TITLE Process for high throughput screening of cps-based  
JOURNAL immuno-agonist/antagonist  
Patent: WO 0222809-A 67 21-MAR-2002;  
Coley Pharmaceutical GmbH (DE)  
FEATURES  
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RESULT 13  
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LOCUS AX546865  
DEFINITION Sequence 4 from Patent WO02053141.  
ACCESSION AX546865  
VERSION AX546865.1 GI:25812009  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
REFERENCE 1  
AUTHORS Bratzler, R.L.  
TITLE Inhibition of angiogenesis by nucleic acids  
JOURNAL Patent: WO 02053141-A 4 11-JUL-2002;  
Coley Pharmaceutical Group, Inc. (US)  
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Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14  
AX546917/c 18 bp DNA linear PAT 01-MAR-2003  
LOCUS AX546917  
DEFINITION Sequence 56 from Patent WO02053141.  
ACCESSION AX546917  
VERSION AX546917.1 GI:25812061  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
REFERENCE 1  
AUTHORS  
TITLE  
JOURNAL  
Patent: WO 02053141-A 56 11-JUL-2002;  
Coley Pharmaceutical Group, Inc. (US)  
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REFERENCE 1  
AUTHORS Bratzler, R.L.  
TITLE Inhibition of angiogenesis by nucleic acids  
JOURNAL Patent: WO 02053141-A 56 11-JUL-2002;  
Coley Pharmaceutical Group, Inc. (US)  
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Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15  
BD009122/c 18 bp DNA linear PAT 31-JAN-2002  
LOCUS BD009122  
DEFINITION Immunostimulatory nucleic acid molecules.  
ACCESSION BD009122  
VERSION BD009122.1 GI:18637495  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Krieg, A.M. and Kline, J.N.  
TITLE Immunostimulatory nucleic acid molecules  
JOURNAL Patent: JP 2001503267-A 74 13-MAR-2001;  
UNIVERSITY OF IOWA RESEARCH FOUNDATION  
COMMENT OS Artificial Sequence  
PN JP 2001503267-A/74  
PD 13-MAR-2001  
PF 30-OCT-1997 JP 1998520784  
PR 30-OCT-1996 US 08/738652  
PI ARTHUR M KRIEG, JOEL N KLINE  
PC C07H21/00, C07H21/02, C07H21/04, A61K31/175, A61K31/335, A61K31/47,  
PC A61K31/70  
CC  
FH  
FT  
Key Location/Qualifiers  
1..18  
/organism="Artificial Sequence".  
Location/Qualifiers  
1..18  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

ORIGIN  
Query Match 100.0%; Score 18; DB 6; Length 18;  
Best Local Similarity 88.9%; Pred. No. 4.8e+02;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGCAGCGGUA 18  
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18 AGAGGUGCGCAGCGGTA 1

RESULT 16  
AR052611/c 17 bp DNA linear PAT 29-SEP-1999  
LOCUS AR052611  
DEFINITION Sequence 9 from patent US 5831066.  
ACCESSION AR052611  
VERSION AR052611.1 GI:5975975  
KEYWORDS  
SOURCE  
Unknown.

ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Reed,J.C.  
TITLES Regulation of bcl-2 gene expression  
JOURNAL Patent: US 5831066-A 9 03-NOV-1998;  
FEATURES Location/Qualifiers  
source 1..17  
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ORIGIN  
Query Match 94.4%; Score 17; DB 6; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.5e+03;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GAGGGUCCGACGCGGUA 18  
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Db 17 GAGGGTCGACGCGGTA 1

RESULT 17  
BD187524 17 bp DNA linear PAT 17-JUL-2003  
LOCUS REGULATION OF bcl-2 GENE EXPRESSION.  
ACCESSION BD187524  
VERSION BD187524.1 GI:32997263  
KEYWORDS JP 2003026609-A/9.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Reed,J.C.  
TITLES REGULATION OF bcl-2 GENE EXPRESSION  
JOURNAL Patent: JP 2003026609-A 9 29-JAN-2003;  
AUTHORS John C REED  
FEATURES OS Artificial Sequence  
PN JP 2003026609-A/9  
PD 29-JAN-2003  
PF 19-JUN-2002 JP 2002178753  
PR 20-SEP-1993 US 08/124256  
PI John C Reed  
CC Description of Artificial Sequence: Designed DNA based on bcl-  
CC 2 gene Location/Qualifiers.  
FH Key Location/Qualifiers  
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/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

ORIGIN  
Query Match 94.4%; Score 17; DB 6; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.5e+03;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GAGGGUCCGACGCGGUA 18  
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Db 17 GAGGGTCGACGCGGTA 1

RESULT 18  
AR630675 17 bp DNA linear PAT 14-FEB-2005  
LOCUS AR630675  
DEFINITION Sequence 9 from patent US 6641541.  
ACCESSION AR630675  
VERSION AR630675.1 GI:59766403  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Reed,J.C.

TITLE Regulation of BCL-2 gene expression  
JOURNAL Patent: US 6841541-A 9 11-JAN-2005;  
AUTHORS The Trustees of the University of Pennsylvania; Philadelphia, PA  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 94.4%; Score 17; DB 6; Length 17;  
Best Local Similarity 88.2%; Pred. No. 1.5e+03;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GAGGGUCCGACGCGGUA 18  
|||||:|||||:|  
Db 17 GAGGGTCGACGCGGTA 1

RESULT 19  
AY207027 289 bp DNA linear BCT 17-MAR-2003  
LOCUS Acinetobacter sp. S429\_2 16S ribosomal RNA gene, partial sequence.  
DEFINITION AY207027  
ACCESSION AY207027.1 GI:29027585  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Acinetobacter sp. S429\_2  
Acinetobacter sp. S429\_2  
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
Moraxellaceae; Acinetobacter.  
REFERENCE 1 (bases 1 to 289)  
AUTHORS Vandroekhoven,K., Wattiau,P., De mot,R. and Springael,D.  
TITLES Acinetobacter sp. diversity in environmental samples assessed by an  
Acinetobacter 16S rDNA specific PCR-DGGE system  
JOURNAL Unpublished  
AUTHORS 2 (bases 1 to 289)  
Vandroekhoven,K., Wattiau,P., De mot,R. and Springael,D.  
Direct Submission  
Submitted (24-DEC-2002) Environmental Technology, Vito (Flemisch  
Institute for Technological Research), Boeretang 200, Mol 2400,  
Belgium  
FEATURES Location/Qualifiers  
source 1..289  
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Query Match 91.1%; Score 16.4; DB 1; Length 289;  
Best Local Similarity 83.3%; Pred. No. 1.9e+03;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db 110 AGAGGGTCGACGCGGTA 127

RESULT 20  
AX513690 32 bp DNA linear PAT 06-OCT-2002  
LOCUS AX513690  
DEFINITION Sequence 79 from Patent W00226757.  
ACCESSION AX513690  
VERSION AX513690.1 GI:23559810  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Kandimala,B.R., Zhao,Q., Yu,D. and Agrawal,S.  
TITLES Modulation of Immunostimulatory activity of Immunostimulatory

oligonucleotide analogs by positional chemical changes  
Patent: WO 0226757-A 79 04-APR-2002;

JOURNAL  
HYBRIDON, INC. (US)  
Location/Qualifiers

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ORIGIN

Query Match 88.9%; Score 16; DB 6; Length 32;  
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16 AGGGTGCACGCGGTA 1

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AX513691/c 32 bp DNA linear PAT 05-OCT-2002  
LOCUS AX513691  
DEFINITION Sequence 80 from Patent WO0226757.  
ACCESSION AX513691  
VERSION AX513691.1 GI:23559811  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.

REFERENCE  
1 Kandimalla, E.R., Zhao, Q., Yu, D. and Agrawal, S.  
Modulation of immunostimulatory activity of immunostimulatory  
oligonucleotide analogs by positional chemical changes  
Patent: WO 0226757-A 80 04-APR-2002;  
JOURNAL  
HYBRIDON, INC. (US)  
Location/Qualifiers

FEATURES  
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/note="3' linkage"  
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ORIGIN

Query Match 88.9%; Score 16; DB 6; Length 32;  
Best Local Similarity 87.5%; Pred. No. 4.3e+03;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGGGTGCACGCGGUA 18  
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Db 32 AGGGTGCACGCGGTA 17

RESULT 22  
AC138105/c 101451 bp DNA linear HTG 13-DEC-2002  
LOCUS AC138105  
DEFINITION Mus musculus clone RP23-114F22, LOW-PASS SEQUENCE SAMPLING.  
ACCESSION AC138105  
VERSION AC138105.1 GI:26665790  
KEYWORDS HTG; HTGS\_PHASE0.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Theria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS

1 (bases 1 to 101451)  
Birren, B., Nusbaum, C. and Lander, E.  
Mus musculus, clone RP23-114F22  
Unpublished  
2 (bases 1 to 101451)  
Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,  
Barra, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B.,  
Canarata, T., Chang, J., Chararo, B., Choepel, Y., Collymore, A.,  
Cook, A., Cooke, P., DeRellano, K., Dewar, K., Diaz, J. S., Dodge, S.,  
Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,  
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N.,  
Hagos, B., Horton, L., Hulme, M., Iliev, I., Johnson, R., Jones, C.,  
Kamat, A., Karatas, A., Kelle, C., Landers, T., Levine, R.,  
Lindblad-Toh, K., Liu, G., Maclean, C., MacDonald, P., Major, J.,  
Matthews, C., McCarthy, M., Melidiri, J., Menous, L., Mihova, T.,  
Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,  
Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,  
Peterson, K., Phukhang, P., Pierre, N., Raymond, C., Retta, R.,  
Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schnupack, R.,  
Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N.,  
Stojanovic, N., Talamas, J., Testaye, S., Theodore, J., Topham, K.,  
Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X.,  
Wyman, D., Young, G., Zainoun, J., Zemdek, L., Zimmer, A. and Zody, M.

TITLE  
JOURNAL  
COMMENT  
Submitted (13-DEC-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIRB  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence.submissions@genome.wi.mit.edu

Project Information  
Center project name: 114\_F\_22  
Center clone name: 114\_F\_22

NOTE: This record contains 78 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
1 1187: contig of 1187 bp in length  
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\* 2490: contig of 1203 bp in length  
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\* 2591 2590: contig of 1166 bp in length  
\* 3756: contig of 1166 bp in length  
\* 3757 3856: gap of 100 bp  
\* 3857 4942: contig of 1086 bp in length  
\* 4943 5042: gap of 100 bp  
\* 5043 6213: contig of 1171 bp in length  
\* 6214 6313: gap of 100 bp  
\* 6314 7531: contig of 1218 bp in length  
\* 7532 7531: gap of 100 bp  
\* 7532 8845: contig of 1214 bp in length  
\* 8846 8945: gap of 100 bp  
\* 8946 10075: contig of 1130 bp in length  
\* 10076 10175: gap of 100 bp  
\* 10176 11316: contig of 1141 bp in length  
\* 11317 11416: gap of 100 bp  
\* 11417 12599: contig of 1183 bp in length  
\* 12600 12699: gap of 100 bp  
\* 12700 13909: contig of 1210 bp in length  
\* 13910 14009: gap of 100 bp  
\* 14010 15320: contig of 1211 bp in length  
\* 15321 15320: gap of 100 bp

15321 16571: contig of 1251 bp in length  
\* 16572 16671: gap of 100 bp  
\* 16732 17839: contig of 1168 bp in length  
\* 17840 17939: gap of 100 bp  
\* 17940 19118: contig of 1179 bp in length  
\* 19119 19218: gap of 100 bp  
\* 19219 20438: contig of 1220 bp in length  
\* 20439 20538: gap of 100 bp  
\* 20539 21768: contig of 1230 bp in length  
\* 21769 21868: gap of 100 bp  
\* 21869 23075: contig of 1207 bp in length  
\* 23076 23175: gap of 100 bp  
\* 23176 24381: contig of 1206 bp in length  
\* 24382 24481: gap of 100 bp  
\* 24482 25689: contig of 1208 bp in length  
\* 25690 25790: gap of 100 bp  
\* 25790 26988: contig of 1199 bp in length  
\* 26989 27088: gap of 100 bp  
\* 27089 28249: contig of 1161 bp in length  
\* 28250 28349: gap of 100 bp  
\* 28350 29546: contig of 1197 bp in length  
\* 29547 30892: contig of 1246 bp in length  
\* 30893 30992: gap of 100 bp  
\* 30993 32185: contig of 1193 bp in length  
\* 32186 32285: gap of 100 bp  
\* 32286 33507: contig of 1222 bp in length  
\* 33508 33607: gap of 100 bp  
\* 33608 34851: contig of 1244 bp in length  
\* 34852 34951: gap of 100 bp  
\* 34952 36177: contig of 1226 bp in length  
\* 36178 36277: gap of 100 bp  
\* 36278 37514: contig of 1237 bp in length  
\* 37515 37614: gap of 100 bp  
\* 37615 38778: contig of 1164 bp in length  
\* 38779 38878: gap of 100 bp  
\* 38879 40134: contig of 1256 bp in length  
\* 40135 40234: gap of 100 bp  
\* 40235 41412: contig of 1178 bp in length  
\* 41413 41512: gap of 100 bp  
\* 41513 42727: contig of 1215 bp in length  
\* 42728 42827: gap of 100 bp  
\* 42828 44042: contig of 1215 bp in length  
\* 44043 44142: gap of 100 bp  
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\* 80956 82128: contig of 1173 bp in length  
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\* 83542 84760: contig of 1219 bp in length  
\* 84761 84860: gap of 100 bp  
\* 84861 86083: contig of 1223 bp in length  
\* 86084 86183: gap of 100 bp  
\* 86184 87401: contig of 1218 bp in length  
\* 87402 87501: gap of 100 bp  
\* 87502 88707: contig of 1206 bp in length  
\* 88708 88807: gap of 100 bp  
\* 88808 90003: contig of 1196 bp in length  
\* 90004 90103: gap of 100 bp  
\* 90104 91253: contig of 1150 bp in length  
\* 91254 91353: gap of 100 bp  
\* 91354 92484: contig of 1131 bp in length

Query Match 88.9% Score 16; DB 14; Length 101451;  
Best Local Similarity 87.5% Pred. No. 1.1e+03;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GAGGUGUCGACGCGGU 17  
DB 29716 GAGGUGUCGACGCGGT 29701

RESULT 23  
CT005253\_2  
WPCOMMENT

Sequence split into 7 fragments LOCUS CT005253 Accession CT005253

Fragment Name	Begin	End
CT005253_0	1	110000
CT005253_1	100001	210000
CT005253_2	200001	310000
CT005253_3	300001	410000
CT005253_4	400001	510000
CT005253_5	500001	610000
CT005253_6	600001	622648

Continuation (3 of 7) of CT005253 from base 200001 (CT005253 *Leishmania* major strain Frie

Query Match 88.9% Score 16; DB 14; Length 110000;  
Best Local Similarity 93.8% Pred. No. 1.1e+03;  
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGUCGACGCGG 16

Db 29363 AGAGGCTCCGACCGG 29378

# RESULT 24 AC021215/c LOCUS

AC021215 191504 bp DNA 1linear HTG 07-JUL-2000  
Homo sapiens chromosome 17 clone RP11-497H17, WORKING DRAFT

SEQUENCE, 30 unordered pieces.

AC021215 AC021215.4 GI:8570248

VERSION HTG: HTGS PHAS81, HTGS\_DRAFT.

KEYWORDS Homo sapiens (human)

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Homo.

1 (bases 1 to 191504)

Waterston, R.H.

The sequence of Homo sapiens clone

Unpublished

2 (bases 1 to 191504)

Waterston, R.H.

Direct Submission

Submitted (15-JAN-2000)

Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA

On Jun 17, 2000 this sequence version replaced gi:7232172.

COMMENT

----- Genome Center -----  
Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: http://genome.wustl.edu/gsc/index.shtml

Project Information

Center project name: H NH0497H17

Summary Statistics

Sequencing vector: MJ3; 88%

Chemistry: Dye-terminator Big Dye; 12% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 168128 bases at least Q40

Consensus quality: 175861 bases at least Q30

Consensus quality: 181010 bases at least Q20

Insert size: 193000; agarose-fp

Insert size: 188604; sum-of-contigs

Quality coverage: 3.80 in Q20 bases; agarose-fp

Quality coverage: 3.98 in Q20 bases; sum-of-contigs

-----

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 30 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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\* 12923 13022: gap of unknown length  
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60559..66583
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gap              /estimated_length=unknown
66584..66683
misc_feature      /estimated_length=unknown
66684..74323
/notes="assembly_name:Contig24"
gap              /estimated_length=unknown
74324..74423
misc_feature      /estimated_length=unknown
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Query Match      88.9%; Score 16; DB 14; Length 191504;
Best Local Similarity 87.5%; Pred. No. 9.8e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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RESULT 25
AF432629/c      544 bp      DNA      linear      ENV 03-MAY-2004
LOCUS      AF432629

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```

DEFINITION      Uncultured bacterium clone S52.30PG 16S ribosomal RNA gene, partial
sequence.
ACCESSION      AF432629
VERSION      AF432629.1 GI:27363039
KEYWORDS      ENV.
SOURCE      uncultured bacterium
ORGANISM      Bacteria; environmental samples.
REFERENCE      1 (bases 1 to 544)
AUTHORS      Chow,M.L., Radomski,C.C., McDermott,J.M., Davies,J. and
Axelrod,P.E.
TITLE      Molecular characterization of bacterial diversity in lodgepole pine
(Pinus contorta) rhizosphere soils from British Columbia forest
soils differing in disturbance and geographic source
JOURNAL      FEMS Microbiol. Ecol. 42, 347-357 (2002)
AUTHORS      Harris,J.K., Chow,M.L., Chittaranjan,S., Radomski,C.C.,
McDermott,J.M., Davies,J., Pace,N.R. and Axelrod,P.E.
TITLE      Expansion of the bacterial phylogenetic tree: Significant
survey-points for further mapping of bacterial diversity
JOURNAL      Unpublished
AUTHORS      3 (bases 1 to 544)
REFERENCE      Chow,M.L., Radomski,C.C., McDermott,J.M., Davies,J. and
Axelrod,P.E.
TITLE      Direct Submission
JOURNAL      Submitted (12-Oct-2001) BC Research Inc., 3650 Westbrook Mall,
Vancouver, BC V6S 2L2, Canada
FEATURES      Location/Qualifiers
source      1..544
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             /mol_type="genomic DNA"
             /db_xref="taxon:77133"
             /clone="S52.30PG"
             /environmental_sample
             /note="from lodgepole pine rhizosphere soil from the
British Columbia Ministry of Forests Long-Term Soil
Productivity (LTSP) installation near Prince George, BC,
Canada"
             <1..>544
             /product="16S ribosomal RNA"

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ORIGIN
Query Match      85.6%; Score 15.4; DB 3; Length 544;
Best Local Similarity 82.4%; Pred. No. 5.3e+03;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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CY      2 GAGGGTCCGACGCGGUA 18
DB      137 GAGGGTCCGACGCGGUA 121

RESULT 26
AY988985/c      625 bp      DNA      linear      ENV 02-MAY-2005
LOCUS      AY988985
DEFINITION      Uncultured soil bacterium clone LJA-6F04 16S ribosomal RNA gene,
partial sequence.
ACCESSION      AY988985
VERSION      AY988985.1 GI:62913134
KEYWORDS      ENV.
SOURCE      uncultured soil bacterium
ORGANISM      Bacteria; environmental samples.
REFERENCE      1 (bases 1 to 625)
AUTHORS      Schloos,P.D. and Handelsman,J.
TITLE      The last word: toward a sample based census of bacteria in soil
JOURNAL      Unpublished
AUTHORS      2 (bases 1 to 625)
REFERENCE      Schloos,P.D. and Handelsman,J.
TITLE      Direct Submission
JOURNAL      Submitted (29-MAR-2005) Department of Plant Pathology, University
of Wisconsin-Madison, 1630 Linden Drive, Madison, WI 53705, USA
FEATURES      Location/Qualifiers
source      1..625

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/organism="uncultured soil bacterium"  
/mol\_type="genomic DNA"  
/isolation\_source="soil"  
/db\_xref="taxon:164851"  
/clone="11A.6P04"  
/environmental\_sample  
/country="USA\_Aleaska"  
<1..>625  
/product="16S ribosomal RNA"

ORIGIN

Query Match 85.6%; Score 15.4; DB 3; Length 625;  
Best Local Similarity 82.4%; Pred. No. 5.2e+03;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGGUA 18  
|||||:|||||:|||||:  
119 GAGGGTCGTACGCGGTA 103

Db

RESULT 27  
DQ123679/c 849 bp DNA linear ENV 02-AUG-2005  
LOCUS  
DEFINITION Uncultured soil bacterium clone PAH-Bio-08 16S ribosomal RNA gene,  
partial sequence.  
ACCESSION DQ123679 GI:71384051  
VERSION  
KEYWORDS ENV.  
SOURCE uncultured soil bacterium  
ORGANISM uncultured soil bacterium  
REFERENCE 1 (bases 1 to 849)  
AUTHORS Singleton,D.R., Sangaiiah,R., Gold,A., Ball,L.M. and Aitken,M.D.  
TITLE 'Division of Labor' in the Bacterial Degradation of Polycyclic  
Aromatic Hydrocarbons in a Bioreactor Treating Contaminated Soil  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 849)  
AUTHORS Singleton,D.R., Sangaiiah,R., Gold,A., Ball,L.M. and Aitken,M.D.  
TITLE Direct Submission  
JOURNAL Submitted (11-JUL-2005) Environmental Sciences & Engineering,  
University of North Carolina, CB#7431, Chapel Hill, NC 27599, USA  
FEATURES  
source  
1..849  
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/mol\_type="genomic DNA"  
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/clone="PAH-Bio-08"  
/environmental\_sample  
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/product="16S ribosomal RNA"

ORIGIN

Query Match 85.6%; Score 15.4; DB 3; Length 849;  
Best Local Similarity 82.4%; Pred. No. 4.9e+03;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGGUA 18  
|||||:|||||:|||||:  
115 GAGGGTCGTACGCGGTA 99

Db

RESULT 28  
DQ123747/c 855 bp DNA linear ENV 02-AUG-2005  
LOCUS  
DEFINITION Uncultured soil bacterium clone PAH-Bio-87 16S ribosomal RNA gene,  
partial sequence.  
ACCESSION DQ123747 GI:71384119  
VERSION  
KEYWORDS ENV.  
SOURCE uncultured soil bacterium  
ORGANISM uncultured soil bacterium  
REFERENCE 1 (bases 1 to 855)  
AUTHORS Singleton,D.R., Sangaiiah,R., Gold,A., Ball,L.M. and Aitken,M.D.  
TITLE 'Division of Labor' in the Bacterial Degradation of Polycyclic  
Aromatic Hydrocarbons in a Bioreactor Treating Contaminated Soil  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 855)  
AUTHORS Singleton,D.R., Sangaiiah,R., Gold,A., Ball,L.M. and Aitken,M.D.  
TITLE Direct Submission  
JOURNAL Submitted (11-JUL-2005) Environmental Sciences & Engineering,  
University of North Carolina, CB#7431, Chapel Hill, NC 27599, USA  
FEATURES  
source  
1..855  
/organism="uncultured soil bacterium"  
/mol\_type="genomic DNA"  
/isolation\_source="PAH-contaminated soil"  
/db\_xref="taxon:164851"  
/clone="PAH-Bio-87"  
/environmental\_sample  
<1..>855  
/product="16S ribosomal RNA"

ORIGIN

Query Match 85.6%; Score 15.4; DB 3; Length 855;  
Best Local Similarity 82.4%; Pred. No. 4.9e+03;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGGUA 18  
|||||:|||||:|||||:  
115 GAGGGTCGTACGCGGTA 99

Db

1 (bases 1 to 855)  
AUTHORS Singleton,D.R., Sangaiiah,R., Gold,A., Ball,L.M. and Aitken,M.D.  
TITLE 'Division of Labor' in the Bacterial Degradation of Polycyclic  
Aromatic Hydrocarbons in a Bioreactor Treating Contaminated Soil  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 855)  
AUTHORS Singleton,D.R., Sangaiiah,R., Gold,A., Ball,L.M. and Aitken,M.D.  
TITLE Direct Submission  
JOURNAL Submitted (11-JUL-2005) Environmental Sciences & Engineering,  
University of North Carolina, CB#7431, Chapel Hill, NC 27599, USA  
FEATURES  
source  
1..855  
/organism="uncultured soil bacterium"  
/mol\_type="genomic DNA"  
/isolation\_source="PAH-contaminated soil"  
/db\_xref="taxon:164851"  
/clone="PAH-Bio-87"  
/environmental\_sample  
<1..>855  
/product="16S ribosomal RNA"

ORIGIN

Query Match 85.6%; Score 15.4; DB 3; Length 855;  
Best Local Similarity 82.4%; Pred. No. 4.9e+03;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGGUA 18  
|||||:|||||:|||||:  
115 GAGGGTCGTACGCGGTA 99

Db

RESULT 29  
RS0252692/c 1029 bp DNA linear ENV 18-AUG-2000  
LOCUS  
DEFINITION Rhizosphere soil bacterium clone RSC-II-71, 16S rRNA gene  
(partial).  
ACCESSION AJ252692  
VERSION AJ252692 GI:9857208  
KEYWORDS 16S ribosomal RNA; 16S rRNA gene.  
SOURCE rhizosphere soil bacterium RSC-II-71  
ORGANISM rhizosphere soil bacterium RSC-II-71  
REFERENCE 1  
AUTHORS Lukow,T.  
TITLE Vergleichende Charakterisierung der bakteriellen  
Rhizosphärenenzymeigenschaften transgener versus nicht-transgener  
Kartoffelpflanzen  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1029)  
AUTHORS Lukow,T.  
TITLE Direct Submission  
JOURNAL Submitted (16-AUG-1999) Lukow T., Biogeochemie, Max-Planck-Institut  
für terrestrische Mikrobiologie, Karl-von-Frisch-Strasse, 35043  
Marburg, GERMANY  
FEATURES  
source  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:102490"  
/clone="RSC-II-71"  
1..1029  
/gene="16S rRNA"  
<1..>1029  
/gene="16S rRNA"  
/product="16S ribosomal RNA"

ORIGIN

Query Match 85.6%; Score 15.4; DB 3; Length 1029;  
Best Local Similarity 82.4%; Pred. No. 4.8e+03;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGGUA 18  
|||||:|||||:|||||:  
115 GAGGGTCGTACGCGGTA 99

Db

Db 172 GAAGTCCGACCGCGTA 156

RESULT 30  
LOCUS AY102340/c  
DEFINITION uncultured bacterium clone a13154 16S ribosomal RNA gene, partial sequence.  
ACCESSION AY102340  
VERSION AY102340.1 GI:21322295  
KEYWORDS ENV.  
SOURCE uncultured bacterium  
ORGANISM Bacteria; environmental samples.  
REFERENCE 1 (bases 1 to 1330)  
AUTHORS Ellis, R.J., Morgan, P., Weightman, A.J. and Fry, J.C.  
TITLE Cultivation-Dependent and -Independent Approaches for Determining Bacterial Diversity in Heavy-Metal-Contaminated Soil  
JOURNAL Appl. Environ. Microbiol. 69 (6), 3223-3230 (2003)  
PUBMED 12788719  
REFERENCES 2 (bases 1 to 1330)  
AUTHORS Ellis, R.J., Morgan, P., Weightman, A.J. and Fry, J.C.  
TITLE Direct Submission  
JOURNAL Submitted (08-MAY-2002) Imperial College at Silwood Park, NERC Center for Population Biology, Ascot, Berks SL5 7PY, UK  
LOCATION/Qualifiers  
1. 1330  
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/environmental\_sample  
<1. >1330  
/product="16S ribosomal RNA"

ORIGIN

RNA

Query Match 85.6%; Score 15.4; DB 3; Length 1330;  
Best Local Similarity 82.4%; Pred. No. 4.6e+03;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGCGCGACCGCGTA 18  
||||:|||||  
Db 130 GAGGCTCGTACCGCGTA 114

RESULT 31  
LOCUS AY102345/c  
DEFINITION uncultured bacterium clone a13101 16S ribosomal RNA gene, partial sequence.  
ACCESSION AY102345  
VERSION AY102345.1 GI:21322300  
KEYWORDS ENV.  
SOURCE uncultured bacterium  
ORGANISM Bacteria; environmental samples.  
REFERENCE 1 (bases 1 to 1331)  
AUTHORS Ellis, R.J., Morgan, P., Weightman, A.J. and Fry, J.C.  
TITLE Cultivation-Dependent and -Independent Approaches for Determining Bacterial Diversity in Heavy-Metal-Contaminated Soil  
JOURNAL Appl. Environ. Microbiol. 69 (6), 3223-3230 (2003)  
PUBMED 12788719  
REFERENCES 2 (bases 1 to 1331)  
AUTHORS Ellis, R.J., Morgan, P., Weightman, A.J. and Fry, J.C.  
TITLE Direct Submission  
JOURNAL Submitted (08-MAY-2002) Imperial College at Silwood Park, NERC Center for Population Biology, Ascot, Berks SL5 7PY, UK  
LOCATION/Qualifiers  
1. 1331  
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/clone="a13101"

FEATURES  
source

ORIGIN

RNA

Query Match 85.6%; Score 15.4; DB 3; Length 1331;  
Best Local Similarity 82.4%; Pred. No. 4.6e+03;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGCGCGACCGCGTA 18  
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Db 131 GAGGCTCGTACCGCGTA 115

RESULT 32  
LOCUS BC082645/c  
DEFINITION Xenopus laevis hypothetical LOC494668, mRNA (cDNA clone MGC:81662 IMAGE:6864519), complete cds.  
ACCESSION BC082645  
VERSION BC082645.1 GI:52139140  
KEYWORDS MGC.  
SOURCE Xenopus laevis (African clawed frog)  
ORGANISM Xenopus laevis  
Xenopus laevis (African clawed frog)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus; Xenopus.  
REFERENCE 1 (bases 1 to 1871)  
AUTHORS Klein, S.L., Strausberg, R.L., Wagner, L., Pontius, J., Clifton, S.W. and Richardson, P.  
TITLE Genetic and genomic tools for Xenopus research: The NIH Xenopus Initiative  
JOURNAL Dev. Dyn. 225 (4), 384-391 (2002)  
PUBMED 12454917  
REFERENCES 2 (bases 1 to 1871)  
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altchul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marisina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Tishiyuki, S., Abramson, R.D., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hilly, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywicki, M.I., Stalaka, U., Smalins, D.E., Scherch, A., Schein, J.B., Jones, S.J. and Marra, M.A.  
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
PUBMED 12477932  
REFERENCES 3 (bases 1 to 1871)  
AUTHORS Klein, S. and Gerhard, D.S.  
TITLE Direct Submission  
JOURNAL Submitted (15-SEP-2004) National Institutes of Health, Xenopus Gene Collection (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD 20892-7510, USA  
NIH-MGC Project  
Contract: XGC help desk  
Email: ggc@bcrc.mcgill.nh.gov  
Tissue Procurement: Martha Rebbeck, Steven L. Klein, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Genome Sequence Centre,  
BC Cancer Agency, Vancouver, BC, Canada  
info@bcgsc.bc.ca

REMARK  
COMMENT

Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Odi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Lilia Prabh, Paraneh Saeedi, JR Santos, Angelique Scherch, Ursula Skalska, Duane Smalish, Jeff Stott, Miranda Tsai, George Yang, Jacque Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNLT at: <http://image.llnl.gov>  
Series: IRK Plate: 159 Row: 1 Column: 20  
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

## FEATURES

source

1.1871  
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/mol\_type="mRNA"  
/db\_xref="taxon:8355"  
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/clone\_lib="NICHD\_XGC\_Emb1"  
/lab\_host="DH10B"  
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RCYRCGKEGHWKCEPLDQWALELCEPEYPPSPDPYKPRSAVRYAIVKQVFD  
BEERSIVYQRYRVPSSYDAIILERRVNALPGASTISYERLIDSPFYERHLLPP  
POLPSYTYRERSPIRSSASSSMETRYTERRLSPILRSPAPDPRCRSDSYERVO  
YF"

## CDS

## gene

## ORIGIN

Query Match 85.6%; Score 15.4; DB 5; Length 1871;  
Best Local Similarity 88.2%; Pred. No. 4.3e+03;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGATCGCAGCGGGA 18  
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DB 872 GAGGCGCCGACGCGGA 856

RESULT 33  
BC073203/c 2394 bp mRNA 1linear VRT 03-AUG-2004  
LOCUS  
DEFINITION  
IMAGE:5156366, complete cds.

ACCESSION  
BC073203  
VERSION  
BC073203.1  
KEYWORDS  
MGC.  
SOURCE  
Xenopus laevis (African clawed frog)  
Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
Xenopodinae; Xenopus; Xenopus.  
1 (bases 1 to 2394)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
12454917  
Klein, S.L., Strauberg, R.L., Wagner, L., Pontius, J., Clifton, S.W.  
and Richardson, P.  
Genetic and genomic tools for Xenopus research: The NIH Xenopus  
Initiative  
Dev. Dyn. 225 (4), 384-391 (2002)

## REFERENCE

AUTHORS

2 (bases 1 to 2394)  
Strauberg, R.L., Feinold, E.A., Grouse, L.H., Derge, J.G.,  
Klausner, R.D., Collins, P.S., Wagner, L., Sherman, C.M., Schuler, G.D.,  
Altschuler, S.F., Zeeberg, B., Butow, K.H., Schaefer, C.F., Bhat, N.K.,  
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P.,  
Ditchenko, L., Marusik, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Stapleton, M., Soares, M.B., Donald, M.F., Casavant, T.L.,  
Scheer, T.B., Brownstein, M.J., Udell, T.B., Tothlyki, S.,  
Carinci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
Abramson, R.D., Mullany, S.V., Bosak, S.A., McSwan, P.J.,  
McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hui, S.W.,  
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
Pahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,  
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
Bonifard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalish, D.E.,  
Scherch, A., Schein, J.R., Jones, S.J. and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
3 (bases 1 to 2394)  
Klein, S. and Gerhardt, D.S.  
Direct Submission  
Submitted (14-JUN-2004) National Institutes of Health, Xenopus Gene  
Collection (XGC), National Institute of Child Health and Human  
Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD  
20892-7510, USA  
NIH-MGC Project  
Contact: XGC help desk  
Email: [xgc@bbsrc.ox.ac.uk](mailto:xgc@bbsrc.ox.ac.uk)  
Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLT)  
DNA Sequencing by: Genome Sequence Centre,  
BC Cancer Agency, Vancouver, BC, Canada  
info@bcsc.bc.ca

## REMARK

COMMENT

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/ILNLT at: <http://image.llnl.gov>  
Series: IRK Plate: 153 Row: 1 Column: 1  
This clone was selected for full length sequencing because it  
passed the following selection criteria: Hexamer frequency ORF  
analysis, Similarity but not identity to protein.

## FEATURES

source

1.2394  
/organism="Xenopus laevis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8355"  
/clone="MGC:80472 IMAGE:5156366"  
/tissue\_type="Embryo, stage 10"  
/clone\_lib="NICHD\_XGC\_Emb1"  
/lab\_host="DH10B"  
/note="Vector: pCMV-SPORT6"  
1.2394  
/gene="MGC80472"  
/db\_xref="GeneID:44116"  
554.1564  
/gene="MGC80472"  
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/protein\_id="AAH73203.1"  
/db\_xref="GI:49255990"



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Query Match      85.6%; Score 15.4; DB 2; Length 132418;
Best Local Similarity   82.4%; Pred. No. 2.1e+03;
Matches    14; Conservative     2; Mismatches    1; Indels    0; Gaps    0;

Db              2690 GAAGGTGACGCCGGTA 2706

Qy             2 GAGGATUGCACC GGCGUA 18
               |||||:|||||::|
LOCUS          AC159420                      142479 bp DNA linear INV 02-APR-2005
DEFINITION     Trypanosoma brucei chromosome 8 clone RPCI93-26A17, complete sequence.
ACCESSION      AC159420
VERSION        AC159420.1 GI:62175571
KEYWORDS       HTG.
SOURCE         Trypanosoma brucei
ORGANISM       Eukaryote; Euglenozoa; Kinetoplastida; Trypanosomatidae;
REFERENCE      1 (bases 1 to 142479)
AUTHORS        Ghedin,B., Blandin,G., Bartholomeu,D., Caler,E., Haas,B., Hamrick,L., Shalim,J., Hou,L., Djikeng,A., Feldblum,T., Hostetler,J., Johnson,J., Jones,K., Koo,H.L., Larkin,C., Pai,G., Peterson,J., Khalak,H.G., Salzberg,S., Simpson,A.J., Tallon,L., Van Aken,S., Wanless,D., White,O., Wortman,J., Fraser,C.M. and El-Sayed,N.M.A.
COMMENT        Unpublished
                2 (bases 1 to 142479)
                Haas,B., Blandin,G. and El-Sayed,N.
                Direct Submission
                Submitted (02-APR-2005) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, nelsayed@tigr.org
                BAC clone RPCI93-26A17 from Trypanosoma brucei chromosome 8. Putative protein coding regions (>30 codons) were predicted by combining the output of the gene finding algorithm GLIMMER with similarity data and manual annotation of open reading frames. Further refinement of gene models (additions, deletions and alterations to boundary coordinates) were done manually based on detailed comparisons with the T. cruzi and L. major genomes. Genes on BACs were assigned a systematic name based on the chromosome and the BAC from which they originated (e.g. Tb03.27P10.410). Gene products were assigned a putative function when they shared significant similarity with experimentally characterized gene products or when they contained functionally known protein domains. Gene products were labelled either "hypothetical protein", or "hypothetical protein, conserved" in the case of products showing significant similarity with proteins or domains of unknown function from other organisms. Gene products of unknown function with predicted orthologs in Trypanosoma cruzi and Leishmania major genomes were automatically classified as conserved proteins. Short predicted coding sequences (less than 150 codons) with no additional evidence of coding potential were labelled "hypothetical protein, unlikely".
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                     /chromosome="8"
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                     /note="synonym: Tb08.26A17.20, hypothetical protein, conserved"
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CDS	10984..11649	/locus_tag="TB927.8.2300" /note="synonym: Tb08.26A17.80; hypothetical protein, conserved" 10984..>11649 /locus_tag="TB927.8.2300" /product="hypothetical protein, conserved" 10984..11649 /locus_tag="TB927.8.2300" /codon_start=1 /product="hypothetical protein, conserved" /protein_id="AAK69720.1" /db_xref="GI:62175587" /translation="MDVYKRSANMLMTKGIITELRSPPALVCTIRRFKHPMSGEVTL YVPIIAPHYERFRLTDAMHLTNPFMDKYLCEGRLPQAGTALARRHEVFRLLPFLS IAPVNDIKKFGIVERRDPLSRNAYQMLDGAAPPDPRARRAIERIIGVAADATKTV CGMGVHLVMTYTRRTIGTYVESEBEELVEVMKRWVIGCFMGITTFMMVVALYRML RPF"
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 Db 136646 GAGGTCGACGCGGTA 136662

RESULT 36  
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 LOCUS AC099556  
 DEFINITION Trypanosoma brucei chromosome VIII clone RPCI93-26A17, \*\*\*  
 SEQUENCING IN PROGRESS \*\*\*

ACCESSION AC099556  
 VERSION AC099556.10 GI:20043112  
 KEYWORDS HTG; HTGS PHASE2.  
 SOURCE Trypanosoma brucei  
 ORGANISM Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;  
 Trypanosoma.

REFERENCE 1 (bases 1 to 144820)  
 AUTHORS El-Sayed, N.M., Ghedin, E., Song, J., Larkin, C., Wanless, D., Jones, K., Peterson, J., Hou, L., Zhao, H., Mason, T., Millscher, J., Pal, G., Van Aken, S., Utecht, T., Khalak, H.G., Gerard, C., Leech, V., Ull, E., Melville, S., White, O., Adams, M.D., Donelson, J.E. and Fraser, C.M.  
 TITLE Trypanosoma brucei GUTat10.1 RPCI93-26A17 BAC genomic sequence  
 JOURNAL Unpublished  
 COMMENT 2 (bases 1 to 144820)  
 El-Sayed, N.M., Khalak, H. and Adams, M.D.  
 DIRECT SUBMISSION  
 Submitted (16-NOV-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA  
 3 (bases 1 to 144820)  
 El-Sayed, N.M., Khalak, H. and Adams, M.D.  
 DIRECT SUBMISSION  
 Submitted (05-APR-2002) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA  
 On Apr 5, 2002 this sequence version replaced gi:14425288.  
 NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 1 contigs. Gaps between the contigs  
 \* are represented as runs of N. The order of the pieces  
 \* is believed to be correct as given, however the sizes  
 \* of the gaps between them are based on estimates that have  
 \* provided by the submitter.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.  
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ORIGIN

Query Match 85.6%; Score 15.4; DB 14; Length 144820;  
 Best Local Similarity 82.4%; Pred. No. 2e+03;  
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGUGCAGCGCGUA 18  
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 Db 137827 GAGGTCGACGCGGTA 137843

RESULT 37  
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 LOCUS AC007862  
 DEFINITION Trypanosoma brucei chromosome 2 clone RPCI93-10C8, complete  
 SEQUENCING IN PROGRESS \*\*\*

ACCESSION AC007862  
 VERSION AC007862.7 GI:62358417  
 KEYWORDS HTG.  
 SOURCE Trypanosoma brucei

ORGANISM Trypanosoma brucei  
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;  
 Trypanosoma.

REFERENCE 1 (bases 1 to 150671)  
 AUTHORS Ghedin, E., Blandin, G., Bartholomew, D., Caler, E., Haas, B., Hannick, L., Shallow, J., Hou, L., Djikeng, A., Feldblyum, T., Hoestler, J., Johnson, J., Jones, K., Koo, H.L., Larkin, C., Pal, G., Peterson, J., Khalak, H.G., Salzberg, S., Simpson, A.J., Tallon, L., Van Aken, S., Wanless, D., White, O., Wortman, J., Fraser, C.M. and El-Sayed, N.M.A.  
 TITLE Unpublished  
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 150671)  
 AUTHORS El-Sayed, N.M., Khalak, H. and Adams, M.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-JUN-1999) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA  
 3 (bases 1 to 150671)  
 Haas, B., Blandin, G. and El-Sayed, N.  
 DIRECT SUBMISSION  
 Submitted (07-APR-2005) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, nelsayed@igrr.org.  
 On Apr 7, 2005 this sequence version replaced gi:14787186.  
 BAC clone RPCI93-10C8 from Trypanosoma brucei chromosome 2.  
 putative protein coding regions (>30 codons) were predicted by  
 combining the output of the gene finding algorithm Glimmer with  
 similarity data and manual annotation of open reading frames.  
 Further refinement of gene models (additions, deletions and  
 alterations to boundary coordinates) were done manually based on  
 detailed comparisons with the T. cruzi and L. major genomes. Genes  
 on BACs were assigned a systematic name based on the chromosome and  
 the BAC from which they originated (e.g. TP03.27F10.410). Gene  
 products were assigned a putative function when they shared  
 significant similarity with experimentally characterized gene  
 products or when they contained functionally known protein domains.  
 Gene products were labelled either 'hypothetical protein', or  
 'hypothetical protein, conserved' in the case of products showing  
 significant similarity with proteins or domains of unknown function  
 from other organisms. Gene products of unknown function with  
 predicted orthologs in Trypanosoma cruzi and Leishmania major  
 genomes were automatically classified as conserved proteins. Short  
 predicted coding sequences (less than 150 codons) with no  
 additional evidence of coding potential were labelled 'hypothetical  
 protein, unlikely'.  
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repeat\_region

repeat\_region

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repeat\_region

gene



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Query Match 85.6%; Score 15.4; DB 2; Length 150671;  
Best Local Similarity 82.4%; Pred. No. 2e+03;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 AAGGGUGGACGGCGU 17  
Db 26280 AAGGGGTCGCCCGCGT 26296  
RESULT 38  
AC091290/C  
LOCUS  
DEFINITION  
Mus musculus strain C57BL6/J chromosome 7 clone Rf23-27G15, WORKING  
DRAFT SEQUENCE, 28 unordered pieces.  
ACCESSION  
AC091290  
VERSION  
AC091290.9 GI:20127973  
KEYWORDS  
HTG; HTGS PHASE1; HTGS\_DRAFT.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 266178)  
Li, J., Montgomerie, K. T., Grille, G., Chiu, D., Decker, J., Pusina, M.,  
Goltz, J., Halder, A., Hall, L., Han, J., Ioshikhes, I. P., Lee, B.,





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LVPFNLTAEBQVADILIIYQVCTDWSQNGSLKDRLLPTEKAIHILGASVDFPI  
LBOIQPHLLEIYTAQTOIFRSLKEFEVCSILBQYCRKMYHLVORPEOKEKES  
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TSRLP"

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9451..10215  
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/note="ABC-type amino acid transport/signal transduction  
systems, periplasmic component

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/codon\_start=1  
/evidence=not experimental  
/transl\_table=11  
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/protein\_id="CAE80657.1"  
/db\_xref="GI:39576493"  
/db\_xref="UniProt/TREMBL:O6MJA4"  
/translacion="MAVIMRMLIALFLISANTSHTSRTTITLITHEAPPMALPD  
KGAIFPALAKVLKKGGEYLVNFAVPSWRARAKQTDPLIDGYAVRAIENADLEFS  
EYNLESFVNLARXKDHPIEMNKVODLSKYVAGNVOGVLARGVELADQGXIKETTT  
TONNNILKATKRVDIYPSDAFVPEPYLATDPTKRYKYNKKQINSKPIVIBRYGALK  
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/locus\_tag="Bd2878"  
complement(10225..10647)  
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/note="InterPro: HNH nuclease, () Putative HNH family  
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hypothetical protein"  
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Query Match 85.6%; Score 15.4; DB 1; Length 344249;  
Best local Similarity 82.4%; Pred. No. 1.8e+03;  
Matches 14; Insertive 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGGTGGCAGCGCGU 17  
DB 3451 AGCGGGTGGCAGCGCGT 3435

RESULT 40  
BX248356/c  
LOCUS  
DEFINITION  
Corynebacterium diptheriae gravis NCTC13129, complete genome;  
segment 3/8.  
ACCESSION  
BX248356 BX248353  
VERSION  
BX248356.1 GI:38199583  
KEYWORDS  
complete genome.  
SOURCE  
Corynebacterium diptheriae  
ORGANISM  
Corynebacterium diptheriae  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.  
1 (bases 1 to 347625)  
Cerdano-Tarraga,A.M., Estratiou,A., Dover,L.G., Holden,M.T.,  
Pallen,M., Bentley,S.D., Besra,G.S., Churcher,C., James,K.D., De  
Zoyza,A., Chillingworth,T., Cronin,A., Dowd,L., Feltwell,T.,  
Hamlin,N., Holroyd,S., Jagels,K., Moule,S., Quail,M.A.,  
Rabinowitch,B., Rutherford,K.M., Thomson,N.R., Unwin,L.,  
Whitehead,S., Barrett,B.G. and Parkhill,J.  
The complete genome sequence and analysis of Corynebacterium  
diptheriae NCTC13129  
Nucleic Acids Res. 31 (22), 6516-6523 (2003)  
14602910  
2 (bases 1 to 347625)  
Cerdano-Tarraga,A.M.  
Direct Submission  
Submitted (03-Oct-2003) Cerdano-Tarraga A.M., submitted on behalf  
of the Pathogen Sequencing Unit, Sanger Institute, Wellcome Trust  
Genome Campus, Hinxton, Cambridge CB10 1SA E-mail:  
amc@sanger.ac.uk

JOURNAL  
PUBMED  
AUTHORS  
TITLE  
JOURNAL

FEATURES  
source  
Location/Qualifiers  
1. .347625  
/organism="Corynebacterium diphtheriae"  
/mol\_type="genomic DNA"  
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/note="biotype gravis"  
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/db\_xref="GI:38199584"  
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probability 0.667 between residues 22 and 23"  
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487. .1365  
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487. .1365  
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535. .603  
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1389. .2246  
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/note="Signal peptide predicted for DIP0718 by SignalP 2.0  
HMM (Signal peptide probability 0.699) with cleavage site  
probability 0.667 between residues 22 and 23"  
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257. .484  
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(EMBL:AB007142) (97 aa) fasta scores: E(): 4.5e-11, 51.38%  
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/transl\_table=11  
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/protein\_id="CAE49241.1"  
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(EMBL:Z95120) (285 aa) fasta scores: E(): 1.7e-44, 46.69%  
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/db\_xref="InterPro:IPR006025"  
/db\_xref="UniProt/TREMBL:O6N1P8"  
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TTTTATVGAPATATSAQSKGPDAPORPDALITELSGPEFTKGGRTRVQNA  
GAHAGHDKEVFTYIVSENGINTAYAGDDAFAAVVADLTLPKSKWTDKRGFEH  
DGAVKDPRLRIOLSSVDITHGICGNIMETSCFVIGNIRVINSRRVRAKPRQG  
DGAIVROYLINEVGGIGIPAHNEPCGKNGELAPIMQOTLSISNELPAIDNETTN  
DDGAVCSANPMPYFPA"  
535. .603  
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1165. .1194  
/locus tag="DIP0720"  
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1389. .2246  
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43.03% id in 1120 aa"
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/db_xref="GOA:O6NIP5"
/db_xref="InterPro:IPR000212"
/db_xref="UniProt/TrEMBL:O6NIP5"
/translation="MLSPQLSCALQKPPPTQADVISPLAFTLVVAGAGKTE
TAAARVWLVASGLVDPDVLGITFRKAQOOLSKRIDRLQAGIDNIDIDPTGA
LATKLEAIPTVSTVSYAGRLISEYGLLPSVSRLLSQEELFOIASIVSAHTGA
LMTNSPNTVSTLISVSEMDNHWSPDIEBSAFLAMIDVATSKRPSKVV
KRDPTVLENNELPLVQOKTHADNHTFTSGEOMSLARLAENQVASQRNVOI
IMDEYQDTHGADRVLLKSLFAGTAVTAGDPMOSTIGRKATNANLEFLDFGSG
SPATKELTVSFNPEVDILANRVSRELLAGSPVGLGADIMALSDRAVNSGR
PSGMDERSYVADHLAQAEQHDGHPFLAAVLVRKRKSAIILEOQGVPELVG
LAGLGIPEVADILVALTLVRPYTOAMRIAGSPVGLGADIMALSDRAVNSGR
DRAATTELSDPLERLKOIADPTPSDOSIYGLAVALDRLDRLSSDGPYSKGS
EKLRTLAALRIYRTKNSLSPDLFADIERPFGITRTVLOREDPSDCACTAHLDK
FAEVODFSRIPEANLSLUDYLSLASEENGLPEEVOVTVADRVOLTVHAKGLEW
QHVAVLHADANTYVARASTWLTNVAASVPALRGADGDLVGAPEIIDPTDPAEL
AAGKAHIADPFQVAAEENARLPYVAITPAEQVLTASADPSKRPVLPYELTALR
NPPDSVEEMHGEADYVPPAPQAVFPNPTIYVGAADVFAAMQKODPLISDDLF
EEMKEKVSALIEHEQLSA PYAVNITGVLTATDITVNLAKNBNPQORRRPVPKPN
STAKGTATHEMERNRFGABALIDETELFGISELDDSLDLKRAFLDSBNADRTPE

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Query Match 85.6%; Score 15.4; DB 1; Length 347625;  
 Best Local Similarity 82.4%; Pred. No. 1.8e+03;  
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCG 17  
 DB 86034 AGAGGTCGACGCGT 86018

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RESULT 41
AR052610/c 17 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 8 from patent US 5831066.
DEFINITION AR052610
ACCESSION AR052610
VERSION AR052610.1 GI:5975974
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Reed, J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 8 03-NOV-1998;
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Location/Qualifiers
1..17
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ORIGIN

Query Match 83.3%; Score 15; DB 6; Length 17;  
 Best Local Similarity 93.3%; Pred. No. 1.5e+04;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCG 15  
 DB 15 AGAGGTCGACGCG 1

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RESULT 42
BD187523/c 17 bp DNA linear PAT 17-JUL-2003
LOCUS Regulation of bcl-2 GENE EXPRESSION.
DEFINITION BD187523
ACCESSION BD187523
VERSION BD187523.1 GI:32997262
KEYWORDS JP 2003026609-A/8.
SOURCE synthetic construct

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ORGANISM synthetic construct  
 other sequences; artificial sequences.  
 1 (bases 1 to 17)  
 REFERENCE  
 AUTHORS Reed, J.C.  
 TITLE REGULATION OF bcl-2 GENE EXPRESSION  
 JOURNAL Patent: JP 2003026609-A 8 29-JAN-2003;  
 COMMENT John C REED  
 OS Artificial Sequence  
 PN JP 2003026609-A/8  
 PD 29-JAN-2003  
 PF 19-JUN-2002 JP 2002178753  
 PR 20-SEP-1993 US 08/124256  
 PI John C Reed  
 CC Description of Artificial Sequence: Designed DNA based on bcl-2  
 CC  
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ORIGIN

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QY 1 AGAGGUGCGACGCG 15  
 DB 15 AGAGGTCGACGCG 1

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RESULT 43
BD192460/c 17 bp DNA linear PAT 17-JUL-2003
LOCUS Compositions and methods for the delivery of oligonucleotides via
DEFINITION the alimentary canal.
ACCESSION BD192460
VERSION BD192460.1 GI:33002199
KEYWORDS JP 2002510319-A/25.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Teng, C.L. and Hardee, G.
TITLE Compositions and methods for the delivery of oligonucleotides via
JOURNAL the alimentary canal
JOURNAL Patent: JP 2002510319-A 25 02-APR-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002510319-A/25
PD 02-APR-2002
PF 01-JUL-1998 JP 1999507295
PR 01-JUL-1997 US 08/866829
PI CHING TROU TENG GREG HARDEE
PC C1201/68; A61K9/127; A61K48/00; C07H21/04
CC Description of Artificial Sequence: Novel Sequence FH Key
Location/Qualifiers
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RESULT 44  
AR630674/c  
LOCUS AR630674  
DEFINITION Sequence 8 from patent US 6841541.  
ACCESSION AR630674  
VERSION AR630674.1 GI:59766401  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Reed,J.C.  
TITL Regulation of BCL-2-gene expression  
JOURNAL Patent: US 6841541-A 8 11-JAN-2005;  
The Trustees of the University of Pennsylvania; Philadelphia, PA  
FEATURES  
source location/Qualifiers  
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ORIGIN  
Query Match 83.3%; Score 15; DB 6; Length 17;  
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Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGUCCGACCGCG 15  
15 AGAGGGTCCGACCGCG 1

RESULT 45  
AR653968/c  
LOCUS AR653968  
DEFINITION Sequence 25 from patent US 6887906.  
ACCESSION AR653968  
VERSION AR653968.1 GI:67584835  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Teng,C.-L. and Harddee,G.  
TITL Compositions and methods for the delivery of oligonucleotides via  
JOURNAL the alimentary canal  
Patent: US 6887906-A 25 03-MAY-2005;  
ISISpharmaceuticals, Inc.; Carlsbad, CA  
FEATURES  
source location/Qualifiers  
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ORIGIN  
Query Match 83.3%; Score 15; DB 6; Length 17;  
Best Local Similarity 93.3%; Pred. No. 1.5e+04;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGUCCGACCGCG 15  
15 AGAGGGTCCGACCGCG 1

RESULT 46  
G22341  
LOCUS G22341  
DEFINITION human STS wt-11635, sequence tagged site.  
ACCESSION G22341  
VERSION G22341.1 GI:1342667  
KEYWORDS STS; STS sequence; primer; sequence tagged site.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 (bases 1 to 426)  
AUTHORS Hudson,T.  
TITL Whitehead Institute/MIT Center for Genome Research, Physically  
JOURNAL Mapped STS  
COMMENT Unpublished (1995)

Contact: Thomas Hudson  
Whitehead Institute/MIT Center for Genome Research  
Whitehead Institute for Biomedical Research  
9 Cambridge Center, Cambridge MA 02142 USA  
Tel: 617 252 1900  
Fax: 617 252 1902  
Email: thudson@genome.wi.mit.edu

Primer A: AAAGGAACCAACAAATG  
Primer B: TCTAGTCTCGACGACATTGG  
STS size: 125  
PCR profile:  
Presoak:  
Denaturation: 56 degrees C  
Annealing: 56 degrees C  
Polymerization:  
PCR Cycles: 35  
Thermal Cycler:  
Protocol:  
Template: 10 ng  
Primer: each 5 pM  
dNTPs: each 4 mM  
Taq Polymerase: 0.025 units/ul  
Total Vol: 20 ul

Buffer:  
MgCl2: 1.5 mM  
KCl: 50 mM  
Tris-HCl: 10 mM  
pH: 9.3

Derived from dbEST (genbank accession R09557).  
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Best Local Similarity 86.7%; Pred. No. 8.8e+03;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGGGUCCGACCGCGU 17  
318 AGGGTCCGACCGCGT 332

RESULT 47  
BD186637  
LOCUS BD186637  
DEFINITION Nucleic acids isolated from neuroblastoma.  
ACCESSION BD186637  
VERSION BD186637.1 GI:31878837  
KEYWORDS WO 02097093-A/58.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 779)  
AUTHORS Nakagawara,A.



TITLE Nucleic acids isolated from neuroblastoma  
JOURNAL Patent: WO 02097093-A 58 05-DEC-2002;  
COMMENT CHINA PREF. HISAIMITSU PHARMACEUTICAL CO INC, AKIRA NAKAGAMARA  
OS Homo sapiens (human)  
PN WO 02097093-A/58  
PD 05-DEC-2002  
PR 30-MAY-2002 WO 2002JP005294  
PR 30-MAY-2001 JP 01P 162775, 24-AUG-2001 JP 01P 255226 PI  
AKIRA NAKAGAMARA  
PC C12N15/11, C12Q1/68, G01N33/53, G01N33/566  
CC nb1a-10589-f  
FH Key Location/Qualifiers  
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QY 2 GAGGGUCCGACGCGG 16  
DB 75 GAGGGTCCGACGCGG 89

RESULT 48  
CQ729047 1936 bp DNA linear PAT 03-FEB-2004  
LOCUS Sequence 14981 from Patent WO02068579.  
DEFINITION CQ729047  
ACCESSION CQ729047  
VERSION CQ729047.1 GI:42299514  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE  
1 Venter, C.J., Adams, M.C., Li, P.W. and Myers, B.W.  
Kite, such as nucleic acid arrays, comprising a majority of  
humanexons or transcripts, for detecting expression and other uses  
thereof  
JOURNAL Patent: WO 02068579-A 14981 06-SEP-2002;  
FEATURES  
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ORIGIN  
Query Match 83.3%; Score 15; DB 6; Length 1936;  
Best Local Similarity 93.3%; Pred. No. 6.8e+03;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGG 16  
DB 34 GAGGGTCCGACGCGG 48

RESULT 49  
AX333656 1936 bp DNA linear PAT 09-JAN-2002  
LOCUS Sequence 4165 from Patent WO0194629.  
DEFINITION AX333656  
ACCESSION AX333656  
VERSION AX333656.1 GI:18124375  
KEYWORDS  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE  
1 Young, P.B., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,  
Horrigan, S., Soppet, D.R. and Weaver, Z.  
Cancer gene determination and therapeutic screening using signature  
gene sets  
JOURNAL Patent: WO 0194629-A 4165 13-DEC-2001;  
Avalon Pharmaceuticals (US)  
FEATURES  
source Location/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 83.3%; Score 15; DB 6; Length 1936;  
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Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 34 GAGGGTCCGACGCGG 48

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LOCUS Sequence 2179 from Patent WO03039443.  
DEFINITION AX780022  
ACCESSION AX780022  
VERSION AX780022.1 GI:32697016  
KEYWORDS  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE  
1 Haeflrich, T., Schoch, C., Kern, W., Kohlmann, A., Schmittger, S.,  
Dugas, M., Bils, R., Bros, B. and Mergenthaler, S.  
Novel genetic markers for leukemias  
JOURNAL Patent: WO 03039443-A 2179 15-MAY-2003;  
Deutsches Krebsforschungszentrum (DB) ;  
Ludwig-Maximilians-Universitaet Muenchen (DB) ; Haeflrich, Torsten,  
PD Dr. Dr. (DB) ; Schoch, Claudia (DB) ; Kern, Wolfgang (DB)  
FEATURES  
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ORIGIN  
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Best Local Similarity 93.3%; Pred. No. 6.8e+03;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 34 GAGGGTCCGACGCGG 48

Search completed: March 18, 2006, 19:20:49  
Job time : 1013.54 secs

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OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 18:34:54 ; Search time 361.731 Seconds  
(without alignments)  
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Title: US-10-800-926-1

Perfect score: 18

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Scoring table: IDENTITY NUC  
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Searched: 4996997 seqs, 3332346308 residues

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

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13: geneeqn2004bs:\*  
14: geneeqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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C 19	18	100.0	18	10	ACR36780

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C 22	18	100.0	18	12	AD004787	Ad004787 Cpg oligo
C 23	18	100.0	18	13	ADU89320	Adu89320 Allergic
C 24	18	100.0	18	13	ADU89372	Adu89372 Allergic
C 25	18	100.0	18	14	ADV11411	Adv11411 Reverse B
C 26	18	100.0	18	14	ADW79934	Adw79934 Bacterial
C 27	18	100.0	18	14	ADZ88546	Adz88546 Cpg OD117
C 28	18	100.0	18	14	AEI6652	Aei6652 Cpg immun
C 29	18	100.0	18	14	AEI6249	Aei6249 NK lytic
C 30	18	100.0	18	16	ABK90354	Abk90354 Bcl-2/CRE
C 31	17	94.4	17	2	AAQ86651	Aaq86651 Bcl-2 ant
C 32	17	94.4	17	6	ABK90272	Abk90272 Bcl-2-car
C 33	17	94.4	17	2	ABO78530	Abg78530 Antisense
C 34	17	94.4	17	6	ABL54157	Abi54157 Bcl-2 ant
C 35	17	94.4	17	13	ADT93917	Adt93917 Antisense
C 36	17	94.4	17	14	ADW13838	Adw13838 Bcl-2 ant
C 37	16.4	91.1	16	4	AAH48722	Aah48722 Proto-onc
C 38	15	83.3	15	2	AAO86650	Aao86650 Bcl-2 ant
C 39	15	83.3	15	2	AAV28172	Aav28172 Antisense
C 40	15	83.3	15	2	AAH18693	Aah18693 Target bc
C 41	15	83.3	15	2	AAK23684	Aak23684 Deletion
C 42	15	83.3	15	6	ABK90271	Abk90271 Bcl-2-car
C 43	15	83.3	15	6	ABQ78529	Abq78529 Antisense
C 44	15	83.3	15	6	ABL54156	Abi54156 Bcl-2 ant
C 45	15	83.3	15	17	ADW13837	Adw13837 Bcl-2 ant
C 46	15	83.3	15	17	ADZ88115	Adz88115 Human bcl
C 47	15	83.3	15	11	ADM36038	Adm36038 Immunost
C 48	15	83.3	15	11	ADM35932	Adm35932 DNA oligo
C 49	15	83.3	15	12	ADQ17851	Adq17851 Human sof
C 50	15	83.3	15	9	ACH47428	Ach47428 Human inf
C 51	15	83.3	15	9	ACH47428	Ach47428 Human col
C 52	15	83.3	15	14	ACL60828	ACL60828 Human neu
C 53	15	83.3	15	8	ABT32212	Abt32212 Human neu
C 54	15	83.3	15	6	ABL65828	Abi65828 Lung can
C 55	15	83.3	15	10	ADP81623	Adp81623 Leukemia
C 56	15	83.3	15	12	ADQ59204	Adq59204 MSI-H car
C 57	15	83.3	15	12	ADQ23481	Adq23481 Human sof
C 58	14.8	82.2	14	5	AAH27725	Aah27725 Control O
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C 94	14	77.8	16	14	AB828243	Human Bcl	Ab828243	C 167	13.8	76.7	2951	4	ABL14158	AbL14158 Drosophill
C 95	14	77.8	17	14	AA866652	Ab866652 Bcl-2 ant	Aa866652	C 168	13.8	76.7	3506	13	ADM50782	AdM50782 Chinese m
C 96	14	77.8	17	2	AAV28174	Antisense	AaV28174	C 169	13.8	76.7	3768	14	ADX58500	AdX58500 SARS coro
C 97	14	77.8	17	2	AAV28173	Antisense	AaV28173	C 170	13.8	76.7	5973	4	ABL17320	AbL17320 Drosophill
C 98	14	77.8	17	2	AAV18659	Target Dc	AaV18659	C 171	13.8	76.7	6497	4	ABL29730	AbL29730 Drosophill
C 99	14	77.8	17	2	AAV18659	Target Dc	AaV18659	C 172	13.8	76.7	6816	6	ABX16826	AbX16826 Human T-c
C 100	14	77.8	17	2	AAV23685	Deletion	AaV23685	C 173	13.8	76.7	6816	8	ABX93560	AbX93560 Human CDN
C 101	14	77.8	17	2	AAV23686	Deletion	AaV23686	C 174	13.8	76.7	6816	12	ADH69224	AdH69224 Human T-CC
C 102	14	77.8	17	6	ABX90273	Bcl-2-car	AbX90273	C 175	13.8	76.7	6855	6	AAV16827	AaV16827 Human T-c
C 103	14	77.8	17	6	ABQ78531	Antisense	AbQ78531	C 176	13.8	76.7	6855	8	ABX93561	AbX93561 Human CDN
C 104	14	77.8	17	6	ABV54158	Bcl-2 ant	AbV54158	C 177	13.8	76.7	6855	12	ADH69266	AdH69266 Human TCC
C 105	14	77.8	17	14	ADM13839	AbW13839 Bcl-2 ant	AdW13839	C 178	13.8	76.7	6866	6	ABL22667	AbL22667 Human tm
C 106	14	77.8	17	14	ADZ84117	Human bcl	AdZ84117	C 179	13.8	76.7	6866	6	ABL49320	AbL49320 Human pol
C 107	14	77.8	17	14	ADZ84117	Human bcl	AdZ84117	C 180	13.8	76.7	8346	6	ABX28327	AaX28327 DNA trans
C 108	14	77.8	575	5	AAH56923	P patens	AaH56923	C 181	13.8	76.7	9302	4	AAV31567	AaV31567 Human DNA
C 109	14	77.8	575	5	AAH56923	Lipid bio	AaH56923	C 182	13.8	76.7	9302	6	ABQ66891	AbQ66891 Human pol
C 110	14	77.8	1269	8	ABV77479	A. margin	AbV77479	C 183	13.8	76.7	9302	10	ADC11178	AdC11178 Human DNA
C 111	14	77.8	1498	13	ADX29771	Plant ful	AdX29771	C 184	13.8	76.7	9356	14	AC64651	AcL64519 M. xanthu
C 112	14	77.8	191	13	ADX49438	Plant ful	AdX49438	C 185	13.8	76.7	10016	4	ABL17322	AbL17322 Drosophill
C 113	14	77.8	4317	12	ADN11920	Thaateph	AdN11920	C 186	13.8	76.7	10557	6	AAV18240	AaV18240 Reference
C 114	14	77.8	4317	14	ADZ10196	ADZ10196 Osmotic P	AdZ10196	C 187	13.8	76.7	14180	4	ABL17324	AbL17324 Drosophill
C 115	14	77.8	6376	4	ABL29886	Drosophill	AbL29886	C 188	13.8	76.7	15782	14	AC64651	AcL64651 M. xanthu
C 116	14	77.8	15362	4	AAI36491	Human mus	AAI36491	C 189	13.8	76.7	17062	4	ABL14164	AbL14164 Drosophill
C 117	14	77.8	15362	8	ABX59479	Human mus	AbX59479	C 190	13.8	76.7	25617	9	ACCS8256	AcCS8256 Novobioc
C 118	14	77.8	15362	12	ADJ30229	Human mus	AdJ30229	C 191	13.8	76.7	50000	4	AAV4867	AaV4867 Nucleotid
C 119	14	77.8	15535	92	AAI36490	Human mus	AAI36490	C 192	13.8	76.7	50000	12	ADL14227	AdL14227 Novel hum
C 120	14	77.8	15535	8	ABX59478	Human mus	AbX59478	C 193	13.8	76.7	53178	4	AAV59543	AaV59543 Propionib
C 121	14	77.8	15535	12	ADJ30228	CDNA enco	AdJ30228	C 194	13.8	76.7	53178	8	ACR64472	AcF64472 Propionib
C 122	14	77.8	43576	3	AA668609	Human mus	Aa668609	C 195	13.8	76.7	61103	11	ACN43866	AcN43866 Human gen
C 123	13.8	76.7	24	5	AAV59071	Bacteriop	AaV59071	C 196	13.8	76.7	81145	4	AAV54868	AaV54868 Genomic n
C 124	13.8	76.7	100	8	ACD72758	MLP relat	AcD72758	C 197	13.8	76.7	101433	14	AB6A1169_3	AB6A1169_3 Continuation
C 125	13.8	76.7	364	3	AAI803859	Human sec	AaI803859	C 198	13.8	76.7	110000	11	ADM27081_01	ADM27081_01 Continuation
C 126	13.8	76.7	412	4	AAI803859	Human sec	AaI803859	C 199	13.8	76.7	110000	11	ADM27081_01	ADM27081_01 Continuation
C 127	13.8	76.7	450	3	AAH82147	Human pol	AaH82147	C 200	13.8	76.7	112460	6	ABX83567	AbX83567 Human CDN
C 128	13.8	76.7	480	9	AAH82147	N. mening	AaH82147	C 201	13.8	76.7	149158	12	ADP74211	AdP74211 Equine he
C 129	13.8	76.7	592	6	ABQ36718	Oligonuc	AbQ36718	C 202	13.8	76.7	149261	12	ADP74212	AdP74212 Equine he
C 130	13.8	76.7	592	6	ABQ36719	Oligonuc	AbQ36719	C 203	13.8	76.7	150071	12	ADP74216	AdP74216 Equine he
C 131	13.8	76.7	677	14	ACL161007	Human col	AcL161007	C 204	13.8	76.7	150223	12	ADP74201	AdP74201 Equine he
C 132	13.8	76.7	699	6	AAI43849	Human sig	AaI43849	C 205	13.8	76.7	203654	10	ABX116034	AbX116034 Human gen
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C 135	13.8	76.7	726	5	AAH85562	CDNA enco	AaH85562	C 208	13.8	76.7	347001	12	ADP43517	AdP43517 Human MAd
C 136	13.8	76.7	750	13	ADO82721	Plant ful	AdO82721	C 209	13.8	76.7	347001	14	ABEA00291	AeA00291 EGFP sIgn
C 137	13.8	76.7	920	12	ADJ92563	Human 2P1	AdJ92563	C 210	13.4	74.4	109	2	AAAT33338	AaT33338 Human gen
C 138	13.8	76.7	1107	11	ABD09837	Human DNA	AbD09837	C 211	13.4	74.4	179	6	ABK03327	AbK03327 Human G-P
C 139	13.8	76.7	1107	11	ABD09837	pseudomon	AaB09837	C 212	13.4	74.4	293	6	ABL72412	AbL72412 Corn taas
C 140	13.8	76.7	1215	8	ACA68126	Human sec	AaC68126	C 213	13.4	74.4	382	3	AAV57209	AbV57209 Bucealypu
C 141	13.8	76.7	1215	8	ACA68126	Human sec	AaC68126	C 214	13.4	74.4	426	8	ABX44832	AbX44832 Bovine BS
C 142	13.8	76.7	1222	13	ADSV57116	Bacterial	AaD57116	C 215	13.4	74.4	440	4	AAI87782	AaI87782 Human pol
C 143	13.8	76.7	1236	14	ACL731174	M. xanthu	AcL731174	C 216	13.4	74.4	442	8	AAH39195	AaH39195 Bovine BS
C 144	13.8	76.7	1284	11	ADM65876	Human nuc	AdM65876	C 217	13.4	74.4	448	14	ABE15166	AaE15166 C. glutam
C 145	13.8	76.7	1287	13	ADS48250	Bacterial	AaD48250	C 218	13.4	74.4	471	5	AAH68273	AaH68273 C. glutam
C 146	13.8	76.7	1289	3	AAH67990	Human MTC	AaH67990	C 219	13.4	74.4	471	8	ACA01787	AcA01787 C. glutam
C 147	13.8	76.7	1338	4	ABL29731	Plant ful	AbL29731	C 220	13.4	74.4	496	9	ACH45635	AcH45635 Human foe
C 148	13.8	76.7	1341	13	ADSV61915	Novel can	AdS61915	C 221	13.4	74.4	545	13	ADSV1808	AdS1808 Novel can
C 149	13.8	76.7	1351	12	ADO26264	C35 promo	AdO26264	C 222	13.4	74.4	563	3	AAV65121	AaV65121 Bucealypu
C 150	13.8	76.7	1375	8	AAH55877	Human pol	AaH55877	C 223	13.4	74.4	594	14	ABE15164	AaE15164 C. glutam
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C 153	13.8	76.7	1482	13	ADSV58719	Bacterial	AaD58719	C 226	13.4	74.4	610	6	ABQ50889	AbQ50889 Oligonuc
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C 155	13.8	76.7	1629	5	AAH81901	DNA enco	AaH81901	C 228	13.4	74.4	700	4	AAH93248	AaH93248 Human inf
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C 157	13.8	76.7	1753	5	ADH61797	Human ova	AdH61797	C 230	13.4	74.4	712	10	ADC72639	AdC72639 DNA Seq I
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C 160	13.8	76.7	2053	14	ACL72722	M. xanthu	AcL72722	C 233	13.4	74.4	1176	14	ACU66876	AcU66876 M. xanthu
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C 165	13.8	76.7	2663	8	ABH57901	DNA enco	AbH57901	C 238	13.4	74.4	1339	14	ADM11614	AdM11614 Eucalypu

C 239	13.4	74.4	1358	3	AAC56342	Aac56342 Pimus rad	C 312	13.4	74.4	3155	6	AAI47361	AAI47361 Human NMD
C 240	13.4	74.4	1368	14	ACI68043	ACI68043 M. xanthu	C 313	13.4	74.4	3155	6	ABX77665	ABX77665 Human N-m
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C 242	13.4	74.4	1407	14	ACI68370	ACI68370 M. xanthu	C 315	13.4	74.4	3155	10	AAI59662	AAI59662 Human NMD
C 243	13.4	74.4	1408	13	ACN39805	ACN39805 Tumour-as	C 316	13.4	74.4	3155	10	ABX98520	ABX98520 Human N-m
C 244	13.4	74.4	1416	12	AD085848	AD085848 Human tum	C 317	13.4	74.4	3155	10	ABX92869	ABX92869 Human N-m
C 245	13.4	74.4	1428	5	AAI26113	AAI26113 C. nasrat	C 318	13.4	74.4	3211	2	AAQ79389	AAQ79389 Human NMD
C 246	13.4	74.4	1428	5	AAI26111	AAI26111 C. nasrat	C 319	13.4	74.4	3211	2	AAV82898	AAV82898 Human N-m
C 247	13.4	74.4	1429	5	AAI26110	AAI26110 C. nasrat	C 320	13.4	74.4	3211	3	AAI28972	AAI28972 Human N-m
C 248	13.4	74.4	1429	5	AAI26112	AAI26112 C. nasrat	C 321	13.4	74.4	3211	3	AAI59021	AAI59021 Human N-m
C 249	13.4	74.4	1457	11	ADP65711	ADP65711 Human hyp	C 322	13.4	74.4	3211	6	AAI19178	AAI19178 Human NMD
C 250	13.4	74.4	1457	11	ADP65792	ADP65792 Human CDN	C 323	13.4	74.4	3211	6	AAI47365	AAI47365 Human NMD
C 251	13.4	74.4	1457	13	ADP625852	ADP625852 Breast ca	C 324	13.4	74.4	3211	6	ABX77669	ABX77669 Human N-m
C 252	13.4	74.4	1500	2	AAV01445	AAV01445 Yeast Rpl	C 325	13.4	74.4	3211	9	ACD98334	ACD98334 Human NMD
C 253	13.4	74.4	1506	5	AAI21041	AAI21041 DNA encod	C 326	13.4	74.4	3211	10	AAI59666	AAI59666 Human NMD
C 254	13.4	74.4	1506	5	AAI292403	AAI292403 DNA encod	C 327	13.4	74.4	3211	10	ABX98524	ABX98524 Human N-m
C 255	13.4	74.4	1539	11	ACI96634	ACI96634 Klebsiell	C 328	13.4	74.4	3211	10	ABX92873	ABX92873 Human N-m
C 256	13.4	74.4	1548	3	AAI29952	AAI29952 Human sec	C 329	13.4	74.4	3274	2	AAQ79397	AAQ79397 Human NMD
C 257	13.4	74.4	1551	11	ABD06705	ABD06705 Pseudomon	C 330	13.4	74.4	3274	2	AAV82906	AAV82906 Human N-m
C 258	13.4	74.4	1563	11	ABD17230	ABD17230 Pseudomon	C 331	13.4	74.4	3274	3	AAI28720	AAI28720 Human N-m
C 259	13.4	74.4	1587	6	ABN5926	ABN5926 Novel hum	C 332	13.4	74.4	3274	3	AAI95029	AAI95029 Human N-m
C 260	13.4	74.4	1684	5	AAI90724	AAI90724 DNA encod	C 333	13.4	74.4	3274	6	ABI19186	ABI19186 Human NMD
C 261	13.4	74.4	1743	5	ABAI9813	ABAI9813 Human ner	C 334	13.4	74.4	3274	6	AAI47373	AAI47373 Human NMD
C 262	13.4	74.4	1752	10	ADCT2652	ADCT2652 S. lepidop	C 335	13.4	74.4	3274	8	ABX77677	ABX77677 Human N-m
C 263	13.4	74.4	1762	4	ABL06501	ABL06501 Drosophil	C 336	13.4	74.4	3274	9	ACD98342	ACD98342 Human NMD
C 264	13.4	74.4	1911	6	AB878674	AB878674 S. carzin	C 337	13.4	74.4	3274	10	AAI59674	AAI59674 Human NMD
C 265	13.4	74.4	1911	14	ABE12644	ABE12644 Eneidylne	C 338	13.4	74.4	3274	10	ABX98532	ABX98532 Human N-m
C 266	13.4	74.4	1911	14	ABE10237	ABE10237 S. carzin	C 339	13.4	74.4	3274	10	ABX92881	ABX92881 Human N-m
C 267	13.4	74.4	1914	13	ADT42243	ADT42243 Bacterial	C 340	13.4	74.4	3351	11	ABD17267	ABD17267 Human NMD
C 268	13.4	74.4	1953	11	ABD17159	ABD17159 Pseudomon	C 341	13.4	74.4	3428	12	ADQ63985	ADQ63985 Human N-m
C 269	13.4	74.4	2000	8	ADA73016	ADA73016 Rice gene	C 342	13.4	74.4	3546	4	ABLI2658	ABLI2658 Drosophil
C 270	13.4	74.4	2000	11	ACI34849	ACI34849 Rice stre	C 343	13.4	74.4	3622	4	ABLI2886	ABLI2886 Drosophil
C 271	13.4	74.4	2000	11	ACI37580	ACI37580 Rice stre	C 344	13.4	74.4	3657	11	ABD09694	ABD09694 Pseudomon
C 272	13.4	74.4	2145	12	ADQ64772	ADQ64772 Novel hum	C 345	13.4	74.4	3663	12	ADJ95524	ADJ95524 Equine he
C 273	13.4	74.4	2340	4	AAI54358	AAI54358 Pseudomon	C 346	13.4	74.4	3731	2	AAQ79394	AAQ79394 Human NMD
C 274	13.4	74.4	2340	8	ACA42750	ACA42750 Pseudomon	C 347	13.4	74.4	3731	2	AAV82903	AAV82903 Human N-m
C 275	13.4	74.4	2514	14	ADW16799	ADW16799 Pimus rad	C 348	13.4	74.4	3731	3	AAI28717	AAI28717 Human N-m
C 276	13.4	74.4	2516	8	AAI49613	AAI49613 Human cye	C 349	13.4	74.4	3731	3	AAI95026	AAI95026 Human N-m
C 277	13.4	74.4	2576	8	ACC44326	ACC44326 Gene encod	C 350	13.4	74.4	3731	6	ABI19183	ABI19183 Human NMD
C 278	13.4	74.4	2655	5	AAI26114	AAI26114 C. nasrat	C 351	13.4	74.4	3731	6	AAI47370	AAI47370 Human NMD
C 279	13.4	74.4	2727	2	AAI26114	AAI26114 C. nasrat	C 352	13.4	74.4	3731	8	ABX77674	ABX77674 Human N-m
C 280	13.4	74.4	2763	13	AD0557060	AD0557060 Bacterial	C 353	13.4	74.4	3731	9	ACD98339	ACD98339 Human NMD
C 281	13.4	74.4	2835	2	AAI065490	AAI065490 Human NMD	C 354	13.4	74.4	3731	10	AAI59671	AAI59671 Human NMD
C 282	13.4	74.4	2888	4	ABLI16825	ABLI16825 Drosophil	C 355	13.4	74.4	3731	10	ABX98529	ABX98529 Human N-m
C 283	13.4	74.4	2916	2	AAI066659	AAI066659 Human NMD	C 356	13.4	74.4	3731	10	ABX92878	ABX92878 Human N-m
C 284	13.4	74.4	3007	2	AAQ79395	AAQ79395 Human NMD	C 357	13.4	74.4	3750	8	AAI34706	AAI34706 Human NMD
C 285	13.4	74.4	3007	2	AAV82904	AAV82904 Human N-m	C 358	13.4	74.4	3794	2	AAQ79392	AAQ79392 Human NMD
C 286	13.4	74.4	3007	3	AAI28718	AAI28718 Human N-m	C 359	13.4	74.4	3794	2	AAV82901	AAV82901 Human NMD
C 287	13.4	74.4	3007	3	AAI28718	AAI28718 Human N-m	C 360	13.4	74.4	3794	3	AAI28715	AAI28715 Human NMD
C 288	13.4	74.4	3007	6	ABI19184	ABI19184 Human NMD	C 361	13.4	74.4	3794	3	AAI95024	AAI95024 Human N-m
C 289	13.4	74.4	3007	6	ABAI47371	ABAI47371 Human NMD	C 362	13.4	74.4	3794	6	ABAI9181	ABAI9181 Human NMD
C 290	13.4	74.4	3007	6	ABX77675	ABX77675 Human N-m	C 363	13.4	74.4	3794	6	AAI47368	AAI47368 Human NMD
C 291	13.4	74.4	3007	9	ACD98340	ACD98340 Human NMD	C 364	13.4	74.4	3794	8	ABX77672	ABX77672 Human N-m
C 292	13.4	74.4	3007	9	AAI596672	AAI596672 Human NMD	C 365	13.4	74.4	3794	9	ACD98337	ACD98337 Human NMD
C 293	13.4	74.4	3007	10	ABX98530	ABX98530 Human N-m	C 366	13.4	74.4	3794	10	AAI59669	AAI59669 Human NMD
C 294	13.4	74.4	3007	10	ABX92879	ABX92879 Human N-m	C 367	13.4	74.4	3794	10	ABX98527	ABX98527 Human N-m
C 295	13.4	74.4	3070	2	AAQ79398	AAQ79398 Human NMD	C 368	13.4	74.4	3794	10	ABX92876	ABX92876 Human N-m
C 296	13.4	74.4	3070	2	AAV82907	AAV82907 N-methyl-	C 369	13.4	74.4	3831	11	ACA42615	ACA42615 Pseudomon
C 297	13.4	74.4	3070	2	AAI28721	AAI28721 Human NMD	C 370	13.4	74.4	3861	11	ABD09414	ABD09414 Human NMD
C 298	13.4	74.4	3070	3	AAI28721	AAI28721 Human N-m	C 371	13.4	74.4	3903	11	AAI28718	AAI28718 Human NMD
C 299	13.4	74.4	3070	6	ABI19187	ABI19187 Human NMD	C 372	13.4	74.4	3935	2	AAQ79388	AAQ79388 Human NMD
C 300	13.4	74.4	3070	6	ABAI47374	ABAI47374 Human NMD	C 373	13.4	74.4	3935	2	AAV82897	AAV82897 Human N-m
C 301	13.4	74.4	3070	6	ABX77678	ABX77678 Human N-m	C 374	13.4	74.4	3935	3	AAI28711	AAI28711 Human NMD
C 302	13.4	74.4	3070	9	ACD98343	ACD98343 Human NMD	C 375	13.4	74.4	3935	3	AAI95020	AAI95020 Human N-m
C 303	13.4	74.4	3070	10	AAI59665	AAI59665 Human NMD	C 376	13.4	74.4	3935	6	AAI47364	AAI47364 Human NMD
C 304	13.4	74.4	3070	10	ABX98533	ABX98533 Human N-m	C 377	13.4	74.4	3935	6	ABX77668	ABX77668 Human N-m
C 305	13.4	74.4	3070	10	ABX92882	ABX92882 Human N-m	C 378	13.4	74.4	3935	9	ACD98333	ACD98333 Human NMD
C 306	13.4	74.4	3109	6	ABZ53338	ABZ53338 Human gen	C 379	13.4	74.4	3935	9	AAI59665	AAI59665 Human NMD
C 307	13.4	74.4	3155	2	AAQ79365	AAQ79365 Human N-m	C 380	13.4	74.4	3935	10	ABX98523	ABX98523 Human N-m
C 308	13.4	74.4	3155	2	AAV82894	AAV82894 Human N-m	C 381	13.4	74.4	3935	10	ABX92872	ABX92872 Human N-m
C 309	13.4	74.4	3155	3	AAI28708	AAI28708 Human NMD	C 382	13.4	74.4	3998	10	AAQ79396	AAQ79396 Human NMD
C 310	13.4	74.4	3155	3	AAI95017	AAI95017 Human N-m	C 383	13.4	74.4	3998	2	AAV82905	AAV82905 Human N-m
C 311	13.4	74.4	3155	6	ABI19174	ABI19174 Human NMD	C 384	13.4	74.4	3998	2	AAV82905	AAV82905 Human N-m

C 385	13.4	74.4	3998	3	AAZ38719	AAZ38719 Human NMD	458	13.4	74.4	7654	14	ACL64698	ACL64698 M. xanthu
C 386	13.4	74.4	3998	3	AAA95028	AAA95028 Human N-m	C 459	13.4	74.4	22118	8	ADAI4746	ADAI4746 Mouse 45S
C 387	13.4	74.4	3998	6	AB127162	AB127162 Drosophill	C 460	13.4	74.4	22118	8	ABX11085	ABX11085 Mouse rib
C 388	13.4	74.4	3998	6	AB199185	AB199185 Human NMD	C 461	13.4	74.4	22118	9	ADA37415	ADA37415 Origin of
C 389	13.4	74.4	3998	6	AA147372	AA147372 Human NMD	C 462	13.4	74.4	22118	10	AD61410	AD61410 Mouse rib
C 390	13.4	74.4	3998	8	ABX77676	ABX77676 Human N-m	C 463	13.4	74.4	22118	10	ADFI0518	ADFI0518 Mouse rib
C 391	13.4	74.4	3998	9	ACD98341	ACD98341 Human NMD	C 464	13.4	74.4	22118	10	ACCA4629	ACCA4629 Mouse rib
C 392	13.4	74.4	3998	10	AA059673	AA059673 Human NMD	C 465	13.4	74.4	22118	13	ADRA43948	ADRA43948 Mouse pre
C 393	13.4	74.4	3998	10	ABX98531	ABX98531 Human NMD	C 466	13.4	74.4	22118	14	ABEB25474	ABEB25474 Mouse 45S
C 394	13.4	74.4	3998	10	ABX92880	ABX92880 Human N-m	C 467	13.4	74.4	22715	9	ADA02852	ADA02852 Human CBX
C 395	13.4	74.4	4094	2	AA079393	AA079393 Human NMD	C 468	13.4	74.4	22715	10	ADB72590	ADB72590 Human CBX
C 396	13.4	74.4	4094	2	AA079392	AA079392 Human NMD	C 469	13.4	74.4	22715	10	ADCB8531	ADCB8531 Human CBX
C 397	13.4	74.4	4094	3	AAZ38716	AAZ38716 Human NMD	C 470	13.4	74.4	22715	12	ADM74447	ADM74447 Human car
C 398	13.4	74.4	4094	3	AAA55025	AAA55025 Human N-m	C 471	13.4	74.4	24883	13	ABD33069	ABD33069 Murine ca
C 399	13.4	74.4	4094	6	AB199182	AB199182 Human NMD	C 472	13.4	74.4	25733	13	ACL64752	ACL64752 M. xanthu
C 400	13.4	74.4	4094	6	AA147369	AA147369 Human NMD	C 473	13.4	74.4	26659	14	ACL64774	ACL64774 M. xanthu
C 401	13.4	74.4	4094	8	ABX77673	ABX77673 Human N-m	C 474	13.4	74.4	26729	9	AA160439	AA160439 Human kin
C 402	13.4	74.4	4094	9	ACD98338	ACD98338 Human NMD	C 475	13.4	74.4	28320	14	ACL64759	ACL64759 M. xanthu
C 403	13.4	74.4	4094	10	AA059670	AA059670 Human NMD	C 476	13.4	74.4	28533	11	ACN44308	ACN44308 Mouse gen
C 404	13.4	74.4	4094	10	ABX98528	ABX98528 Human N-m	C 477	13.4	74.4	47670	4	AB116824	AB116824 Drosophill
C 405	13.4	74.4	4094	10	ABX92877	ABX92877 Human N-m	C 478	13.4	74.4	50368	4	AB116768	AB116768 Drosophill
C 406	13.4	74.4	4157	2	AA079391	AA079391 Human NMD	C 479	13.4	74.4	65952	12	ADQ59527	ADQ59527 Human can
C 407	13.4	74.4	4157	2	AA079390	AA079390 Human N-m	C 480	13.4	74.4	66009	14	AD213908	AD213908 Murine ca
C 408	13.4	74.4	4157	3	AAZ38714	AAZ38714 Human NMD	C 481	13.4	74.4	67674	12	ADP81772	ADP81772 Human MD-
C 409	13.4	74.4	4157	3	AAA55023	AAA55023 Human N-m	C 482	13.4	74.4	70383	9	AA160437	AA160437 Human kin
C 410	13.4	74.4	4157	6	AB199180	AB199180 Human NMD	C 483	13.4	74.4	71887	11	ACN44950	ACN44950 Human gen
C 411	13.4	74.4	4157	6	AA147367	AA147367 Human NMD	C 484	13.4	74.4	103765	4	AA199683_43	AA199683_43 Human gen
C 412	13.4	74.4	4157	9	ABX77671	ABX77671 Human N-m	C 485	13.4	74.4	110000	12	ADN46845_07	ADN46845_07 Continuation (14 o
C 413	13.4	74.4	4157	9	ACD98336	ACD98336 Human NMD	C 486	13.4	74.4	110000	12	ADN46845_07	ADN46845_07 Continuation (14 o
C 414	13.4	74.4	4157	10	AA059668	AA059668 Human NMD	C 487	13.4	74.4	110000	12	ADN47591_13	ADN47591_13 Continuation (14 o
C 415	13.4	74.4	4157	10	ABX98526	ABX98526 Human N-m	C 488	13.4	74.4	110000	12	ADN46123_07	ADN46123_07 Continuation (14 o
C 416	13.4	74.4	4157	10	ABX92875	ABX92875 Human N-m	C 489	13.4	74.4	110000	12	ADN47209_13	ADN47209_13 Continuation (14 o
C 417	13.4	74.4	4158	11	ABD06744	ABD06744 Pseudomon	C 490	13.4	74.4	110000	12	ADN46464_07	ADN46464_07 Continuation (14 o
C 418	13.4	74.4	4287	13	AB106500	AB106500 Drosophill	C 491	13.4	74.4	110000	12	ADN47960_13	ADN47960_13 Continuation (14 o
C 419	13.4	74.4	4298	2	AA079370	AA079370 Human N-m	C 492	13.4	74.4	149158	12	ADP74211	ADP74211 Equine he
C 420	13.4	74.4	4298	2	AA079370	AA079370 Human N-m	C 493	13.4	74.4	149261	12	ADP74212	ADP74212 Equine he
C 421	13.4	74.4	4298	3	AAZ38701	AAZ38701 Human NMD	C 494	13.4	74.4	150071	12	ADP74216	ADP74216 Equine he
C 422	13.4	74.4	4298	3	AAA55010	AAA55010 Human N-m	C 495	13.4	74.4	150223	12	ADP74201	ADP74201 Equine he
C 423	13.4	74.4	4298	6	AB199167	AB199167 Human NMD	C 496	13.4	74.4	309400	5	AAH68534	AAH68534 C. glutam
C 424	13.4	74.4	4298	6	AA147354	AA147354 Human NMD	C 497	13.2	73.3	25	AC181324	AC181324 Human mtc	
C 425	13.4	74.4	4298	8	ABX77658	ABX77658 Human NMD	C 498	13.2	73.3	29	AAQ33869	AAQ33869 Sequence	
C 426	13.4	74.4	4298	9	ACD98332	ACD98332 Human NMD	C 499	13.2	73.3	54	AAQ47266	AAQ47266 Lactate d	
C 427	13.4	74.4	4298	10	AA059655	AA059655 Human NMD	C 500	13.2	73.3	100	ACD77872	ACD77872 E. coli X	
C 428	13.4	74.4	4298	10	ABX98513	ABX98513 Human N-m	C 501	13.2	73.3	100	ACD77871	ACD77871 E. coli K	
C 429	13.4	74.4	4298	10	ABX92862	ABX92862 Human N-m	C 502	13.2	73.3	100	ABQ84336	ABQ84336 DPPIII gen	
C 430	13.4	74.4	4361	2	AA079390	AA079390 Human NMD	C 503	13.2	73.3	100	ABQ84337	ABQ84337 DPPIII gen	
C 431	13.4	74.4	4361	2	AA079389	AA079389 Human N-m	C 504	13.2	73.3	125	AACT10486	AACT10486 Human sec	
C 432	13.4	74.4	4361	3	AAZ38713	AAZ38713 Human NMD	C 505	13.2	73.3	192	ADP91968	ADP91968 Novel S.	
C 433	13.4	74.4	4361	3	AAA55022	AAA55022 Human N-m	C 506	13.2	73.3	192	ABAS5838	ABAS5838 Streptoco	
C 434	13.4	74.4	4361	6	AB199179	AB199179 Human NMD	C 507	13.2	73.3	197	AA564683	AA564683 DNA encod	
C 435	13.4	74.4	4361	6	AA147366	AA147366 Human NMD	C 508	13.2	73.3	197	AA5688140	AA5688140 DNA encod	
C 436	13.4	74.4	4361	8	ABX77670	ABX77670 Human N-m	C 509	13.2	73.3	197	AA5688994	AA5688994 DNA encod	
C 437	13.4	74.4	4361	9	ACD98335	ACD98335 Human NMD	C 510	13.2	73.3	197	AA567026	AA567026 DNA encod	
C 438	13.4	74.4	4361	10	AA059667	AA059667 Human NMD	C 511	13.2	73.3	197	AA580086	AA580086 DNA encod	
C 439	13.4	74.4	4361	10	ABX98525	ABX98525 Human N-m	C 512	13.2	73.3	206	ABQ84298	ABQ84298 Human DP	
C 440	13.4	74.4	4361	10	ABX92874	ABX92874 Human N-m	C 513	13.2	73.3	327	ABK76591	ABK76591 Bacillus	
C 441	13.4	74.4	4494	14	ACL71069	ACL71069 Human N-m	C 514	13.2	73.3	333	ABK79782	ABK79782 Bacillus	
C 442	13.4	74.4	4594	2	AA070131	AA070131 NMDAR1-1	C 515	13.2	73.3	380	ADV78134	ADV78134 Zoogloea	
C 443	13.4	74.4	4659	2	AA099964	AA099964 Human exc	C 516	13.2	73.3	387	ABX36272	ABX36272 Human sec	
C 444	13.4	74.4	4659	2	ABX94241	ABX94241 Human exc	C 517	13.2	73.3	394	AA5888139	AA5888139 DNA encod	
C 445	13.4	74.4	4663	6	AB553058	AB553058 cDNA enco	C 518	13.2	73.3	394	AA584682	AA584682 DNA encod	
C 446	13.4	74.4	4953	11	ABD06623	ABD06623 Pseudomon	C 519	13.2	73.3	394	AA567025	AA567025 DNA encod	
C 447	13.4	74.4	5022	12	AA099970	AA099970 Human exc	C 520	13.2	73.3	400	ACF05800	ACF05800 Streptoco	
C 448	13.4	74.4	5636	8	AA559561	AA559561 Propionib	C 521	13.2	73.3	402	AD049127	AD049127 S. pneumo	
C 449	13.4	74.4	5636	8	ACF64490	ACF64490 Propionib	C 522	13.2	73.3	402	AA557353	AA557353 S. pneumo	
C 450	13.4	74.4	6690	4	AB116769	AB116769 Drosophill	C 523	13.2	73.3	402	AA557356	AA557356 S. pneumo	
C 451	13.4	74.4	6988	14	AC164270	AC164270 M. xanthu	C 524	13.2	73.3	414	ACH94487	ACH94487 Klebsiell	
C 452	13.4	74.4	7282	10	ACC49359	ACC49359 Human NMI	C 525	13.2	73.3	418	AACT76880	AACT76880 Human ORF	
C 453	13.4	74.4	7796	3	AAAC64578	AAAC64578 T. gondii	C 526	13.2	73.3	426	AAAC43330	AAAC43330 Arabidops	
C 454	13.4	74.4	8663	5	AAAC30133	AAAC30133 Human lun	C 527	13.2	73.3	468	AAH65562	AAH65562 C. glutam	
C 455	13.4	74.4	8663	10	ADB33470	ADB33470 Human nov	C 528	13.2	73.3	468	ACA000019	ACA000019 C. glutam	
C 456	13.4	74.4	16387	14	AC164663	AC164663 M. xanthu	C 529	13.2	73.3	474	ADP92657	ADP92657 Cotton ex	
C 457	13.4	74.4	17384	10	ACC44721	ACC44721 Cosmid pf	C 530	13.2	73.3	490	ABV10781	ABV10781 Human pro	

531	13.2	73.3	505	9	ACH34904	Acth34904 Human end	c 604	13.2	73.3	1542	13	ADR85495	Adr85495 Aspergill
532	13.2	73.3	506	6	ABK77059	Abk77059 Bacillus	c 605	13.2	73.3	1550	12	ADH16275	Adh16275 Human nuc
533	13.2	73.3	512	6	ABQ44040	Abq44040 Oligonucle	c 606	13.2	73.3	1590	11	ACH94615	Ach94615 Klebsiell
534	13.2	73.3	512	6	ABQ44040	Abq44040 Oligonucle	c 607	13.2	73.3	1591	13	ACH8435	Ach8435 Arabidops
535	13.2	73.3	514	6	ABQ18920	Abq18920 Oligonucle	c 608	13.2	73.3	1611	12	ADQ23250	Adq23250 Human sof
536	13.2	73.3	514	6	ABQ18920	Abq18920 Oligonucle	c 609	13.2	73.3	1617	5	AA93064	AA93064 DNA encod
537	13.2	73.3	521	12	ADQ18372	Adq18372 Human sof	c 610	13.2	73.3	1668	5	AA69002	AA69002 DNA encod
538	13.2	73.3	525	6	ABO39240	Abq39240 Oligonucle	c 611	13.2	73.3	1668	14	ADM16710	Adm16710 Eucalyptu
539	13.2	73.3	525	6	ABO39240	Abq39240 Oligonucle	c 612	13.2	73.3	1682	13	ADR84908	Adr84908 Aspergill
540	13.2	73.3	531	12	ACH72965	Acth72965 Human gen	c 613	13.2	73.3	1702	6	ADD33055	Ad333055 Human bec
541	13.2	73.3	543	8	ABZ36885	Abz36885 Human GEN	c 614	13.2	73.3	1756	6	ADV25578	Adv25578 Human pro
542	13.2	73.3	552	11	ABD10266	Abd10266 Pseudomon	c 615	13.2	73.3	1779	8	ACA25210	Act25210 Prokaryot
543	13.2	73.3	577	6	ABQ43770	Abq43770 Oligonucle	c 616	13.2	73.3	1815	12	ADJ62773	Adj62773 Human CDN
544	13.2	73.3	577	6	ABQ43771	Abq43771 Oligonucle	c 617	13.2	73.3	1815	14	ADZ80550	Adz80550 Syntactin
545	13.2	73.3	589	6	ABQ46551	Abq46551 Oligonucle	c 618	13.2	73.3	1854	13	ADT44511	Adt44511 Bacterial
546	13.2	73.3	589	6	ABQ46550	Abq46550 Oligonucle	c 619	13.2	73.3	1867	6	ABL67923	AbL67923 Ovary can
547	13.2	73.3	621	5	ABV53182	Abv53182 Human pro	c 620	13.2	73.3	1867	6	ABK83449	Abk83449 Human CDN
548	13.2	73.3	624	10	ADK59637	Adk59637 Plant DNA	c 621	13.2	73.3	1883	5	AA669005	AA669005 DNA encod
549	13.2	73.3	629	4	AAK58047	Aak58047 Human imm	c 622	13.2	73.3	1888	9	ACE25366	Act25366 Human EYR
550	13.2	73.3	629	4	AAK58047	Aak58047 Human imm	c 623	13.2	73.3	1901	5	AA882469	AA882469 DNA encod
551	13.2	73.3	637	12	ADD43160	Ad43160 Plant CDN	c 624	13.2	73.3	1928	13	ADR98766	Adr98766 Lung spec
552	13.2	73.3	647	13	ADRI15017	Adri15017 Rat elect	c 625	13.2	73.3	1944	14	ADW64698	Adw64698 Glutconac
553	13.2	73.3	647	14	ABEA47944	Aea47944 Rat growt	c 626	13.2	73.3	1965	14	ACT172528	Act172528 M. xanthu
554	13.2	73.3	666	6	ABQ49000	Abq49000 Oligonucle	c 627	13.2	73.3	1970	6	ABQ81544	Abq81544 Gene up-r
555	13.2	73.3	666	6	ABQ49001	Abq49001 Oligonucle	c 628	13.2	73.3	1981	4	ABU17135	Abu17135 Drosophil
556	13.2	73.3	667	6	ABT07870	Abt07870 Human lun	c 629	13.2	73.3	2000	8	ADA71568	Ada71568 Rice gene
557	13.2	73.3	690	10	ADP00829	Adp00829 Bacterial	c 630	13.2	73.3	2044	13	ADS48703	Ads48703 Bacterial
558	13.2	73.3	714	3	AAK45660	Aak45660 Arabidops	c 631	13.2	73.3	2059	10	ADBS8542	Adbs8542 Toxicity-
559	13.2	73.3	715	3	AAK33148	Aac33148 Arabidops	c 632	13.2	73.3	2059	10	ADBS5150	Adbs5150 Primary r
560	13.2	73.3	716	3	AAK52027	Aac52027 Arabidops	c 633	13.2	73.3	2099	13	ADVA41338	Adv41338 Rat cardi
561	13.2	73.3	740	3	AAAT9339	Aaa9339 Buncalypcu	c 634	13.2	73.3	2155	10	ADCO8395	Adc08395 Rice DNA
562	13.2	73.3	752	5	AAAG4177	Aag4177 DNA encod	c 635	13.2	73.3	2155	10	ADCO8342	Adc08342 Rice DNA
563	13.2	73.3	773	4	AAK57140	Aak57140 Human imm	c 636	13.2	73.3	2212	5	AA670736	Aa670736 DNA encod
564	13.2	73.3	774	4	AAK591490	Aas91490 DNA encod	c 637	13.2	73.3	2297	2	AAV63562	Aav63562 DNA encod
565	13.2	73.3	780	14	ADV78127	Adv78127 Zoolloea	c 638	13.2	73.3	2297	2	AAE24904	Aae24904 Nucleoid
566	13.2	73.3	786	6	ABQ22337	Abq22337 Oligonucle	c 639	13.2	73.3	2298	2	AAZ32678	Aaz32678 Human ves
567	13.2	73.3	814	6	ABQ22337	Abq22337 Oligonucle	c 640	13.2	73.3	2322	5	AAE87441	Aae87441 Corynebac
568	13.2	73.3	814	6	AAK588148	Aa888148 DNA encod	c 641	13.2	73.3	2338	5	AAO40408	Aao40408 Rice phen
569	13.2	73.3	815	8	ACR23777	Act3777 Prokaryot	c 642	13.2	73.3	2413	5	AA93057	Aa93057 DNA encod
570	13.2	73.3	844	12	AD182274	Ad182274 Human DNA	c 643	13.2	73.3	2427	13	ADSA46097	Ads46097 Bacterial
571	13.2	73.3	845	2	AAV83887	Aav83887 Promoter	c 644	13.2	73.3	2504	4	AAQ87446	Aaq87446 TriDoliu
572	13.2	73.3	882	11	ABD10373	Abd10373 Pseudomon	c 645	13.2	73.3	2646	12	ADO57328	Ado57328 DNA encod
573	13.2	73.3	900	5	AAK588147	Aa888147 DNA encod	c 646	13.2	73.3	2650	14	ABEA51127	AbEA51127 Pseudomon
574	13.2	73.3	940	8	ABZ52514	Abz52514 Aspergill	c 647	13.2	73.3	2684	4	ABL04951	AbL04951 Drosophil
575	13.2	73.3	994	6	ABQ32082	Abq32082 Oligonucle	c 648	13.2	73.3	2747	4	ABU10709	Abu10709 Drosophil
576	13.2	73.3	994	6	ABQ32083	Abq32083 Oligonucle	c 649	13.2	73.3	2987	4	ABAO8622	Abao8622 Human str
577	13.2	73.3	1020	4	AAU01888	AaU01888 Human rep	c 650	13.2	73.3	3002	11	ABEB86037	Abeb86037 DNA damag
578	13.2	73.3	1020	4	ABL97181	AbL97181 Human tee	c 651	13.2	73.3	3077	10	ADE58072	Ade58072 Rat gene
579	13.2	73.3	1023	12	ADM36193	Adm36193 Candida a	c 652	13.2	73.3	3077	10	ADBS6068	Adbs6068 Rat gene
580	13.2	73.3	1032	3	AAK38509	Aac38509 Arabidops	c 653	13.2	73.3	3319	5	AA644598	Aa644598 DNA encod
581	13.2	73.3	1035	6	ABQ40400	Abq40400 Oligonucle	c 654	13.2	73.3	3321	5	AA885592	Aa885592 DNA encod
582	13.2	73.3	1035	6	ABQ40401	Abq40401 Oligonucle	c 655	13.2	73.3	3367	2	AAV63191	Aav63191 DNA fcom
583	13.2	73.3	1036	6	ABQ45043	Abq45043 Oligonucle	c 656	13.2	73.3	3367	6	AAQ92041	Aaq92041 Human pol
584	13.2	73.3	1036	6	ABQ45042	Abq45042 Oligonucle	c 657	13.2	73.3	3369	2	AAV52175	Aav52175 Streptoco
585	13.2	73.3	1044	8	ACR48211	Act48211 Prokaryot	c 658	13.2	73.3	3420	13	ADBS5852	Adbs5852 Bacterial
586	13.2	73.3	1079	6	ABQ27779	Abq27779 Oligonucle	c 659	13.2	73.3	3558	10	ADBS6987	Adbs6987 C. neofo
587	13.2	73.3	1079	6	ABQ27778	Abq27778 Oligonucle	c 660	13.2	73.3	3777	6	ADD33048	Ad333048 Human bec
588	13.2	73.3	1098	5	AA860090	Aa860090 DNA encod	c 661	13.2	73.3	3789	14	ADX02206	Adx02206 Human cod
589	13.2	73.3	1101	4	AAAS6186	Aaas6186 Salmonell	c 662	13.2	73.3	3794	5	AA593067	Aa593067 Human encod
590	13.2	73.3	1101	8	ACA52127	Act52127 Prokaryot	c 663	13.2	73.3	3800	2	AAK28141	Aak28141 CCoAOMT P
591	13.2	73.3	1119	3	ADMS56810	Adms56810 Bacterial	c 664	13.2	73.3	3800	3	AAZ60808	Aaz60808 Nucleoid
592	13.2	73.3	1131	10	ADCT5855	Adct5855 DNA homol	c 665	13.2	73.3	3907	10	ADB65908	Adb65908 C. neofo
593	13.2	73.3	1215	2	AAV04470	Aav04470 Gallus ga	c 666	13.2	73.3	3921	13	ADU01914	AdU01914 Novel hum
594	13.2	73.3	1215	9	ACF06116	Actf06116 Bacterial	c 667	13.2	73.3	4237	5	AA886660	Aa886660 DNA encod
595	13.2	73.3	1269	13	ADMS5410	Adms5410 Bacterial	c 668	13.2	73.3	4340	4	AA67040	Aa67040 DNA encod
596	13.2	73.3	1272	13	AD849896	Ad849896 Bacterial	c 669	13.2	73.3	4340	5	ABU17134	Abu17134 Drosophil
597	13.2	73.3	1315	5	AAK54693	Aak54693 DNA encod	c 670	13.2	73.3	4746	4	AAK52577	Aak52577 Human pol
598	13.2	73.3	1357	3	ADP17063	Adp17063 Plant CDN	c 671	13.2	73.3	4874	5	AA884894	Aa884894 DNA encod
599	13.2	73.3	1434	5	AAK56563	Aa56563 DNA encod	c 672	13.2	73.3	4874	6	AB878711	Ab878711 Human CDN
600	13.2	73.3	1434	5	AAK56563	Aa56563 DNA encod	c 673	13.2	73.3	4927	6	AB878720	Ab878720 Human CDN
601	13.2	73.3	1434	5	AAK56563	Aa56563 DNA encod	c 674	13.2	73.3	4986	4	ABU10708	Abu10708 Drosophil
602	13.2	73.3	1452	13	ADBS58692	Adbs58692 Bacterial	c 675	13.2	73.3	5093	10	ADBS52876	Adbs52876 Primary r
603	13.2	73.3	1539	10	ABZ40437	Abz40437 N. gonorr	c 676	13.2	73.3	5197	4	AAK71813	Aak71813 Human imm



677	13.2	73.3	5197	4	AAI62920	AAI62920 Human gen	c 750	13.2	72.3	170506	14	ADZ13520	Adi13520 Human can
678	13.2	73.3	5891	6	ABNL3439	Abi13439 Human imm	c 751	13.2	72.3	171096	13	ADT05874	Adt05874 Cercopith
679	13.2	73.3	6089	6	ABN80255	Abn80255 Human imm	c 752	13.2	72.3	191284	12	ADQ97957	Adq97957 Cercopith
c 680	13.2	73.3	7682	13	ADWR4321	Adw4321 Aspergill	c 753	13.2	73.3	227448	13	ABD32381	Abd32381 Mouse can
681	13.2	73.3	10607	14	ADM27018	Adm27018 Genomic s	754	13.2	73.3	339234	12	ADQ59437	Adq59437 Human can
682	13.2	73.3	10692	14	ACR64497	Act64497 M. xanthu	755	13.2	73.3	339234	14	ADZ13744	Adz13744 Murine ca
683	13.2	73.3	13154	5	ABLI19201	Abli19201 Drosophi1	756	13.2	73.3	349980	5	AAH61610	Aah61610 Neiseeria
c 684	13.2	73.3	13836	5	ABAI16633	Abai16633 Human ner	c 757	13.2	72.2	20	2	AAH68525	Aah68525 C glutam1
c 685	13.2	73.3	14417	4	AAK87584	Aak87584 Human imm	c 758	13	72.2	20	2	AAO66643	Aao66643 Antisense
c 686	13.2	73.3	14417	4	AAK71816	Aak71816 Human imm	c 759	13	72.2	20	2	AAV28169	Aav28169 Antisense
c 687	13.2	73.3	14417	4	AAK73113	Aak73113 Human imm	c 760	13	72.2	20	2	AAI18690	Aai18690 Target bc
c 688	13.2	73.3	14417	4	AAI62923	Aai62923 Human gen	c 761	13	72.2	20	2	AAI23581	Aai23581 Delcton
c 689	13.2	73.3	14417	8	ABZ74674	Abz74674 Secreted	c 762	13	72.2	20	3	AAZ49348	Aaz49348 bcl-2 tar
c 690	13.2	73.3	14417	10	ABZ68196	Abz68196 Human sec	c 763	13	72.2	20	10	AAZ58991	Aaz58991 bcl-2 ant
c 691	13.2	73.3	14426	4	AAK87586	Aak87586 Human imm	c 764	13	72.2	20	13	ADRA4439	Adra4439 bcl-2 spe
c 692	13.2	73.3	14426	4	AAK73099	Aak73099 Human imm	c 765	13	72.2	20	13	ADU67662	Adu67662 bcl-2 gen
c 693	13.2	73.3	14426	4	AAK87568	Aak87568 Human imm	c 766	13	72.2	20	14	ADZ84112	Adz84112 Human bcl
c 694	13.2	73.3	14426	4	AAK71817	Aak71817 Human imm	c 767	13	72.2	228	13	ADR12540	Adr12540 Gene vacc
c 695	13.2	73.3	14426	4	AAK85290	Aak85290 Human imm	c 768	13	72.2	228	13	ADS86591	Ads86591 Trypanoso
c 696	13.2	73.3	14426	4	AAK71814	Aak71814 Human imm	c 769	13	72.2	234	6	ABN79389	Abn79389 Human ORF
c 697	13.2	73.3	14426	4	AAK73115	Aak73115 Human imm	c 770	13	72.2	849	5	AAH64998	Aah64998 C glutam1
c 698	13.2	73.3	14426	4	AAI62921	Aai62921 Human gen	c 771	13	72.2	972	4	AAH68036	Aah68036 Corynebac
c 699	13.2	73.3	14426	8	AAI62924	Aai62924 Human gen	c 772	13	72.2	1335	5	AAH34550	Aah34550 Human DNA
c 700	13.2	73.3	14426	8	ABZ74676	Abz74676 Secreted	c 773	13	72.2	1608	8	ADA70753	Ada70753 Rice gene
c 701	13.2	73.3	14426	8	ABZ74673	Abz74673 Secreted	c 774	13	72.2	1617	8	ACA39689	Aca39689 Prokaryot
c 702	13.2	73.3	14426	10	ABZ68195	Abz68195 Human sec	c 775	13	72.2	1902	6	ABN67223	Abn67223 Streptoco
c 703	13.2	73.3	14426	10	ABZ68195	Abz68195 Human sec	c 776	13	72.2	1905	13	ADN83467	Adn83467 Streptoco
c 704	13.2	73.3	14448	4	AAK71815	Aak71815 Human imm	c 777	13	72.2	2019	6	ADZ28834	Adz28834 Perentia1
c 705	13.2	73.3	14448	4	AAK87580	Aak87580 Human imm	c 778	13	72.2	2160	10	ADG70537	Adg70537 Listeria
c 706	13.2	73.3	14448	4	AAK73111	Aak73111 Human imm	c 779	13	72.2	2478	3	AAH51307	Aah51307 A. terreu
c 707	13.2	73.3	14448	4	AAI62922	Aai62922 Human gen	c 780	13	72.2	3083	2	AAQ79384	Aaq79384 Human N-m
c 708	13.2	73.3	14451	4	AAK73116	Aak73116 Human imm	c 781	13	72.2	3285	4	AAH52089	Aah52089 Mycobacte
c 710	13.2	73.3	14451	4	AAK71818	Aak71818 Human imm	c 782	13	72.2	3612	4	ABLI19705	Abli19705 Drosophi1
c 711	13.2	73.3	14451	4	AAK87587	Aak87587 Human imm	c 783	13	72.2	3612	13	ADO89695	Ado89695 Antagonis
c 712	13.2	73.3	16680	4	ABLI19205	Abli19205 Human gen	c 784	13	72.2	6324	2	AAV58938	Aav58938 Mycobacte
713	13.2	73.3	20188	12	ADN33950	Adn33950 Human CDN	c 785	13	72.2	10095	2	AAV58938	Aav58938 Mycobacte
714	13.2	73.3	20190	12	ADO471539	Ado471539 Human NOV	c 786	13	72.2	31328	3	AAH51295	Aah51295 A. terreu
715	13.2	73.3	20190	12	ADO471539	Ado471539 Human NOV	c 787	13	72.2	36292	13	ADV87726	Adv87726 Streptoco
716	13.2	73.3	22129	4	AAH59632	Aah59632 Streptocob	c 788	13	72.2	36292	13	ADV78979	Adv78979 Streptoco
717	13.2	73.3	22129	8	ACF64561	Acf64561 Proplonib	c 789	13	72.2	36412	10	ADB74383	Adb74383 Mycobacte
718	13.2	73.3	22612	13	ADK67003	Adk67003 Mouse can	c 790	13	72.2	76363	12	ADI09997	Adi09997 Rice cult
719	13.2	73.3	22612	14	ADZ12852	Adz12852 Murine ca	c 791	13	72.2	76363	12	ADI09997	Adi09997 Rice cult
720	13.2	73.3	30390	4	AAH59520	Aah59520 Proplonib	c 792	13	72.2	76363	12	ADK72433	Adk72433 Rice fert
721	13.2	73.3	30390	8	ACF64449	Acf64449 Proplonib	c 793	13	72.2	103599	4	ABX04971	Abx04971 S. cinna
c 722	13.2	73.3	30390	3	AAH61514	Aah61514 N. mening	c 794	13	72.2	103599	4	ABX04971	Abx04971 S. cinna
c 723	13.2	73.3	45265	2	AAZ23902	Aaz23902 Sequence	c 795	13	72.2	104514	11	ACN45168	Acn45168 Mouse gen
c 724	13.2	73.3	49999	2	AAZ23902	Aaz23902 Human LOB	c 796	13	72.2	110000	4	AAI99682_42	Aai99682_42
725	13.2	73.3	51837	13	ABD33453	Abd33453 Human can	c 797	13	72.2	110000	4	AAI99683_42	Aai99683_42
c 726	13.2	73.3	54929	11	AAH594396	Aah594396 Mouse gen	c 798	13	72.2	110000	6	ABN71527_18	Abn71527_18
727	13.2	73.3	56050	4	AAH594396	Aah594396 Proplonib	c 799	13	72.2	110000	6	ABN71527_18	Abn71527_18
728	13.2	73.3	56050	8	ACF64478	Acf64478 Proplonib	c 800	13	72.2	110000	13	ADN81204_19	Adn81204_19
729	13.2	73.3	57137	11	ACN44300	Acn44300 Mouse gen	c 801	13	72.2	137560	5	ADP74816	Adp74816
c 730	13.2	73.3	58540	11	ACN44640	Acn44640 Mouse gen	c 802	13	72.2	349980	12	AAH64966	Aah64966 C glutam1
731	13.2	73.3	71292	11	ACN45142	Acn45142 Human gen	c 803	12.8	71.1	20	12	ADP12127	Adp12127 bet 2 rlg
732	13.2	73.3	71655	14	ADZ13303	Adz13303 Human can	c 804	12.8	71.1	35	12	ADL65326	Adl65326 Rhodobac
c 733	13.2	73.3	104644	6	ABO99653	Abog99653 Human MS4	c 805	12.8	71.1	35	14	ADY30677	Ady30677 Monatin b
c 734	13.2	73.3	110000	3	AAH61489_0	Aah61489_0	c 806	12.8	71.1	35	14	ADX70463	Adx70463 TrypCtopha
735	13.2	73.3	110000	4	AAI99682_20	Aai99682_20	c 807	12.8	71.1	35	14	ADY58746	Ady58746 Primer se
736	13.2	73.3	110000	4	AAI99682_20	Aai99682_20	c 808	12.8	71.1	35	14	AAH01353	Aah01353 PCR prime
c 737	13.2	73.3	110000	8	ABX16390_4	Abx16390_4	c 809	12.8	71.1	45	6	ADR52341	Adr52341 Small int
738	13.2	73.3	110000	11	ABH56454_02	Abh56454_02	c 810	12.8	71.1	50	12	ABZ04062	Abz04062 Human leu
c 739	13.2	73.3	110000	11	ADM27081_14	Adm27081_14	c 811	12.8	71.1	50	12	ADP10308	Adp10308 50-mer o1
c 740	13.2	73.3	110000	11	ADM27081_15	Adm27081_15	c 812	12.8	71.1	51	4	AAI79204	Aai79204 Human s11
c 741	13.2	73.3	110000	11	ACN44150_2	Acn44150_2	c 813	12.8	71.1	51	4	AAI79206	Aai79206 Human s11
742	13.2	73.3	110000	13	ABD3267_0	Abd3267_0	c 814	12.8	71.1	51	4	AAI79194	Aai79194 Human s11
c 743	13.2	73.3	123920	11	ACN44816	Acn44816 Mouse can	c 815	12.8	71.1	100	8	ACD73505	Acd73505 E. coli K
c 744	13.2	73.3	124233	14	ACN41200	Acn41200 Murine gen	c 816	12.8	71.1	100	8	ACD73504	Acd73504 E. coli K
c 745	13.2	73.3	128668	11	ACN44074	Acn44074 Murine ca	c 817	12.8	71.1	111	2	AAQ40257	Aaq40257 Plasmid p
c 746	13.2	73.3	131680	10	ADP29092	Adp29092 Human gen	c 818	12.8	71.1	111	3	AAH89828	Aah89828 Sequence
c 747	13.2	73.3	135005	12	ADQ19501	Adq19501 Human eof	c 819	12.8	71.1	111	4	AAH12746	Aah12746 Plasmid p
c 748	13.2	73.3	132501	13	ADP67269	Adp67269 Human chr	c 820	12.8	71.1	208	2	AAV70845	Aav70845 Sequence
c 749	13.2	73.3	170489	13	ABD33314	Abd33314 Human can	c 821	12.8	71.1	225	11	ABD09839	Abd09839 Pseudomon
							c 822	12.8	71.1	230	6	ABN26088	Abn26088 Human ORF

C 823	12.8	71.1	243	8	ABZ56063	Abz56063	Apergill	C 896	12.8	71.1	583	6	ABQ55663	Abq55663	Human ova
C 824	12.8	71.1	244	4	AAK53931	Aak53931	Murine re	C 897	12.8	71.1	583	10	ACA10301	Act10301	Rice leaf
C 825	12.8	71.1	251	2	AAK12443	Aak12443	Human bia	C 898	12.8	71.1	583	13	ADU53415	Adu53415	Puariatum
C 826	12.8	71.1	254	3	AACT0110	Aact0110	Human sec	C 899	12.8	71.1	583	14	ADZ91418	Adz91418	Puariatum
C 827	12.8	71.1	276	6	ABN17900	Abn17900	Human ORF	C 900	12.8	71.1	585	6	ABQ36158	Abq36158	Oligonuclei
C 828	12.8	71.1	287	10	ABX88742	Abx88742	Corn ear-	C 901	12.8	71.1	585	6	ABQ36159	Abq36159	Oligonuclei
C 829	12.8	71.1	289	2	AAH87219	Aah87219	Human ear-	C 902	12.8	71.1	589	6	ABK54739	Abk54739	Human col
C 830	12.8	71.1	293	10	ABX88989	Abx88989	Corn ear-	C 903	12.8	71.1	594	6	ABQ49814	Abq49814	Oligonuclei
C 831	12.8	71.1	300	2	AAK98289	Aak98289	Human can	C 904	12.8	71.1	594	6	ABQ49815	Abq49815	Oligonuclei
C 832	12.8	71.1	303	12	ADK64500	Adk64500	Cotton cd	C 905	12.8	71.1	595	14	ADY98049	Ady98049	Fungal IT
C 833	12.8	71.1	305	13	ADQ18669	Adq18669	Human bof	C 906	12.8	71.1	597	6	ABN16686	Abn16686	Human ORF
C 834	12.8	71.1	319	5	AD175465	Ad175465	Human ova	C 907	12.8	71.1	597	13	ADQ53310	Adq53310	Novel can
C 835	12.8	71.1	319	5	AD169118	Ad169118	Human ova	C 908	12.8	71.1	599	14	ADY98052	Ady98052	Fungal IT
C 836	12.8	71.1	343	6	ABN77427	Abn77427	Human ORF	C 909	12.8	71.1	601	6	ABQ50119	Abq50119	Oligonuclei
C 837	12.8	71.1	347	6	ABN22254	Abn22254	Human ORF	C 910	12.8	71.1	601	6	ABQ50118	Abq50118	Oligonuclei
C 838	12.8	71.1	352	4	AAH22400	Aah22400	Human rac	C 911	12.8	71.1	607	6	ABQ54458	Abq54458	Human ova
C 839	12.8	71.1	365	2	AAV70847	Aav70847	Sequence	C 912	12.8	71.1	609	4	AAU00402	Aau00402	Human rep
C 840	12.8	71.1	378	7	ADG31202	Adg31202	Human gen	C 913	12.8	71.1	609	4	ABA07480	AbA07480	Human ova
C 841	12.8	71.1	378	7	ADY65590	Ady65590	HTRA gene	C 914	12.8	71.1	629	6	ABQ98527	Abq98527	Human ORF
C 842	12.8	71.1	382	3	AAV72782	Aav72782	5.8S rRNA	C 915	12.8	71.1	646	4	AAH06561	Aah06561	Human CDN
C 843	12.8	71.1	387	3	AAH30645	Aah30645	Human col	C 916	12.8	71.1	660	4	ABL02323	AbL02323	Drosophila
C 844	12.8	71.1	389	14	ADK25718	Adk25718	Novel cel	C 917	12.8	71.1	660	5	ABV37051	Abv37051	Human pro
C 845	12.8	71.1	390	8	ACA25967	Acta25967	Prokaryot	C 918	12.8	71.1	660	6	ABQ39008	Abq39008	Oligonuclei
C 846	12.8	71.1	390	8	ACA23244	Acta23244	Prokaryot	C 919	12.8	71.1	660	6	ABQ33847	Abq33847	Oligonuclei
C 847	12.8	71.1	397	3	ACG98648	Acg98648	Human col	C 920	12.8	71.1	660	6	ABQ39009	Abq39009	Oligonuclei
C 848	12.8	71.1	402	5	ABN75080	Abn75080	Human ORF	C 921	12.8	71.1	660	6	ABQ33846	Abq33846	Oligonuclei
C 849	12.8	71.1	405	5	ABAI3625	Abai3625	Human ner	C 922	12.8	71.1	672	14	ADY98023	Ady98023	Fungal IT
C 850	12.8	71.1	405	5	ABAI9982	Abai9982	Human ner	C 923	12.8	71.1	675	4	AAH51989	Aah51989	Mycobacte
C 851	12.8	71.1	411	8	ACA06161	Acta06161	C. glutam	C 924	12.8	71.1	682	14	ADY98020	Ady98020	Fungal IT
C 852	12.8	71.1	411	8	ACA00388	Acta00388	C. glutam	C 925	12.8	71.1	686	6	ABQ14059	Abq14059	Oligonuclei
C 853	12.8	71.1	414	3	ACG88274	Acg88274	Human col	C 926	12.8	71.1	682	6	ABQ14058	Abq14058	Oligonuclei
C 854	12.8	71.1	414	3	AAAC8334	Aaac8334	Human sec	C 927	12.8	71.1	701	6	ABT22310	Abt22310	Breast ca
C 855	12.8	71.1	427	5	ABV07110	Abv07110	Human pro	C 928	12.8	71.1	734	6	ABQ26163	Abq26163	Oligonuclei
C 856	12.8	71.1	432	8	AAQ48961	Aaq48961	Human met	C 929	12.8	71.1	734	6	ABQ26162	Abq26162	Oligonuclei
C 857	12.8	71.1	435	14	ACL70921	Actl70921	M. xanthu	C 930	12.8	71.1	735	11	ABD16493	Abd16493	Pseudomon
C 858	12.8	71.1	459	9	ACH4573	Ach4573	Human adu	C 931	12.8	71.1	751	6	ABQ18300	Abq18300	Oligonuclei
C 859	12.8	71.1	476	2	AAZ16771	Aaz16771	Human gen	C 932	12.8	71.1	751	6	ABQ18301	Abq18301	Oligonuclei
C 860	12.8	71.1	484	13	ACN52594	Actn52594	Cotton an	C 933	12.8	71.1	752	10	ADCI3584	Adci3584	Human NOV
C 861	12.8	71.1	485	6	ABH83718	Abh83718	Human ova	C 934	12.8	71.1	762	13	ADCI3586	Adci3586	Human NOV
C 862	12.8	71.1	486	9	ACH15311	Ach15311	Human adu	C 935	12.8	71.1	763	13	ADSH8607	Adsh8607	Human hou
C 863	12.8	71.1	492	12	ACH87023	Ach87023	Human gen	C 936	12.8	71.1	763	13	ADU60286	Adu60286	Housekeep
C 864	12.8	71.1	493	12	ACH94062	Ach94062	Human gen	C 937	12.8	71.1	771	13	ADT43154	Adt43154	Bacterial
C 865	12.8	71.1	494	9	ACH37883	Ach37883	Human end	C 938	12.8	71.1	784	6	ABQ37285	Abq37285	Oligonuclei
C 866	12.8	71.1	499	5	ABV11655	Abv11655	Human pro	C 939	12.8	71.1	784	6	ABQ37284	Abq37284	Oligonuclei
C 867	12.8	71.1	507	3	AAFI6380	Aafi6380	Human pro	C 940	12.8	71.1	785	10	ADF28876	Adf28876	Human nor
C 868	12.8	71.1	510	6	ABQ42192	Abq42192	Oligonuclei	C 941	12.8	71.1	786	8	ACA04819	Acta04819	CDNA enco
C 869	12.8	71.1	510	6	ABQ42193	Abq42193	Oligonuclei	C 942	12.8	71.1	795	4	AAI23802	Aai23802	Human bre
C 870	12.8	71.1	511	6	ABX93641	Abx93641	New asper	C 943	12.8	71.1	795	4	AAH07870	Aah07870	Human CDN
C 871	12.8	71.1	513	12	ACH73293	Ach73293	Human gen	C 944	12.8	71.1	813	11	ACT29508	Act29508	Rice abio
C 872	12.8	71.1	526	13	ADU12508	Adu12508	Solid tum	C 945	12.8	71.1	845	6	ABQ22604	Abq22604	Oligonuclei
C 873	12.8	71.1	526	14	ABE53260	Abe53260	Human pro	C 946	12.8	71.1	845	6	ABQ22605	Abq22605	Oligonuclei
C 874	12.8	71.1	528	6	ABQ44954	Abq44954	Oligonuclei	C 947	12.8	71.1	852	10	ACF67588	Actf67588	Photornab
C 875	12.8	71.1	528	12	ABQ44955	Abq44955	Oligonuclei	C 948	12.8	71.1	858	5	AAV77901	Aav77901	DNA encod
C 876	12.8	71.1	535	12	ACH80362	Ach80362	Human gen	C 949	12.8	71.1	867	4	AAI02813	Aai02813	Human rep
C 877	12.8	71.1	537	14	ACT66935	Act66935	M. xanthu	C 950	12.8	71.1	881	13	ADX31657	Adx31657	Human ste
C 878	12.8	71.1	538	6	ABQ49655	Abq49655	Oligonuclei	C 951	12.8	71.1	886	8	ACC57556	Actc57556	Human ste
C 879	12.8	71.1	538	6	ABQ49664	Abq49664	Oligonuclei	C 952	12.8	71.1	900	2	AAV71596	Aav71596	Mycobacte
C 880	12.8	71.1	540	4	AAI00061	Aai00061	Human rep	C 953	12.8	71.1	900	10	AAU59705	Aau59705	M. tuberc
C 881	12.8	71.1	551	3	AACT6609	Aact6609	Human ORF	C 954	12.8	71.1	900	13	ADU64256	Adu64256	Mycobacte
C 882	12.8	71.1	552	12	ADQ24957	Adq24957	Human bof	C 955	12.8	71.1	918	11	ABD16236	Abd16236	Pseudomon
C 883	12.8	71.1	555	4	AAI02812	Aai02812	Human rep	C 956	12.8	71.1	924	11	ACT27592	Act27592	Rice abio
C 884	12.8	71.1	562	6	ABQ52559	Abq52559	Oligonuclei	C 957	12.8	71.1	942	13	ADR12609	Adr12609	Gene vacc
C 885	12.8	71.1	562	6	ABQ52558	Abq52558	Oligonuclei	C 958	12.8	71.1	952	2	AAV63923	Aav63923	Mycobacte
C 886	12.8	71.1	569	6	ABQ21069	Abq21069	Oligonuclei	C 959	12.8	71.1	952	2	AAH81026	Aah81026	Nucleotid
C 887	12.8	71.1	569	6	ABQ21068	Abq21068	Oligonuclei	C 960	12.8	71.1	967	6	ABQ42625	Abq42625	Oligonuclei
C 888	12.8	71.1	573	6	ABQ23260	Abq23260	Oligonuclei	C 961	12.8	71.1	967	6	ABQ42624	Abq42624	Oligonuclei
C 889	12.8	71.1	573	6	ABQ23261	Abq23261	Oligonuclei	C 962	12.8	71.1	970	2	AAZ41416	Aaz41416	Human nor
C 890	12.8	71.1	573	12	ADJ339109	Adj339109	Plant CDN	C 963	12.8	71.1	971	6	ABQ16240	Abq16240	Oligonuclei
C 891	12.8	71.1	577	10	ADJ13732	Adj13732	C. glutam	C 964	12.8	71.1	971	6	ABQ16241	Abq16241	Oligonuclei
C 892	12.8	71.1	578	10	ABT22373	Abt22373	Breast ca	C 965	12.8	71.1	976	6	ABR93132	AbR93132	DNA seque
C 893	12.8	71.1	579	6	ABQ42902	Abq42902	Oligonuclei	C 966	12.8	71.1	993	11	ABD03398	Abd03398	Pseudomon
C 894	12.8	71.1	579	6	ABQ42903	Abq42903	Oligonuclei	C 967	12.8	71.1	996	14	ADZ75692	Adz75692	Xanthomon
C 895	12.8	71.1	583	3	AAFP09374	Aafp09374	Pnearium	C 968	12.8	71.1	999	12	ADQ85696	Adq85696	Human tum

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C 969 12.8 71.1 999 13 ADQ86772 Human tum
C 970 12.8 71.1 999 13 ADQ82260 Plant ful
C 971 12.8 71.1 1008 6 AB161976 Colom ade
C 972 12.8 71.1 1008 10 ADF76529 Novel hum
C 973 12.8 71.1 1010 4 AAI60629 Novel hum
C 974 12.8 71.1 1010 13 ADP97395 Human pol
C 975 12.8 71.1 1015 4 AAI58843 Human pol
C 976 12.8 71.1 1015 5 ADQ99064 DNA encod
C 977 12.8 71.1 1015 5 ADQ98064 DNA encod
C 978 12.8 71.1 1018 3 AAF21892 Novel hum
C 979 12.8 71.1 1020 11 ADI31337 Human bre
C 980 12.8 71.1 1020 13 ADQ83404 Human lym
C 981 12.8 71.1 1023 8 ACA25958 Prokaryot
C 982 12.8 71.1 1043 14 ADQ49508 Insulin s
C 983 12.8 71.1 1047 5 AAS85011 DNA encod
C 984 12.8 71.1 1047 10 ADF53767 Alcohol d
C 985 12.8 71.1 1047 12 ADI18257 Coryneb
C 986 12.8 71.1 1047 14 ADV69576 Coryneb
C 987 12.8 71.1 1047 14 ACI67776 M. xanthu
C 988 12.8 71.1 1052 14 ADQ62795 Human CDN
C 989 12.8 71.1 1052 14 ADY15209 DNA encod
C 990 12.8 71.1 1052 14 ADQ49144 Insulin s
C 991 12.8 71.1 1065 14 ACU73167 M. xanthu
C 992 12.8 71.1 1069 11 ACU27795 Rice abio
C 993 12.8 71.1 1084 6 ABQ47759 Oligonuc
C 994 12.8 71.1 1084 6 ABQ47758 Oligonuc
C 995 12.8 71.1 1103 6 AAF18132 Lung canc
C 996 12.8 71.1 1123 6 ABQ38699 Oligonuc
C 997 12.8 71.1 1123 6 ABQ38698 Oligonuc
C 998 12.8 71.1 1152 12 ADMA6685 DNA encod
C 999 12.8 71.1 1155 6 ABQ94237 FLO11 gen
1000 12.8 71.1 1158 6 AAI38737 Coryneb

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## ALIGNMENTS

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RESULT 1
AAV52546/c
ID AAV52546 standard; DNA, 18 BP.
XX
AC AAV52546;
XX
DT 20-NOV-1998 (first entry)
XX
DE Unmethylated CpG dinucleotide 1761.
XX
KW Unmethylated CpG dinucleotide; immune response; bacterial meningitis;
KW natural killer cell activation; NK cell; Th2 response; neonatal sepsis;
KW pulmonary disorder; asthma; environmentally induced airway disease;
KW bacterial infection; endotoxaemia; therapy; cystic fibrosis;
KW inflammatory bowel disease; ss.
XX
OS Synthetic.
XX
PN WO9837919-A1.
XX
PD 03-SEP-1998.
XX
PF 25-FEB-1998; 98WO-US003678.
XX
PR 28-FEB-1997; 97US-0039405P.
XX
PA (IOWA ) UNIV IOWA RES FOUNDD.
XX
PI Schwartz DA, Krieg AM;
XX
DR WPI; 1998-480941/41.
XX
PT Use of nucleic acids containing an unmethylated CpG - for treating a
PT subject having or at risk of having an acute decrement in air flow or
PT inhibiting an inflammatory response.
XX

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PS Example 4; Page 35; 65pp; English.
XX
XX This sequence represents an unmethylated CpG dinucleotide, and can be
CC having, in the method of the invention. The method is for treating a subject
CC using, or at risk of having an acute decrement in air flow, comprising
CC administering a nucleic acid sequence containing at least one
CC unmethylated CpG. The nucleic acids containing an unmethylated CpG
CC dinucleotide affect an immune response in a subject by activating natural
CC killer cells (NK) or redirecting a subject's immune response from a Th2
CC to a Th1 response by inducing monocytic and other cells to produce Th1
CC cytokines. They can be used to treat pulmonary disorders having an
CC immunologic component, such as asthma or environmentally induced airway
CC disease. They can also be used to treat diseases associated with Gram-
CC positive bacterial infections or endotoxaemia including bacterial
CC meningitis, neonatal sepsis, cystic fibrosis, inflammatory bowel disease
CC and liver cirrhosis, Gram-negative pneumonia, Gram-negative abdominal
CC abscess, haemorrhagic shock, disseminated intravascular coagulation, or
CC an inflammatory response to lipopolysaccharide
XX
SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

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Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 88.9%; Pred. No. 10;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 AGAGGCGCGCAGCGGUA 18
Db 18 AGAGGCGCGCAGCGGTA 1

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RESULT 2
AAV27720/c
ID AAV27720 standard; DNA, 18 BP.
XX
AC AAV27720;
XX
DT 01-OCT-1998 (first entry)
XX
DE Immunostimulatory oligodeoxyribonucleotide of the invention.
XX
KW Immunostimulatory; oligodeoxyribonucleotide; ODN;
KW unmethylated CpG dinucleotide; activate; lymphocyte; immune response;
KW Th2; Th1; cytokine; treatment; prevention; asthma; autoimmune disease;
KW desensitisation therapy; artificial adjuvant; antibody generation; ss.
XX
OS Synthetic.
XX
PN WO9818810-A1.
XX
PD 07-MAY-1998.
XX
PF 30-OCT-1997; 97WO-US019791.
XX
PR 30-OCT-1996; 96US-00738652.
XX
PA (IOWA ) UNIV IOWA RES FOUNDD.
XX
PI Krieg AM, Kline JN;
XX
DR WPI; 1998-272127/24.
XX
PT New immunostimulatory nucleic acid molecules - which contain at least one
PT unmethylated CpG dinucleotide, used for treating e.g. tumours, infections
PT or autoimmune disease.
XX
PS Disclosure; Page 49; 109pp; English.
XX
XX AAV27641-751 represent immunostimulatory oligodeoxyribonucleotides (ODNs)
CC of the invention. The ODNs contain at least one unmethylated CpG
CC dinucleotide, and have the formula: 5' N1X1CGX2N2 3', where at least one
CC nucleotide separates consecutive CpGs, X1 is adenine, guanine, or
CC thymine, X2 is cytosine or thymine, N1 is any nucleotide and N1+N2 is 0-26
CC bases with the provision that N1 and N2 does not contain a CCGG tetramer

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CC or more than one CCG or CGG trimer OR 5' NX1X2CGX3X4N 3', where at least  
 CC one nucleotide separates consecutive Cpgs, X1 and X2 are selected from  
 CC GpT, GpC, GpA, ApT and ApA, X3 and X4 are selected from TpT or CpT, N is  
 CC any nucleotide and NX1X2 is 0-26 bases with the provision that N1 and N2  
 CC does not contain a CCGG tetramer or more than one CCG or CGG trimer. The  
 CC ODNs activate lymphocytes in a subject and redirect a subject's immune  
 CC response from a Th2 to a Th1 (e.g. by inducing monocytic cells and other  
 CC cells to produce Th1 cytokines, including IL-12, IFN-gamma and GM-CSF).  
 CC The ODNs can be used to treat or prevent an asthmatic disorder,  
 CC autoimmune diseases, in desensitisation therapy, as an adjuvant  
 CC adjuvant during antibody generation in a mammal such as a mouse or a  
 CC human

XX  
 CC  
 SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 10;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGAGGGUCCACGCGGUA 18  
 |||||:|||||:|  
 DB 18 AGAGGTCGACGCGGTA 1

## RESULT 3

AAZ41906/C  
 ID AAZ41906 standard; DNA; 18 BP.

XX  
 AC AAZ41906;

XX  
 DT 24-JAN-2000 (first entry)

XX  
 DE IL-12 secretion inducing Cpg oligonucleotide 51.

XX Cpg oligonucleotide; phosphorothioate; interleukin-12; IL-12; secretion;  
 KW human PMBC; immune response; cancer; HIV; bacterial disease; asthma;  
 KW neoplastic disorder; jaagsiekte; B cell; NK cell; ss; cytokine;  
 KW antigen presenting cell; infection; allergic disease.

XX  
 OS Synthetic.

XX  
 PN WO951259-A2.

XX  
 PD 14-OCT-1999.

XX  
 PF 02-APR-1999; 99WO-US007335.

XX  
 PR 03-APR-1998; 98US-0080729P.

XX  
 PA (IOWA) UNIV IOWA RES FOUND.

XX  
 PI Krieger AM, Weiner G;

XX  
 DR WPI; 1999-620169/53.

XX  
 PT Novel synergistic combinations of immunostimulatory oligonucleotides and  
 PT immunopotentiating cytokines are useful for stimulating the immune  
 PT system.

XX  
 PS Example 8; Page 80; 91pp; English.

XX  
 CC Sequences AAZ41856-241949 are phosphorothioate Cpg oligonucleotides which  
 CC are used in the invention to induce interleukin-12 (IL-12) secretion from  
 CC human PMBC. The invention comprises stimulating an immune response in a  
 CC subject comprising administering to a subject exposed to an antigen, an  
 CC immunopotentiating cytokine and an immunostimulatory Cpg oligonucleotide  
 CC to induce a synergistic antigen specific immune response. The methods are  
 CC useful for treating cancer by stimulating an antigen specific immune  
 CC response against a cancer antigen. The methods can also be used to treat  
 CC neoplastic disorders in humans, including but not limited to: sarcoma,  
 CC carcinoma, fibroma, lymphoma, melanoma, neuroblastoma, retinoblastoma,  
 CC and glioma. The methods are also useful for treating infectious diseases,  
 CC e.g. viral diseases such as HIV, bacterial diseases, and fungal diseases.

CC The methods may also be used to treat allergic diseases, e.g. asthma. The  
 CC methods and compositions may also be applied to treat cancer and tumours  
 CC in non human subjects, e.g. cats and dogs. Neoplasias affecting  
 CC agricultural livestock may also be treated and include leukaemia,  
 CC haemangioepithelioma and bovine ocular neoplasia. Chronic, infectious,  
 CC contagious diseases of sheep and goats caused by the bacterium  
 CC Corynebacterium pseudotuberculosis, and contagious lung tumour of sheep  
 CC caused by jaagsiekte may also be treated. Cpg oligonucleotides can be  
 CC useful in activating B cells, NK cells, and antigen presenting cells,  
 CC such as monocytes and macrophages. Cpg oligonucleotides enhance antibody  
 CC dependent cellular cytotoxicity and can be used as an adjuvant in  
 CC conjunction with tumour antigens to protect against a tumour challenge

XX  
 CC  
 SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 10;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGAGGGUCCACGCGGUA 18  
 |||||:|||||:|  
 DB 18 AGAGGTCGACGCGGTA 1

## RESULT 4

AAZ47982/C  
 ID AAZ47982 standard; DNA; 18 BP.

XX  
 AC AAZ47982;

XX  
 DT 08-MAR-2000 (first entry)

XX  
 DE Immune remodeling inducing Cpg oligonucleotide SEQ ID NO:60.

XX Haematopoiesis; regulation; Cpg oligonucleotide; phosphorothioate;  
 KW immune remodeling; thrombopoiesis; anaemia; immune system; cancer;  
 KW immune response; allergic reaction; infectious disease; asthma;  
 KW thrombocytopoiesis; immunohaemolytic disorder; genetic disorder;  
 KW haemoglobinopathy; kidney failure; chronic inflammatory disorder;  
 KW rheumatoid arthritis; ss.

XX  
 OS Synthetic.

XX  
 PN WO9518118-A2.

XX  
 PD 18-NOV-1999.

XX  
 PF 14-MAY-1999; 99WO-1B001285.

XX  
 PR 14-MAY-1998; 98US-0085516P.

XX  
 PR 02-FEB-1999; 99US-00241653.

XX  
 PA (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.

XX  
 PA (CPGI-) CPG IMMUNOPHARMACEUTICALS INC.

XX  
 PI Wagner H, Lipford G;

XX  
 DR WPI; 2000-062261/05.

XX  
 PT Use of Cpg containing oligonucleotides for, e.g. inducing an antigen-  
 PT specific immune response.

XX  
 PS Example 1; Page 66; 116pp; English.

XX  
 CC The present invention describes a method using Cpg containing  
 CC oligonucleotides (ONs) for regulating immune system remodeling and for  
 CC regulating haematopoiesis. The method for inducing an antigen-specific  
 CC immune response comprises: (1) administering an ON having a sequence  
 CC including at least the formula (1), and (2) exposing the subject to an  
 CC antigen at least 3 days after the ON is administered to the subject to  
 CC produce an antigen-specific immune response; 5' X1CGX2 3' (1), where the  
 CC ON = includes at least 8 nucleotides; C and G = unmethylated, and X1 and  
 CC X2 = nucleotides. The method can be used for inducing an immune response

CC against an antigen such as cells, cell extracts, proteins,  
CC polyaccharides, polyaccharide conjugates, lipids, glycolipids,  
CC carbohydrate, viral extracts, viruses, bacteria, fungi, parasites and  
CC allergens. It can be used in a subject at risk of developing cancer or an  
CC allergic reaction. It can also be used for treating an infectious  
CC disease, allergic diseases and asthma, as well as thrombocytopaenia which  
CC is drug-induced, due to an autoimmune disorder such as idiopathic  
CC thrombocytopenic purpura, or resulting from accidental or therapeutic  
CC radiation exposure. It can also be used for treating anaemia such as drug  
CC -induced anaemia, immunohaemolytic disorder, genetic disorders such as  
CC haemoglobinopathy and inherited haemolytic anaemia, inadequate production  
CC despite adequate iron stores, chronic disease such as kidney failure, and  
CC chronic inflammatory disorder such as rheumatoid arthritis, or anaemia  
CC resulting from accidental or therapeutic radiation exposure. AA247932 to  
CC AA248029 represent phosphorothioate Cpg oligonucleotides used in the  
CC exemplification of the present invention

SO Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 18;  
Best Local Similarity 88.9%; Pred. No. 10;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18  
DB 18 AGAGGUGCGACGCGGTA 1

RESULT 5  
AA247644/C  
ID AA247644 standard; DNA; 18 BP.  
XX AA247644;  
AC  
XX  
XX  
DT 01-MAR-2000 (first entry)  
XX  
XX  
DB Parasitic infection preventing exemplary oligonucleotide SEQ ID NO:50.  
XX  
XX  
XX Immune system; immunostimulatory; parasitic infection; parasite;  
XX Cpg oligonucleotide; antigen presenting cell; natural killer cell;  
XX granulocyte; malaria; helminth disease; tick; mite; ss.  
XX  
XX Synthetic.  
XX  
XX MO9956755-A1.  
XX  
XX 11-NOV-1999.  
XX  
XX 06-MAY-1999; 99MO-US009863.  
XX  
XX 06-MAY-1998; 98US-0084512P.  
XX  
XX (IOWA ) UNIV IOWA RES FOUND.  
XX (OTTA-) OTTAWA CIVIC LOEB RES INST.  
XX (USNA ) US SEC OF NAVY.  
XX  
XX Gramzinski RA, Krieg AM, Davis HU, Hoffman SL;  
XX WPI, 2000-062123/05.  
XX  
XX Treating and preventing parasitic infections using Cpg oligonucleotides.  
XX  
XX Disclosure; Page 20; 74pp; English.  
XX  
XX The present invention describes a method for treating and preventing  
XX parasitic infection by administration of unmethylated Cpg  
XX oligonucleotides. The Cpg oligonucleotides are able to stimulate the  
XX innate immune system via the activation of immune cells, such as antigen  
XX presenting cells, natural killer cells and granulocytes. The Cpg  
XX oligonucleotides and the method can be used to treat and prevent  
XX parasitic diseases, such as malaria, helminth diseases, tick and mites in  
XX humans, animals and poultry. The oligonucleotides may be administered in  
XX conjunction with parasitocides or other therapeutic compounds after an

CC organism has been diagnosed to be infected with parasites. Diseases which  
CC can be treated or prevented include those caused by Plasmodium  
CC falciparum, P. ovale, P. malariae, P. vivax, P. knowlesi, Babesia  
CC microti, B. divergens, Trypanosoma cruzi, T. gambiense, T. rhodesiense,  
CC Schistosoma mansoni, Toxoplasma gondii, Trichinella spiralis, Leishmania  
CC major, L. donovani, L. braziliensis, and L. tropica. The parasite is  
CC especially capable of causing malaria. The present sequence represents a  
CC parasitic infection preventing exemplary oligonucleotide sequence from  
CC the present invention

SO Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 18;  
Best Local Similarity 88.9%; Pred. No. 10;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18  
DB 18 AGAGGUGCGACGCGGTA 1

RESULT 6  
AAH50628/C  
ID AAH50628 standard; DNA; 18 BP.  
XX AAH50628;  
AC  
XX  
XX  
DT 22-AUG-2001 (first entry)  
XX  
XX  
XX Natural killer cell lytic activity inducing oligonucleotide SEQ ID NO:60.  
XX  
XX  
XX Immunostimulatory; inducing; natural killer cell; lytic activity;  
XX unmethylated Cpg dinucleotide; immune response; B cell proliferation;  
XX Th1; immune activation; interleukin 6; IL-6; interferon gamma; IFN-gamma;  
XX cytokine; ss.  
XX  
XX Homo sapiens.  
XX Synthetic.  
XX  
XX US6239116-B1.  
XX  
XX 29-MAY-2001.  
XX  
XX 30-OCT-1997; 97US-00960774.  
XX  
XX 30-OCT-1996; 96US-00738652.  
XX  
XX (IOWA ) UNIV IOWA RES FOUND.  
XX (COLE-) COLEBY PHARM GROUP INC.  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Krieg AM, Kline JN;  
XX WPI, 2001-380456/40.  
XX  
XX Methods for inducing IL-6, interferon-gamma or IL-12, or stimulating  
XX natural killer cell lytic activity in a human, comprise administering to  
XX the subject or exposing a natural killer cell to immunostimulatory  
XX nucleic acids.  
XX  
XX Disclosure; Col 32; 74pp; English.  
XX  
XX The present invention describes methods for inducing interleukin 6 (IL-  
XX 6), interferon-gamma (IFN-gamma) or IL-12, or for stimulating natural  
XX killer cell lytic activity. The methods comprise administering to the  
XX subject or exposing a natural killer cell to an immunostimulatory nucleic  
XX acid. Also described are: (1) inducing IL-6 in a subject comprising  
XX administering to the subject to induce IL-6 in the subject the  
XX immunostimulatory nucleic acid; (2) stimulating natural killer cell lytic  
XX activity comprising exposing a natural killer cell to the  
XX immunostimulatory nucleic acid to stimulate natural killer cell lytic  
XX activity; (3) inducing interferon-gamma in a subject to treat an immune  
XX system deficiency comprising administering to the subject to induce

CC interferon-gamma production, the immunostimulatory nucleic acid; and (4)  
 CC inducing IL-12 in a subject comprising administering to the subject the  
 CC immunostimulatory nucleic acid. The methods are useful for inducing IL-6,  
 CC interferon-gamma or IL-12, or stimulating natural killer cell lytic  
 CC activity in a subject, particularly a human. The methods are particularly  
 CC useful for modulating an immune response. AAH50571 to AAH50671 represent  
 CC oligonucleotide sequences used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;  
 XX  
 Query Match 100.0%; Score 18; DB 4; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 10;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGAGGUGCGCAGCGGUA 18  
 DB 18 AGAGGUGCGCAGCGGUA 1  
 XX  
 RESULT 7  
 AAF98931/c  
 ID AAF98931 standard; DNA; 18 BP.  
 XX  
 AC AAF98931;  
 XX  
 DT 12-JUN-2001 (first entry)  
 XX  
 DE Immunostimulatory nucleic acid #47.  
 XX  
 KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
 KW immunostimulatory; tumour; viral infection; bacterial infection;  
 KW fungal infection; parasitic infection; cancer; asthma;  
 KW infectious disease; allergy; immune deficiency; phosphorochloate; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200122972-A2.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 25-SEP-2000; 2000MO-US026383.  
 XX  
 PR 25-SEP-1999; 99US-0156113P.  
 PR 27-SEP-1999; 99US-0156135P.  
 PR 23-AUG-2000; 2000US-0227436P.  
 XX  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.  
 PI Krieg AM, Schetter C, Vollmer J;  
 PI WPI; 2001-273485/28.  
 DR  
 XX  
 PT Vaccinating against tumors, infectious diseases, allergies and asthma  
 PT using immunostimulatory Py-rich and TG nucleic acids.  
 XX  
 PS Disclosure; Page 39; 338pp; English.  
 XX  
 CC The present invention relates to a method for stimulating an immune  
 CC response. The method comprises administering an immunostimulatory nucleic  
 CC acid to a non-rodent subject in sufficient quantity to stimulate an  
 CC immune response. The present sequence is one such immunostimulatory  
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
 CC also useful for preventing cancer, asthma, infectious disease, allergy or  
 CC immune deficiency. The present sequence can also be used to redirect a  
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
 CC present sequence may have a phosphorochloate backbone

XX  
 SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;  
 XX  
 Query Match 100.0%; Score 18; DB 4; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 10;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGAGGUGCGCAGCGGUA 18  
 DB 18 AGAGGUGCGCAGCGGUA 1  
 XX  
 RESULT 8  
 AAF98888/c  
 ID AAF98888 standard; DNA; 18 BP.  
 XX  
 AC AAF98888;  
 XX  
 DT 12-JUN-2001 (first entry)  
 XX  
 DE Immunostimulatory nucleic acid #4.  
 XX  
 KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;  
 KW immunostimulatory; tumour; viral infection; bacterial infection;  
 KW fungal infection; parasitic infection; cancer; asthma;  
 KW infectious disease; allergy; immune deficiency; phosphorochloate; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200122972-A2.  
 XX  
 PD 05-APR-2001.  
 XX  
 PF 25-SEP-2000; 2000MO-US026383.  
 XX  
 PR 25-SEP-1999; 99US-0156113P.  
 PR 27-SEP-1999; 99US-0156135P.  
 PR 23-AUG-2000; 2000US-0227436P.  
 XX  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.  
 PI Krieg AM, Schetter C, Vollmer J;  
 PI WPI; 2001-273485/28.  
 DR  
 XX  
 PT Vaccinating against tumors, infectious diseases, allergies and asthma  
 PT using immunostimulatory Py-rich and TG nucleic acids.  
 XX  
 PS Disclosure; Page 38; 338pp; English.  
 XX  
 CC The present invention relates to a method for stimulating an immune  
 CC response. The method comprises administering an immunostimulatory nucleic  
 CC acid to a non-rodent subject in sufficient quantity to stimulate an  
 CC immune response. The present sequence is one such immunostimulatory  
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
 CC also useful for preventing cancer, asthma, infectious disease, allergy or  
 CC immune deficiency. The present sequence can also be used to redirect a  
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
 CC present sequence may have a phosphorochloate backbone  
 XX  
 SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;  
 XX  
 Query Match 100.0%; Score 18; DB 4; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 10;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGAGGUGCGCAGCGGUA 18



Db 18 AGAGGTCGACGCGGTA 1

## RESULT 9

ABST7572/C  
ID ABST7572 standard; DNA; 18 BP.

AC ABST7572;

DT 13-DEC-2002 (first entry)

DE Angiogenesis inhibitory oligonucleotide #56.

XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
KM tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
KM diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
KM corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
KM rubecosis; Osler-Webber Syndrome; myocardial angiogenesis;  
KM plaque neovascularisation; telangiectasia; haemophilic joint;  
KM angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
KM scleroderma; hypertrophic scar.

OS Synthetic.

PN WO200253141-A2.

PD 11-JUL-2002.

PF 14-DEC-2001; 2001WO-US048458.

PR 14-DEC-2000; 2000US-0255534P.

PA (COLE-) COLEY PHARM GROUP INC.

PI Bratzler RL;

DR WPI; 2002-566690/60.

XX Inhibiting angiogenesis in a subject, involves administering at least one  
PT antiangiogenic nucleic acid molecule to the subject.

PS Claim 2; Page 20; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising  
CC administering at least one antiangiogenic nucleic acid molecule. Also  
CC included is a kit comprising a first container housing the antiangiogenic  
CC nucleic acids, and instructions for administering them to a subject  
CC having a condition characterised by unwanted angiogenesis. The method is  
CC useful for inhibiting angiogenesis associated with solid tumour growth,  
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
CC rubecosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
CC acid of the invention

XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 18;

Best Local Similarity 88.9%; Pred. No. 10;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGTCGACGCGGTA 18  
DB 18 AGAGGTCGACGCGGTA 1

## RESULT 10

ABST7520/C  
ID ABST7520 standard; DNA; 18 BP.

XX ABST7520;

DT 13-DEC-2002 (first entry)

DE Angiogenesis inhibitory oligonucleotide #4.

XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
KM tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
KM diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
KM corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
KM rubecosis; Osler-Webber Syndrome; myocardial angiogenesis;  
KM plaque neovascularisation; telangiectasia; haemophilic joint;  
KM angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;  
KM scleroderma; hypertrophic scar.

OS Synthetic.

PN WO200253141-A2.

PD 11-JUL-2002.

PF 14-DEC-2001; 2001WO-US048458.

PR 14-DEC-2000; 2000US-0255534P.

PA (COLE-) COLEY PHARM GROUP INC.

PI Bratzler RL;

DR WPI; 2002-566690/60.

XX Inhibiting angiogenesis in a subject, involves administering at least one  
PT antiangiogenic nucleic acid molecule to the subject.

PS Claim 2; Page 19; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising  
CC administering at least one antiangiogenic nucleic acid molecule. Also  
CC included is a kit comprising a first container housing the antiangiogenic  
CC nucleic acids, and instructions for administering them to a subject  
CC having a condition characterised by unwanted angiogenesis. The method is  
CC useful for inhibiting angiogenesis associated with solid tumour growth,  
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
CC rubecosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,  
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
CC acid of the invention

XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 18;

Best Local Similarity 88.9%; Pred. No. 10;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGTCGACGCGGTA 18  
DB 18 AGAGGTCGACGCGGTA 1

## RESULT 11

ABL39077/C  
ID ABL39077 standard; DNA; 18 BP.

AC ABL39077;

DT 16-APR-2002 (first entry)

DE Immunostimulatory nucleic acid SEQ ID NO: 485.





XX 15-UTL-1994; 94US-00276358.  
 PR 07-FEB-1995; 95US-00386063.  
 PR 30-OCT-1996; 96US-00738652.  
 PR 30-OCT-1997; 97US-00960774.  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 XX Krieger AM, Hartmann G;  
 PI WPI; 2002-689667/74.  
 DR  
 XX  
 PT Activating a dendritic cell for cancer immunotherapy or for treating  
 PT infectious or allergy disease, by contacting a dendritic cell with an  
 PT isolated nucleic acid containing at least one unmethylated CpG  
 PT dinucleotide.  
 XX  
 XX Example 6; Col 32; 52pp; English.  
 PS  
 CC This invention relates to a novel method for activating or causing  
 CC maturation of a dendritic cell. The method comprises contacting a  
 CC dendritic cell with an isolated nucleic acid containing at least one  
 CC unmethylated CpG dinucleotide in an amount effective to activate or cause  
 CC maturation of the dendritic cell, where the activation is performed ex  
 CC vivo. The method of the invention may have cytostatic or anticancer  
 CC activities. The method of the invention is useful for cancer  
 CC immunotherapy or for treating an infectious disease or allergy, by  
 CC administering an activated dendritic cell that expresses a specific cancer,  
 CC microbial or allergy causing antigen, to a subject having a cancer  
 CC including the cancer antigen, to a subject having an infection with a  
 CC microorganism including the microbial antigen or to a subject having an  
 CC allergic reaction to the allergy causing antigen, where the activated  
 CC dendritic cell is prepared using the method of the invention. The method  
 CC is useful for generating a high yield of dendritic cells by administering  
 CC an isolated nucleic acid containing at least one unmethylated CpG  
 CC dinucleotide, where the nucleic acid is 8-80 bases in length in an amount  
 CC effective to activate the dendritic cells to a subject, and isolating  
 CC dendritic cells from the subject. The use of CpG allows the generation of  
 CC mature dendritic cells from peripheral blood within two days in a well  
 CC defined system. The application of CpG for this purpose is superior to  
 CC granulocyte macrophage-colony stimulating factor (GM-CSF), which is  
 CC currently used for this purpose. CpG oligonucleotides have a longer half  
 CC life, are less expensive, and show a greater magnitude of immune effects.  
 CC The present sequence represents a CpG oligonucleotide used in the method  
 CC of the invention  
 CC  
 SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 18; DB 6; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 10;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGAGGCGCGACGCGGUA 18  
 Db |||||:|||||:|||||:  
 18 AGAGGCGCGACGCGGTA 1  
 RESULT 14  
 ACD99318/c  
 ID ACD99318 standard; DNA; 18 BP.  
 AC ACD99318;  
 XX  
 DT 25-SEP-2003 (first entry)  
 XX  
 DE Immunostimulatory nucleic acid #4.  
 XX  
 KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
 KW anticancer; gene therapy; vaccine; non-allergic inflammatory disease;  
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
 XX  
 XX Synthetic.

XX US2003050268-A1.  
 PN  
 XX 13-MAR-2003.  
 PD  
 XX 29-MAR-2002; 2002US-00112653.  
 XX  
 XX 29-MAR-2001; 2001US-0279642P.  
 PR  
 XX (KRIEGER) KRIEGER A M.  
 PA (BERG/) BERG D J.  
 XX  
 PI Krieger AM, Berg DJ;  
 PI WPI; 2003-521815/49.  
 DR  
 XX  
 PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
 PT disease by administering an immunostimulatory nucleic acid.  
 XX  
 PS Disclosure; Page 8; 229pp; English.  
 CC  
 CC The invention describes a method of treating non-allergic inflammatory  
 CC disease comprising administering to a subject having or at risk of  
 CC developing a non-allergic inflammatory disease an immunostimulatory  
 CC nucleic acid for prevention or treatment of the disease. The method is  
 CC useful for treating non-allergic inflammatory diseases, such as  
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
 CC This sequence represents an immunostimulatory nucleic acid  
 CC  
 SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 18; DB 9; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 10;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGAGGCGCGACGCGGUA 18  
 Db |||||:|||||:|||||:  
 18 AGAGGCGCGACGCGGTA 1  
 RESULT 15  
 ADB36390/c  
 ID ADB36390 standard; DNA; 18 BP.  
 AC ADB36390;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Immunostimulatory nucleic acid #4.  
 XX  
 KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
 KW hypo-responsive subject; immunostimulatory.  
 XX  
 XX Synthetic.  
 OS  
 XX US2003087848-A1.  
 PN  
 XX 08-MAY-2003.  
 PD  
 XX  
 XX 02-FEB-2001; 2001US-00776479.  
 PF  
 XX 03-FEB-2000; 2000US-0179991P.  
 PR  
 XX (BRATZLER) BRATZLER R L.  
 PA (PETERSEN) PETERSEN D M.  
 PA (FOURON) FOURON Y.  
 XX  
 PI Bratzler RL, Petersen DM, Fouron Y;  
 PI WPI; 2003-657977/62.  
 DR  
 XX

PT Treating and/or preventing allergy or asthma using an immunostimulatory  
nucleic acid alone or in combination with an asthma/allergy medicament.  
XX  
PS Disclosure; Page 5; 221pp; English.  
XX  
CC The invention relates to a method of treating or preventing allergy or  
asthma which comprises administering to a subject a poly-G nucleic acid  
in an aerosol formulation. The methods and compositions of the present  
invention are useful for diagnosing and/or treating asthma and allergy  
especially in a hypo-responsive subject. The present sequence represents  
an immunostimulatory nucleic acid of the invention.  
XX  
SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;  
Query Match 100.0%; Score 18; DB 9; Length 18;  
Best Local Similarity 88.9%; Pred. No. 10;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGAGGUGCGACGCGGUA 18  
DB 18 AGAGGTCGACGCGGTA 1  
RESULT 16  
ADB36433/c  
ID ADB36433 standard; DNA; 18 BP.  
XX  
AC ADB36433;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Immunostimulatory nucleic acid #47.  
XX  
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
hypo-responsive subject; immunostimulatory.  
OS Synthetic.  
XX  
PN US2003087848-A1.  
XX  
PD 08-MAY-2003.  
XX  
PF 02-FEB-2001; 2001US-00776479.  
XX  
PR 03-FEB-2000; 2000US-0179991P.  
XX  
PA (BRAT/) BRATZLER R L.  
PA (PETE/) PETERSEN D M.  
PA (FOUR/) FOURON Y.  
XX  
PI Bratzler RL, Petersen DM, Fouron Y;  
XX  
DR WPI; 2003-657977/62.  
XX  
PT Treating and/or preventing allergy or asthma using an immunostimulatory  
nucleic acid alone or in combination with an asthma/allergy medicament.  
XX  
PS Disclosure; Page 6; 221pp; English.  
XX  
CC The invention relates to a method of treating or preventing allergy or  
asthma which comprises administering to a subject a poly-G nucleic acid  
in an aerosol formulation. The methods and compositions of the present  
invention are useful for diagnosing and/or treating asthma and allergy  
especially in a hypo-responsive subject. The present sequence represents  
an immunostimulatory nucleic acid of the invention.  
XX  
SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;  
Query Match 100.0%; Score 18; DB 9; Length 18;  
Best Local Similarity 88.9%; Pred. No. 10;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGAGGUGCGACGCGGUA 18

DB 18 AGAGGTCGACGCGGTA 1  
RESULT 17  
AAD60215/c  
ID AAD60215 standard; DNA; 18 BP.  
XX  
AC AAD60215;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Oligonucleotide 1761 used for activating dendritic cells.  
XX  
KW Dendritic cell activation; cancer immunotherapy; infectious disease;  
allergy; cell therapy; ss.  
OS Undefined.  
XX  
PN US2003100527-A1.  
XX  
PD 29-MAY-2003.  
XX  
PF 03-JUN-2002; 2002US-00161229.  
XX  
PR 15-JUN-1994; 94US-00276358.  
PR 07-FEB-1995; 95US-00386063.  
PR 30-OCT-1996; 96US-00738652.  
PR 30-OCT-1997; 97US-00960774.  
PR 13-NOV-1998; 98US-00191170.  
XX  
PA (IOWA ) UNIV IOWA RES FOUND.  
XX  
PI Krieg AM, Hartmann G;  
XX  
DR WPI; 2003-706674/67.  
XX  
PT Activating a dendritic cell useful for treating cancer, infectious  
diseases or allergies, comprises contacting the dendritic cell with an  
amount of an isolated nucleic acid that contains at least one  
unmethylated CpG dinucleotide.  
XX  
PS Example 6; Page 18; 51pp; English.  
XX  
CC The invention relates to a method of activating a dendritic cell. The  
method involves contacting the dendritic cell with an isolated nucleic  
acid containing at least one unmethylated CpG dinucleotide, where the  
nucleic acid is about 8-80 bases in length, in an amount that activates  
the dendritic cell. The compositions and methods of the invention are  
useful for cancer immunotherapy, or for treating an infectious disease  
(e.g. viral, bacterial or fungal infections) or allergy. The invention is  
useful in cell therapy. The present sequence is an oligonucleotide used  
for activating dendritic cells  
XX  
SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;  
Query Match 100.0%; Score 18; DB 10; Length 18;  
Best Local Similarity 88.9%; Pred. No. 10;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGAGGUGCGACGCGGUA 18  
DB 18 AGAGGTCGACGCGGTA 1  
RESULT 18  
ADG68160/c  
ID ADG68160 standard; DNA; 18 BP.  
XX  
AC ADG68160;  
XX  
DT 11-MAR-2004 (first entry)  
XX

DE Unmethylated CpG dinucleotide-containing oligonucleotide #58.  
 XX Unmethylated CpG dinucleotide; immune activation; Th1 pattern;  
 KM cytokine production; NK lytic activity; B-cell proliferation;  
 KM asthmatic disorder; autoimmune disorder; CpG-associated disorder;  
 KM CpG-mediated leukocyte activation; endosomal acidification;  
 KM systemic lupus erythematosus; sepsis; inflammatory bowel disease;  
 KM psoriasis; gingivitis; arthritis; Crohn's disease; Grave's disease;  
 KM asthma; cancer; bacterial infection; viral infection; fungal infection;  
 KM parasitic infection; ss.  
 XX Synthetic.  
 OS  
 XX US2003191079-A1.  
 PN  
 XX 09-OCT-2003.  
 PD  
 XX 27-NOV-2002; 2002US-00306522.  
 PF  
 XX 15-JUL-1994; 94US-00276358.  
 PR 07-FEB-1995; 95US-00386063.  
 PR 30-OCT-1996; 96US-00738652.  
 PR 30-OCT-1997; 97US-00960774.  
 PR 31-JUL-2000; 2000US-00630319.  
 PR 02-JUL-2002; 2002US-00187489.  
 XX  
 XX (IOWA ) UNIV IOWA RES FOUND.  
 PA  
 XX  
 PI Kriegl AM, Kliman D, Steinberg AD;  
 XX  
 XX WPI; 2003-831664/77.  
 DR  
 XX  
 PT New isolated nucleic acid sequence containing at least one unmethylated  
 PT CpG dinucleotide, useful for preventing or treating autoimmune or other  
 PT CpG-associated disorders, e.g. sepsis, arthritis, Grave's disease, asthma  
 PT or cancer.  
 PT  
 XX Disclosure; SEQ ID NO 60; 70pp; English.  
 XX  
 XX The invention relates to nucleic acid sequences containing at least one  
 CC unmethylated CpG dinucleotide. The invention also relates to methods of  
 CC stimulating immune activation in a subject, where the stimulation is  
 CC predominantly a Th1 pattern of immune activation, comprising  
 CC administering a nucleic acid sequence of the invention, or optionally,  
 CC where the nucleic acid sequence acts as an adjuvant, a method of  
 CC stimulating cytokine production in a subject comprising administering a  
 CC nucleic acid sequence, a method of stimulating NK lytic activity in a  
 CC subject comprising administering a nucleic acid sequence, a method of  
 CC stimulating B-cell proliferation in a subject comprising administering a  
 CC nucleic acid sequence, a method for treating a subject having an  
 CC asthmatic disorder by administering a nucleic acid sequence in a  
 CC pharmaceutical carrier, and a method for treating a subject having an  
 CC autoimmune or other CpG-associated disorder by inhibiting CpG-mediated  
 CC leukocyte activation, comprising administering an inhibitor of endosomal  
 CC acidification in a pharmaceutical carrier. The methods are useful in  
 CC preventing or treating autoimmune or other CpG-associated disorders, such  
 CC as systemic lupus erythematosus, sepsis, inflammatory bowel disease,  
 CC psoriasis, gingivitis, arthritis, Crohn's disease, Grave's disease,  
 CC asthma, cancer or infections (e.g. viral, fungal, bacterial or parasitic  
 CC infections). This sequence represents an oligonucleotide containing an  
 CC unmethylated CpG dinucleotide, used in the scope of the invention.  
 CC  
 XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;  
 SQ

Query Match 100.0%; Score 18; DB 10; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 10;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGTCCGACGCGGTA 18  
 |||||:|||||:  
 DB 18 AGAGGGTCCGACGCGGTA 1

RESULT 19  
 ACF36780/C  
 ID ACF36780 standard; DNA; 18 BP.  
 XX  
 AC ACF36780;  
 XX  
 DT 06-NOV-2003 (first entry)  
 XX  
 XX Immunostimulatory CpG oligonucleotide, SEQ ID NO:75.  
 DE  
 XX Human TLR3; Toll-like receptor 3; TLR3 signal transduction pathway;  
 KM immunostimulant; drug screening; CpG oligonucleotide; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX WO2003031573-A2.  
 PN  
 XX 17-APR-2003.  
 PD  
 XX 03-OCT-2002; 2002WO-US031460.  
 PF  
 XX 05-OCT-2001; 2001US-0327520P.  
 PR  
 XX (COLE-) COLEF PHARM GMBH.  
 PA  
 XX Lipford G;  
 PI  
 XX  
 DR WPI; 2003-393438/37.  
 XX  
 PT Identifying an immunostimulatory compound by contacting a functional Toll  
 PT -like receptor (TLR) 3 with a test compound, and detecting a test  
 PT response mediated by the TLR3 signal transduction pathway.  
 PT  
 XX Disclosure; Page 18; 104pp; English.  
 PS  
 XX The invention relates to a method for identifying an immunostimulatory  
 CC compound which comprises contacting a functional Toll-like receptor 3  
 CC (TLR3) with a test compound, and detecting a test response mediated by  
 CC the TLR3 signal transduction pathway. A test compound is deemed to be  
 CC immunostimulatory when the test response exceeds the negative control  
 CC sequence, or equals or exceeds the reference response. The method is  
 CC useful for identifying compounds that modulate TLR3 signaling activity,  
 CC particularly immunostimulatory compounds. The method may also be used in  
 CC screening for species specificity of an immunostimulatory compound.  
 CC Sequences ACF36744-ACF36822 represent exemplary immunostimulatory CpG  
 CC oligonucleotides which may be used to stimulate TLR3 signalling activity  
 CC according to the invention  
 CC  
 XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;  
 SQ

Query Match 100.0%; Score 18; DB 10; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 10;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGTCCGACGCGGTA 18  
 |||||:|||||:  
 DB 18 AGAGGGTCCGACGCGGTA 1

RESULT 20  
 ADI01100/C  
 ID ADI01100 standard; DNA; 18 BP.  
 XX  
 AC ADI01100;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 XX Immunostimulatory CpG-related oligodeoxynucleotide - SEQ ID NO: 60.  
 DE  
 XX cancer; immunostimulatory; cytostatic; virostatic; fungicide;  
 KM antibacterial; antiparasitic; antiasmatic; brain; lung; ovary; breast;  
 KM prostate; colon; leukemia; carcinoma; sarcoma; tumour; viral; fungal;  
 KM bacterial; parasitic; asthmatic; ss; CpG; unmethylated cytosine-guanine.

XX OS Unidentified.  
 XX PN US653292-B1.  
 XX PD 25-NOV-2003.  
 XX XX  
 XX PF 21-JUN-1999; 99US-00337619.  
 XX XX  
 XX PR 15-JUL-1994; 94US-00276358.  
 XX PR 07-FEB-1995; 95US-00386063.  
 XX PR 30-OCT-1996; 96US-00738652.  
 XX PR 30-OCT-1997; 97US-00960774.  
 XX XX  
 XX PA (IOWA ) UNITV IOWA RES FOUND.  
 XX PI Krleg AM, Wehner G;  
 XX XX  
 XX DR WPI; 2004-088215/09.  
 XX XX  
 XX PT Treatment and/or prevention of cancer and other disorders, e.g. tumor and  
 XX PT viral infection, involves administering an immunostimulatory nucleic  
 XX PT acid.  
 XX PS Disclosure; SEQ ID NO 60; 71bp; English.  
 XX XX  
 XX CC The invention relates to a novel method whereby cancer is treated and/or  
 XX CC prevented by administering an immunostimulatory nucleic acid. The method  
 XX CC of the invention has cytostatic, virucide, fungicide, antibacterial,  
 XX CC antiparasitic and antiasthmatic activities and may be useful for treating  
 XX CC colon cancer, including brain, lung, ovary, breast, prostate and  
 XX CC colon cancers, as well as leukemia, carcinoma, sarcoma and tumour.  
 XX CC Furthermore, the method may be utilized to address viral, fungal,  
 XX CC bacterial or parasitic infection and asthmatic disorders. The current  
 XX CC sequence is that of the immunostimulatory Cpg (unmethylated cytosine-  
 XX CC guanine)-related oligodeoxynucleotide (ODN) of the invention.  
 XX XX  
 XX SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;  
 XX XX  
 XX Query Match 100.0%; Score 18; DB 12; Length 18;  
 XX Best Local Similarity 88.9%; Pred. No. 10;  
 XX Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGAGGUGCCACGCCGUA 18  
 Db |||||:|||||:|  
 18 AGAGGUGCCACGCCGUA 1  
 RESULT 21  
 ADM99069/C  
 ID ADM99069 standard; DNA; 18 BP.  
 XX AC ADM99069;  
 XX XX  
 XX DT 29-JUL-2004 (first entry)  
 XX XX  
 XX DE Immunostimulatory Cpg containing oligonucleotide seqid 60.  
 XX XX  
 XX KW antiallergic; antiarthritic; antiasthmatic; antibacterial;  
 KW antiinflammatory; antiparasitic; antipsoriatic; antithyroid; cytostatic;  
 KW dermatological; fungicide; gastrointestinal; immunosuppressive; virucide;  
 KW unethylated Cpg dinucleotide; asthmatic disorder; cancer; infection;  
 KW allergy; endosomal acidification; autoimmune disorder;  
 KW Cpg associated disorder; systemic lupus erythematosus; sepsis;  
 KW inflammatory bowel disease; psoriasis; gingivitis; arthritis;  
 KW Crohn's disease; Grave's disease; asthma; lymphocyte activation;  
 KW Th1 immune response; Th2 immune response; ss.  
 XX XX  
 XX OS Synthetic.  
 XX PN US2004087538-A1.  
 XX PD 06-MAY-2004.  
 XX XX

XX PF 21-NOV-2003; 2003US-00719493.  
 XX XX  
 XX PR 15-JUL-1994; 94US-00276358.  
 XX PR 07-FEB-1995; 95US-00386063.  
 XX PR 30-OCT-1996; 96US-00738652.  
 XX PR 30-OCT-1997; 97US-00960774.  
 XX PR 21-JUN-1999; 99US-00337619.  
 XX XX  
 XX PA (IOWA ) UNITV IOWA RES FOUND.  
 XX PI Krleg AM, Wehner G;  
 XX XX  
 XX DR WPI; 2004-374746/35.  
 XX XX  
 XX PT New isolated nucleic acid sequence containing at least one unmethylated  
 XX PT Cpg dinucleotide, useful for treating autoimmune or other Cpg associated  
 XX PT disorder, e.g. systemic lupus erythematosus, sepsis, psoriasis,  
 XX PT gingivitis, asthma.  
 XX PS Disclosure; SEQ ID NO 60; 70bp; English.  
 XX XX  
 XX CC The invention describes an isolated nucleic acid sequence containing at  
 XX CC least one unmethylated Cpg dinucleotide. The nucleic acid is useful for  
 XX CC treating an asthmatic disorder, and may also be used for treating cancer,  
 XX CC viral, fungal, bacterial, or parasitic infections. The nucleic acid may  
 XX CC also be used for treating allergies, and as a synthetic adjuvant.  
 XX CC Administration of an inhibitor of endosomal acidification is useful for  
 XX CC treating autoimmune or other Cpg associated disorders, such as systemic  
 XX CC lupus erythematosus, sepsis, inflammatory bowel disease, psoriasis,  
 XX CC gingivitis, arthritis, Crohn's disease, Grave's disease and asthma. This  
 XX CC sequence represents an immunostimulatory Cpg containing oligonucleotide  
 XX CC of the invention.  
 XX XX  
 XX SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;  
 XX XX  
 XX Query Match 100.0%; Score 18; DB 12; Length 18;  
 XX Best Local Similarity 88.9%; Pred. No. 10;  
 XX Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGAGGUGCCACGCCGUA 18  
 Db |||||:|||||:|  
 18 AGAGGUGCCACGCCGUA 1  
 RESULT 22  
 AD004787/C  
 ID AD004787 standard; DNA; 18 BP.  
 XX AC AD004787;  
 XX XX  
 XX DT 26-AUG-2004 (first entry)  
 XX XX  
 XX DE Cpg oligonucleotide #60 tested for immunostimulatory activity.  
 XX XX  
 XX KW Unethylated Cpg dinucleotide; immune response; T helper cell; Th;  
 KW immune activation; cytokine production;  
 KW natural killer cell lytic activity; NK; B cell proliferation;  
 KW asthmatic disorder; autoimmune disorder; Cpg associated disorder;  
 KW systemic lupus erythematosus; sepsis; inflammatory bowel disease;  
 KW psoriasis; gingivitis; arthritis; parasitic; antiinflammatory;  
 KW cancer; viral; fungal; bacterial; parasitic; antiparasitic;  
 KW dermatological; immunosuppressive; antibacterial; antipsoriatic;  
 KW antiarthritic; antithyroid; cytostatic; virucide; fungicide;  
 KW antiparasitic; ss.  
 XX XX  
 XX OS Synthetic.  
 XX PN US2004106568-A1.  
 XX PD 03-JUN-2004.  
 XX XX  
 XX PF 25-JUL-2003; 2003US-00627331.  
 XX XX

XX 15-JUL-1994; 94US-00276358.  
PR 07-FEB-1995; 95US-00386063.  
PR 30-OCT-1996; 96US-00738652.  
PR 30-OCT-1997; 97US-00960774.  
PR 31-JUL-2000; 2000US-00630319.  
PR 02-JUL-2002; 2002US-00187489.  
XX  
PA (IOWA ) UNIV IOWA RES FOUND.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA (COLE-) COLEY PHARM GROUP INC.  
PI Krieg AM, Kliman D, Steinberg AD;  
XX  
DR WPI; 2004-419485/39.  
XX  
XX New nucleic acid sequence containing unmethylated cytosine-guanine (Cpg)  
PT dinucleotide, useful for modulating immune response, e.g. stimulating Th1  
PT pattern of immune activation, cytokine production, or B cell  
PT proliferation.  
XX  
PS Disclosure; SEQ ID NO 60; 72pp; English.  
XX  
CC The present invention relates to oligonucleotide sequences containing at  
CC least one unmethylated Cpg dinucleotide that are able of modulating an  
CC immune response such as stimulating T helper cell (Th) pattern of immune  
CC activation, cytokine production, natural killer cell (NK) lytic activity,  
CC and B cell proliferation in a subject, preferably human. The  
CC immunostimulatory oligonucleotides of the invention are useful for  
CC treating asthmatic disorders, autoimmune or other Cpg associated  
CC disorders (e.g. systemic lupus erythematosus, sepsis, inflammatory bowel  
CC disease, psoriasis, gingivitis, arthritis, Crohn's disease, Grave's  
CC disease), cancer, and viral, fungal, bacterial, and parasitic diseases.  
CC The present sequence represents an unmethylated Cpg dinucleotide  
CC oligonucleotide that is tested for its ability to modulate an immune  
CC response.  
XX  
SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 100.0%; Score 18; DB 12; Length 18;  
Best Local Similarity 88.9%; Pred. No. 10;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGAGGGUCCGACCGCGGUA 18  
DB 18 AGAGGGTCCGACCGCGGTA 1  
XX  
RESULT 23  
ADU89320/c  
ID ADU89320 standard; DNA; 18 BP.  
XX  
AC ADU89320;  
XX  
DT 10-FEB-2005 (first entry)  
XX  
DE Allergic response suppressor oligonucleotide #4.  
XX  
XX ss; antiasthmatic; antiallergic; dermatological; antiinflammatory;  
XX antibacterial; virucide; immunoglobulin B antagonist; allergy;  
XX immunostimulator; asthma; rhinitis; urticaria; dermatitis;  
XX bacterial infection; viral infection.  
XX  
OS Synthetic.  
XX  
PN US2004235774-A1.  
XX  
PD 25-NOV-2004.  
XX  
XX 23-APR-2004; 2004US-00831778.  
XX  
XX 03-FEB-2000; 2000US-0179991P.  
XX  
PR 02-FEB-2001; 2001US-00776479.  
XX

XX (BRAT/) BRATZLER R L.  
PA (PETE/) PETERSEN D M.  
PA (FOUR/) FOURON Y.  
XX  
PI Bratzler RL, Petersen DM, Fouron Y;  
XX  
XX WPI; 2004-833006/82.  
XX  
XX Suppressing allergies, including asthma, rhinitis, urticaria and atopic  
PT dermatitis, in a subject, comprises administering a first and second dose  
PT of an immunostimulatory nucleic acid.  
XX  
PS Disclosure; SEQ ID NO 4; 235pp; English.  
XX  
XX  
CC The invention relates to a method of suppressing a symptom of an allergic  
CC response in a subject by administering a first and second dose of an  
CC immunostimulatory nucleic acid that comprises a nucleotide sequence  
CC comprising 5'-cg-3', and where the second dose is administered from 1 day  
CC to 8 weeks after the first dose. The methods and compositions of the  
CC present invention are useful for the treatment or prevention of asthma  
CC and allergy, including rhinitis, urticaria and atopic dermatitis, using  
CC an immunostimulatory nucleic acid alone or in combination with other  
CC medications. They can also be used in preventing bacterial and viral  
CC infections. This sequence represents an oligonucleotide used in the  
CC method of the invention.  
XX  
SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 100.0%; Score 18; DB 13; Length 18;  
Best Local Similarity 88.9%; Pred. No. 10;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGAGGGUCCGACCGCGGUA 18  
DB 18 AGAGGGTCCGACCGCGGTA 1  
XX  
RESULT 24  
ADU89372/c  
ID ADU89372 standard; DNA; 18 BP.  
XX  
AC ADU89372;  
XX  
DT 10-FEB-2005 (first entry)  
XX  
DE Allergic response suppressor oligonucleotide #56.  
XX  
XX ss; antiasthmatic; antiallergic; dermatological; antiinflammatory;  
XX antibacterial; virucide; immunoglobulin B antagonist; allergy;  
XX immunostimulator; asthma; rhinitis; urticaria; dermatitis;  
XX bacterial infection; viral infection.  
XX  
OS Synthetic.  
XX  
PN US2004235774-A1.  
XX  
PD 25-NOV-2004.  
XX  
XX 23-APR-2004; 2004US-00831778.  
XX  
XX 03-FEB-2000; 2000US-0179991P.  
XX  
PR 02-FEB-2001; 2001US-00776479.  
XX  
XX (BRAT/) BRATZLER R L.  
XX (PETE/) PETERSEN D M.  
XX (FOUR/) FOURON Y.  
XX  
XX Bratzler RL, Petersen DM, Fouron Y;  
XX  
XX WPI; 2004-833006/82.  
XX  
XX Suppressing allergies, including asthma, rhinitis, urticaria and atopic

PT dermatitis, in a subject, comprises administering a first and second dose  
 PT of an immunostimulatory nucleic acid.  
 PS Disclosure; SEQ ID NO 56; 235pp; English.  
 XX  
 CC The invention relates to a method of suppressing a symptom of an allergic  
 CC response in a subject by administering a first and second dose of an  
 CC immunostimulatory nucleic acid that comprises a nucleotide sequence  
 CC comprising 5'-cg-3', and where the second dose is administered from 1 day  
 CC to 8 weeks after the first dose. The methods and compositions of the  
 CC present invention are useful for the treatment or prevention of asthma  
 CC and allergy, including rhinitis, urticaria and atopic dermatitis, using  
 CC an immunostimulatory nucleic acid alone or in combination with other  
 CC medicaments. They can also be used in preventing bacterial and viral  
 CC infections. This sequence represents an oligonucleotide used in the  
 CC method of the invention.  
 CC  
 SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 18; DB 13; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 10;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 AGAGGUGCGCAGCGGUA 18  
 |||||:|||||:|||||:  
 18 AGAGGTCGACGCGGTA 1  
 DB  
 RESULT 25  
 ADV11411/c  
 ID ADV11411 standard; DNA; 18 BP.  
 AC ADV11411;  
 XX  
 DT 24-FEB-2005 (first entry)  
 XX  
 DE Reverse sequence of Bcl-2 antisense DNA.  
 XX  
 KW Oligonucleic acid-bearing composite; liposome;  
 KW 2-O-(2-diehyllaminoethyl)carbamoyl-1,3-O-dioleoylglycerol;  
 KW pharmaceutical; oncogene; bcl-2; cancer; viral infection; inflammation;  
 KW cytostatic; virucide; antiinflammatory; gene therapy; phosphorothioate;  
 KW ds.  
 XX  
 OS Synthetic.  
 OS unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..17  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER=Phosphorothioate backbone"  
 XX  
 PN WO2004105774-A1.  
 XX  
 PD 09-DEC-2004.  
 XX  
 PF 28-MAY-2004; 2004WO-JP007785.  
 XX  
 PR 30-MAY-2003; 2003JP-00154798.  
 PR 12-NOV-2003; 2003JP-00382819.  
 PR 31-MAR-2004; 2004JP-00104036.  
 XX  
 PA (INNSH) NIPPON SHINYAKU CO LTD.  
 XX  
 PI Yano J, Hirabayashi K, Yamaguchi T, Sonoke S;  
 XX  
 DR WPI; 2005-031376/03.  
 XX  
 PT Oligonucleic acid-bearing composite, useful for treating cancer,  
 PT comprises cationic liposome composed of 2-O-(2-  
 PT diehyllaminoethyl)carbamoyl-1,3-O-dioleoylglycerol and phospholipid as  
 PT active ingredient with oligonucleic acid.

XX  
 PS Disclosure; SEQ ID NO 6; 55pp; Japanese.  
 XX  
 CC The invention relates to an oligonucleic acid-bearing composite  
 CC comprising a cationic liposome composed of 2-O-(2-  
 CC diehyllaminoethyl)carbamoyl-1,3-O-dioleoylglycerol and phospholipid as an  
 CC active ingredient, with the oligonucleic acid having 10-15 bases. Also  
 CC disclosed is a pharmaceutical composition for preventing and/or treating  
 CC disease, comprising the oligonucleic acid-bearing composite, where the  
 CC target molecule for the oligonucleic acid-bearing composite, includes  
 CC target DNA, target RNA or target protein. The oligonucleic acid-bearing  
 CC composite has an average particle diameter of 10-100 nm. In the preferred  
 CC oligonucleic acid-bearing composite the phospholipid is lecithin, the  
 CC oligonucleotide is RNA, DNA or its derivative, preferably siRNA (short  
 CC interfering RNA), shRNA, antisense DNA, antisense RNA, DNA enzyme,  
 CC ribozyme or an aptamer. The oligo double-stranded RNA comprises an  
 CC antisense and sense RNA strand with 2 DNA bases at the 3' terminal ends.  
 CC The oligonucleic acid-bearing composite is delivered into a cell  
 CC containing a target molecule (e.g. target DNA, RNA or protein). The  
 CC target molecule of the oligonucleotide includes a viral gene of HIV,  
 CC Hepatitis C virus and Hepatitis B virus, an oncogene such as bcl-2, c-myc  
 CC and bcr-abl gene, and an inflammation related gene such as TNFalpha  
 CC (tumor necrosis factor alpha) and Fas gene, their transcription product,  
 CC translation product and the non-coding region of genomic DNA of arbitrary  
 CC protein. The oligonucleic acid-bearing composite is useful for preparing  
 CC a pharmaceutical composition for treating or preventing diseases such as  
 CC cancer, viral disease or inflammatory disease. The oligonucleic acid  
 CC enables efficient biological activity with respect to the target molecule  
 CC (e.g. target DNA, RNA or protein). This sequence represents the reverse  
 CC sequence of Bcl-2 antisense DNA.  
 CC  
 SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 18; DB 14; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 10;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 AGAGGUGCGCAGCGGUA 18  
 |||||:|||||:|||||:  
 18 AGAGGTCGACGCGGTA 1  
 DB  
 RESULT 26  
 ADM79934  
 ID ADM79934 standard; RNA; 18 BP.  
 AC ADM79934;  
 XX  
 DT 21-APR-2005 (first entry)  
 XX  
 DE Bacterial immunomodulatory CpG oligoribonucleotide, SEQ ID NO:1.  
 XX  
 KW Immune modulation; immune stimulation; bacterial infection; infection;  
 KW endotoxic shock; antibacterial; antimicrobial; immunomodulator;  
 KW immunostimulant; adjuvant; ss.  
 XX  
 OS Bacteria.  
 OS  
 FH Key Location/Qualifiers  
 FT misc\_feature 12..13  
 FT /\*tag= a  
 FT /note= "Cpg dinucleotide"  
 FT misc\_feature 14..15  
 FT /\*tag= b  
 FT /note= "Cpg dinucleotide"  
 XX  
 PN US2005032731-A1.  
 XX  
 PD 10-FEB-2005.  
 XX  
 PF 15-MAR-2004; 2004US-00800926.  
 XX  
 PR 11-MAY-1993; 93US-00059745.  
 XX



PR 20-JAN-1995; 95US-00376175.  
 PR 18-APR-1995; 95US-00517016.  
 PR 29-OCT-1996; 96US-00739264.  
 PR 17-NOV-1998; 98US-00193653.  
 PR 18-JUN-2001; 2001US-00883550.  
 XX  
 PA (MARS/) MARSHALL W E.  
 PI Marshall WB;  
 XX  
 DR WPI; 2005-161694/17.  
 XX  
 PT Composition for modulating and/or stimulating immune system of animal  
 PT useful for withstanding microbial infections and lethality of endotoxic  
 PT shock, comprises low molecular weight oligoribonucleotide from bacteria.  
 XX  
 PS Claim 5; SEQ ID NO 1; 17pp; English.  
 XX  
 CC The invention relates to a composition for modulating and/or stimulating  
 CC the immune system of an animal, comprising bacterial oligoribonucleotides  
 CC (ORN) with a molecular weight of less than 10 kD. The bacterial ORNs are  
 CC preferably ADM79934-ADM79936, contain Cpg motifs and are resistant to  
 CC RNase. Bacteria produce RNase-resistant Cpg ORNs in response to stresses  
 CC such as a change in environment, including the neutral pH they encounter  
 CC when they colonize animals. The immune systems of animals have co-evolved  
 CC to recognize such Cpg ORNs as being derived from bacteria, and has  
 CC adapted a non-toxic alerting response to their release from bacteria. The  
 CC invention also relates to a method for the preparation of the bacterial  
 CC ORNs by subjecting bacteria to one or more periods of stress, separating  
 CC the ORNs and media from the bacteria, and filtering the separated product  
 CC to remove substances with a molecular weight of more than 10 kD; and a  
 CC method of using the filtrate to modulate/stimulate the immune system of  
 CC an animal to withstand microbial infection. The composition and methods  
 CC of the invention are useful for modulating and/or stimulating the immune  
 CC system of animals (including humans, poultry and livestock), particularly  
 CC to withstand microbial infections or the onset of endotoxic shock. The  
 CC compositions may be administered orally (e.g., as a food supplement) or  
 CC parenterally, and may also be administered as an adjuvant for oral or  
 CC parenteral vaccines. The compositions may additionally be used topically  
 CC to protect against ear, nose and vaginal infections. They may further be  
 CC used to extend the viability of monocytes, thereby improving their  
 CC ability to mature into macrophages to fight infection, and may be used to  
 CC downregulate the cytotoxicity of macrophages to prevent them from  
 CC destroying normal T-cells in people with HIV infections. The composition  
 CC of the invention contains ORNs released by either harmless or pathogenic  
 CC bacteria, but is free from bacterial cells. Unlike Cpg  
 CC oligodeoxyribonucleotides (ODNs), the bacterial Cpg ORNs and compositions  
 CC containing them are non-coxic. The present sequence represents a  
 CC specifically claimed bacterial Cpg oligoribonucleotide present in  
 CC compositions of the invention.  
 XX  
 SQ Sequence 18 BP; 4 A; 4 C; 8 G; 0 T; 2 U; 0 Other;  
 Query Match 100.0%; Score 18; DB 14; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGAGGGUGCGACGCGGUA 18  
 DB 1 AGAGGGUGCGACGCGGUA 18  
 AC  
 AC ADZ88546;  
 XX  
 DT 14-JUL-2005 (first entry)  
 XX  
 DE Cpg ODN1761, to induce NK cell lytic activity, SEQ ID NO: 60 #1.  
 XX Immune stimulation; immunotherapy; nucleic acid vaccine;

KW papillomavirus infection; virucide; infection;  
 KW systemic lupus erythematosus; antiinflammatory; dermatological;  
 KW immunosuppressive; dermatological disease; immune disorder;  
 KW metabolic disorder; musculoskeletal disease; tumor; cytotoxic; neoplasm;  
 KW fungal infection; fungicide; parasitic infection; antiparasitic;  
 KW bacterial infection; antibacterial; asthma; antileukemic; inflammation;  
 KW respiratory disease; leukemia; hematological disease; allergy;  
 KW antiallergic; ss.  
 XX  
 OS Unidentified.  
 XX  
 XX US2005101554-A1.  
 XX  
 PD 12-MAY-2005.  
 XX  
 PF 25-JUL-2003; 2003US-00627413.  
 XX  
 PR 15-JUL-1994; 94US-00276358.  
 PR 07-FEB-1995; 95US-00386063.  
 PR 30-OCT-1996; 96US-00738652.  
 PR 30-OCT-1997; 97US-00960774.  
 PR 31-JUL-2000; 2000US-00630319.  
 PR 02-JUL-2002; 2002US-00187489.  
 XX  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GROUP INC.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Krieg AM, Kliman D, Steinberg AD;  
 XX  
 DR WPI; 2005-345416/35.  
 XX  
 PT Treating, preventing or ameliorating a papilloma virus infection  
 PT comprises administering to the subject a composition containing  
 PT unmethylated Cpg dinucleotide.  
 XX  
 PS Disclosure; SEQ ID NO 60; 72pp; English.  
 XX  
 CC The invention relates to unmethylated cytosine-guanine (Cpg)  
 CC dinucleotides that activate lymphocytes and redirect a subject's immune  
 CC response from a antibody (humoral) immune response (Th2) to cellular  
 CC immune response (Th1) thus acting as immunostimulatory compounds. The  
 CC invention is useful for treating, preventing or ameliorating a papilloma  
 CC virus infection, autoimmune disorders (particularly systemic lupus  
 CC erythematosus) and other disorders such as tumor or cancer, viral,  
 CC fungal, bacterial or parasitic infection, asthmatic disorder, allergic  
 CC reaction and leukemia and for stimulating immune activation. The nucleic  
 CC acid sequences of the invention are useful as an adjuvant for generating  
 CC antibodies and in the production of vaccines. The invention is also  
 CC useful in immunotherapy. The present sequence is a Cpg oligonucleotide  
 CC involved in induction of natural killer (NK) cell lytic activity. Note:  
 CC The present sequence is the SEQ ID NO: 60 which is given in the sequence  
 CC listing. This sequence differs from the SEQ ID NO: 60 shown in the  
 CC disclosure (page 19) of the specification.  
 CC  
 XX  
 SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 18; DB 14; Length 18;  
 Best Local Similarity 88.9%; Pred. No. 10;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGAGGGUGCGACGCGGUA 18  
 DB 18 AGAGGGUGCGACGCGGUA 1  
 AC  
 AC ABA16652;  
 XX  
 DT 14-JUL-2005 (first entry)



KW tumourigenesis; hepatitis B infection; human.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX  
 PH Key Location/Qualifiers  
 FT modified\_base 1..57  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "phosphorothioate backbone"  
 XX  
 PN WO200257480-A2.  
 XX  
 PD 25-JUL-2002.  
 XX  
 PF 22-JAN-2002; 2002WO-US001967.  
 XX  
 PR 22-JAN-2001; 2001US-0263244P.  
 XX  
 PA (GENT-) GENTA INC.  
 XX  
 PI Klem RE;  
 XX  
 DR WPI; 2002-590754/63.  
 XX  
 PT Hybrid oligomer comprises a cyclic AMP response element sequence and a  
 PT sequence that hybridizes to the bcl-2 pre-mRNA or mRNA useful for  
 PT preventing or treating cell-proliferative disorders e.g., cancer.  
 XX  
 PS Example 1; Page 58; 78pp; English.  
 XX  
 CC The invention relates to a hybrid oligomer comprising a cyclic AMP  
 CC response element (CRE) sequence and a sequence that hybridizes to the bcl  
 CC -2 pre-mRNA or mRNA. Also included are: (1) inhibiting the growth of  
 CC cancer cells in vitro, which comprises contacting the cancer cells with a  
 CC hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer;  
 CC (2) treating or preventing cancer in a human, which comprises  
 CC administering a hybrid oligomer or a bcl-2 antisense oligomer and a CRE  
 CC decoy oligomer; and (3) a pharmaceutical composition comprising a hybrid  
 CC oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer and a  
 CC carrier. The pharmaceutical composition of the invention is useful for  
 CC preventing or treating cell-proliferative disorders e.g., cancer;  
 CC hyperplasia or tumourigenesis and also bacterial infection, viral  
 CC infection, inflammation, anaphylaxis, allergy, arthritis, asthma,  
 CC autoimmune disorders and parasitic infection. The CRE decoy oligomer and  
 CC bcl-2 antisense oligomer are also useful for preventing or treating  
 CC hepatitis B virus infection. The hybrid oligomers can also be used for  
 CC screening candidate transcription factors or other molecules e.g., gene  
 CC regulatory proteins or for diagnostic assays. The present sequence is a  
 CC Bcl-2/CRE hybrid antisense oligonucleotide  
 XX  
 SQ Sequence 57 BP; 12 A; 17 C; 18 G; 10 T; 0 U; 0 Other;  
 XX  
 Query Match 100.0%; Score 18; DB 6; Length 57;  
 Best Local Similarity 88.9%; Pred. No. 11;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1 AGAGGUGCCACGCGGUA 18  
 |||||:|||||:|||||:  
 Db 37 AGAGGCTCCACGCGGTA 54  
 |||||:|||||:|||||:  
 XX  
 RESULT 31  
 AAQ8651/c  
 ID AAQ8651 standard; DNA; 17 BP.  
 XX  
 AC AAQ8651;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 27-SEP-1995 (first entry)  
 XX  
 DE Bcl-2 antisense oligonucleotide.  
 XX

KW Anticode oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;  
 KW lymphoma; programmed cell death; ss.  
 XX  
 OS Synthetic.  
 XX  
 PH Key Location/Qualifiers  
 FT misc\_feature 1..17  
 FT /tag= a  
 FT /note= "3'-5' (antisense) sequence"  
 XX  
 PN WO9508350-A1.  
 XX  
 PD 30-MAR-1995.  
 XX  
 PF 20-SEP-1994; 94WO-US010725.  
 XX  
 PR 20-SEP-1993; 93US-00124256.  
 XX  
 PA (REED/) REED J C.  
 XX  
 PI Reed JC;  
 XX  
 DR WPI; 1995-139394/18.  
 XX  
 PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment of human  
 PT solid tumours, esp. breast cancer.  
 XX  
 PS Example 12; Page 33; 108pp; English.  
 XX  
 CC Antisense oligonucleotides were tested for their ability to induce  
 CC programmed cell death (DNA fragmentation) in the human lymphoma cell line  
 CC RS1846. The oligonucleotides are phosphodiester targeted against the  
 CC translation initiation site (AAQ8650-55) or the 5'-cap region (AAQ8656-  
 CC 58) of human bcl-2 pre-mRNAs. The AAQ8651 oligonucleotide provided  
 CC pronounced DNA fragmentation. (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 XX  
 SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 94.4%; Score 17; DB 2; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 35;  
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 2 GAGGUGCCACGCGGUA 18  
 |||||:|||||:|||||:  
 Db 17 GAGGCTCCACGCGGTA 1  
 |||||:|||||:|||||:  
 XX  
 RESULT 32  
 ABK90272/c  
 ID ABK90272 standard; DNA; 17 BP.  
 XX  
 AC ABK90272;  
 XX  
 XX 21-OCT-2002 (first entry)  
 DT  
 XX  
 DE Bcl-2-targeting antisense oligonucleotide #9.  
 XX  
 KW Antisense; ss; probe; Bcl-2; cell proliferative disorder; cancer; CRE;  
 KW CAMP response element; bacterial infection; viral infection;  
 KW inflammation; anaphylaxis; allergy; arthritis; asthma; cytostatic;  
 KW autoimmune disorder; parasitic infection; virucide; hyperplasia;  
 KW tumourigenesis; hepatitis B infection; human.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 PN WO200257480-A2.  
 XX  
 PD 25-JUL-2002.  
 XX  
 PF 22-JAN-2002; 2002WO-US001967.  
 XX  
 PR 22-JAN-2001; 2001US-0263244P.  
 XX

XX (GENT-) GENTA INC.  
XX Klem RB;  
XX WPI; 2002-590754/63.  
XX  
XX Hybrid oligomer comprises a cyclic AMP response element sequence and a  
PT sequence that hybridizes to the bcl-2 pre-mRNA or mRNA useful for  
PT preventing or treating cell-proliferative disorders e.g., cancer.  
XX  
XX Disclosure; Page 13; 78pp; English.  
XX  
XX The invention relates to a hybrid oligomer comprising a cyclic AMP  
CC response element (CRE) sequence and a sequence that hybridizes to the bcl  
CC -2 pre-mRNA or mRNA. Also included are: (1) inhibiting the growth of  
CC cancer cells in vitro, which comprises contacting the cancer cells with a  
CC hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer;  
CC (2) treating or preventing cancer in a human, which comprises  
CC administering a hybrid oligomer or a bcl-2 antisense oligomer and a CRE  
CC decoy oligomer; and (3) a pharmaceutical composition comprising a hybrid  
CC oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer and a  
CC carrier. The pharmaceutical composition of the invention is useful for  
CC preventing or treating cell-proliferative disorders e.g., cancer,  
CC hyperplasia or tumorigenesis and also bacterial infection, viral  
CC infection, inflammation, anaphylaxis, allergy, arthritis, asthma,  
CC autoimmune disorders and parasitic infection. The CRE decoy oligomer and  
CC bcl-2 antisense oligomer are also useful for preventing or treating  
CC hepatitis B virus infection. The hybrid oligomers can also be used for  
CC screening candidate transcription factors or other molecules e.g., gene  
CC regulatory proteins or for diagnostic assays. The present sequence is a  
CC Bcl-2 antisense oligonucleotide  
XX  
SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;  
Query Match 94.4%; Score 17; DB 6; Length 17;  
Best Local Similarity 88.2%; Pred. No. 35;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GAGGGUCCGACCGCGUA 18  
DB 17 GAGGGTCGACCGCGTA 1  
RESULT 33  
ABQ78530/c  
ID ABQ78530 standard; DNA; 17 BP.  
XX  
XX  
AC ABQ78530;  
XX  
XX 25-NOV-2002 (first entry)  
DT  
XX  
XX Antisense oligodeoxynucleotide of the human bcl-2 gene.  
DE  
XX  
XX Antisense oligonucleotide; B cell lymphoma/leukemia-2 gene; bcl-2 gene;  
KW cancer; lymphoma; leukemia; chemotherapeutic agent; bone marrow purging;  
KW autoimmune disease; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX US6414134-B1.  
PN  
XX  
XX 02-JUL-2002.  
PD  
XX  
XX 28-NOV-2000; 2000US-00724426.  
PF  
XX  
XX 22-DEC-1988; 88US-00288692.  
PR  
XX 21-FEB-1992; 92US-00840716.  
PR 20-SEP-1993; 93US-00124256.  
PR 05-JUN-1995; 95US-00465485.  
PR 18-MAY-1998; 98US-00080285.  
PR 17-AUG-1999; 99US-00375514.  
XX

PA (UYBE-) UNIV PENNSYLVANIA.  
XX  
XX Reed UC;  
XX  
XX WPI; 2002-641579/69.  
XX  
XX  
XX Novel antisense oligonucleotide complementary to B cell lymphoma/leukemia  
PT -2 mRNA, useful for inhibiting cancer cell growth, for treating  
PT autoimmune disorders, and for ex vivo bone marrow purging.  
XX  
XX  
XX Claim 1; Col 17; 41pp; English.  
XX  
XX  
XX The present sequence represents an antisense oligonucleotide  
CC complementary to B cell lymphoma/leukemia-2 (bcl-2) mRNA. The antisense  
CC oligonucleotide is useful for inhibiting cancer cell (lymphoma or  
CC leukemia cells) growth, for increasing the sensitivity of cancer cells to  
CC cancer chemotherapeutic agents, or for inducing cancer cell death alone  
CC or in combination with any one or more cancer chemotherapeutic agents. It  
CC is also useful for reducing the bcl-2 gene expression or impairing bcl-2  
CC protein function, for ex vivo bone marrow purging, for removing residual  
CC malignant cells from the bone marrow, for inhibiting cancer of neoplastic  
CC cell growth, and for treating autoimmune disease  
XX  
SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;  
Query Match 94.4%; Score 17; DB 6; Length 17;  
Best Local Similarity 88.2%; Pred. No. 35;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GAGGGUCCGACCGCGUA 18  
DB 17 GAGGGTCGACCGCGTA 1  
RESULT 34  
ABL54157/c  
ID ABL54157 standard; DNA; 17 BP.  
XX  
XX  
AC ABL54157;  
XX  
XX 12-JUL-2002 (first entry)  
DT  
XX  
XX Bcl-2 antisense oligonucleotide.  
DE  
XX  
XX B cell lymphoma/leukemia-2; bcl-2; oncogene; antisense; lymphoma;  
KW leukaemia; colon carcinoma; rectal carcinoma; pancreatic cancer;  
KW breast cancer; ovarian cancer; prostate cancer; renal cell carcinoma;  
KW hepatoma; bile duct carcinoma; choriocarcinoma; cervical cancer;  
KW testicular cancer; lung carcinoma; bladder carcinoma; melanoma;  
KW head and neck cancer; brain cancer; cytostatic; human; gene therapy; ss.  
XX  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200217852-A2.  
PN  
XX  
XX 07-MAR-2002.  
PD  
XX  
XX 23-AUG-2001; 2001WO-US026414.  
PF  
XX  
XX 25-AUG-2000; 2000US-0227970P.  
PR 29-SEP-2000; 2000US-0237009P.  
PR 10-NOV-2000; 2000US-00709170.  
XX  
XX (GENT-) GENTA INC.  
PA  
XX  
XX Warrel RP, Klem RB, Fingert H;  
XX  
XX WPI; 2002-371796/40.  
XX  
XX  
XX Treating or preventing cancer, tumors and carcinomas, comprises  
PT administering B cell lymphoma/leukemia-2 antisense oligonucleotide at  
PT high doses for short period for time with one or more cancer  
PT therapeutics.



CC The invention relates to a novel method for treating cancer in a human,  
CC comprising the administration of anticod oligomers for treating bcl-2  
CC gene expressing cancer cells. The invention further comprises: a  
CC pharmaceutical composition comprising an anticod oligomer, and a  
CC pharmaceutical carrier; and increasing the sensitivity of a tumor cell to  
CC a chemotherapeutic agent. The anticod oligomers have cytostatic  
CC activity. The oligomers may be used in gene therapy to treat cancer. The  
CC method is also useful for increasing the sensitivity of a tumor cell to a  
CC chemotherapeutic agent. The types of treatable cancer include non-  
CC Hodgkin's lymphoma, prostate cancer, breast cancer, gastric-intestinal  
CC cancer, or colon cancer. The anticod oligomers are useful for inhibiting  
CC growth of cancer cells or killing tumor cells. This polynucleotide  
CC sequence represents a bcl-2 oligodeoxynucleotide of the invention.  
XX  
SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 94.4%; Score 17; DB 14; Length 17;  
Best Local Similarity 88.2%; Pred. No. 35;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GAGGGTCCGACGCGGTA 18  
DB 17 GAGGGTCCGACGCGGTA 1

RESULT 37  
AAH48722/c  
ID AAH48722 standard; DNA; 20 BP.

AC AAH48722;  
XX  
XX 19-OCT-2001 (first entry)  
XX  
XX Proto-oncogene bcl-2 associated primer SEQ ID 3.  
XX  
XX  
XX Primer: phosphorothioate; somatostatin; cytostatic; virotoxic; asthma;  
XX antiinflammatory; antiaesthematic; cardiac; antitumor therapy; cancer;  
XX viral disease; inflammatory process; somatostatin receptor;  
XX central nervous system disease; cardiovascular disease; SSTR;  
XX proto-oncogene; bcl-2; ss.  
XX  
XX Unidentified.

XX  
XX Key Location/Qualifiers  
XX modified\_base 1..20  
XX /\*tag= a  
XX /mod\_base= OTHER  
XX /note= "phosphorothioate"

XX  
XX DE10006572-A1.  
XX  
XX 23-AUG-2001.  
XX  
XX 14-FEB-2000; 2000DE-01006572.  
XX  
XX 14-FEB-2000; 2000DE-01006572.  
XX  
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX  
XX Eisehnur M, Mier W, Eritia R, Haberkorn U;  
XX  
XX WPI; 2001-530596/59.

XX  
XX New conjugates of oligonucleotides with somatostatin analogs, useful in  
XX antitumor therapy, e.g. of viral, inflammatory or asthmatic disease or  
XX especially tumors overexpressing the somatostatin receptor.

XX  
XX Example 3; Page 9; 16pp; German.

XX  
XX This invention describes a novel oligonucleotide conjugate (1) comprising  
XX (a) an oligonucleotide, at least part of the sequence of which is  
XX complementary to part of an intracellular nucleic acid sequence; and (b)  
XX a somatostatin analog. The products of the invention have cytostatic.

CC virotoxic, antiinflammatory, antiaesthematic and cardiac activity. The use  
CC of (1) is claimed in antitumor therapy, especially of cancer, viral  
CC disease, inflammatory processes or asthmatic, central nervous system or  
CC cardiovascular disease. (1) are especially used for therapy of tumors  
CC overexpressing the somatostatin receptor (SSTR) (e.g. small-cell lung  
CC tumors, breast tumors, brain tumors or other endocrine tumors), but are  
CC also useful for treating viral diseases (e.g. herpes simplex-1  
CC infection), inflammatory disease (typical target RNA the NF-kappa-B),  
CC asthmatic disease (typical target RNA the dopamine receptor), central  
CC nervous system disease (typical target RNA c-myc). (1) are efficiently  
CC taken up by cells and incorporated in target cells (via the SSTR) and are  
CC highly selective for cells overexpressing SSTRs. This sequence  
CC represents a primer used to illustrate the method of the invention  
XX  
SQ Sequence 20 BP; 2 A; 7 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 4; Length 20;  
Best Local Similarity 83.3%; Pred. No. 73;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 AGAGGGTCCGACGCGGTA 18  
DB 18 AGAGGGTCCGACGCGGTA 1

RESULT 38  
AAQ86650/c  
ID AAQ86650 standard; DNA; 17 BP.

AC AAQ86650;  
XX  
XX 25-MAR-2003 (revised)  
XX  
XX 27-SEP-1995 (first entry)  
XX  
XX Bcl-2 antisense oligonucleotide.

XX  
XX Anticod oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;  
XX lymphoma; programmed cell death; ss.  
XX  
XX Synthetic.

XX  
XX Key Location/Qualifiers  
XX misc\_feature 1..17  
XX /\*tag= a  
XX /note= "3'-5' (antisense) sequence"

XX  
XX WO9508350-A1.  
XX  
XX 30-MAR-1995.  
XX  
XX 20-SEP-1994; 94WO-US010725.  
XX  
XX 20-SEP-1993; 93US-00124256.  
XX  
XX (REED/) REED J C.

XX  
XX Reed JC;  
XX  
XX WPI; 1995-139394/18.

XX  
XX Anti-cod oligomers which bind to bcl-2 mRNA - for the treatment of human  
XX solid tumors, esp. breast cancer.

XX  
XX Example 12; Page 33; 108pp; English.

XX  
XX Antisense oligonucleotides were tested for their ability to induce  
XX programmed cell death (DNA fragmentation) in the human lymphoma cell line  
XX RS11846. The oligonucleotides are phosphodiester targeted against the  
XX translation initiation site (AAQ86650-55) or the 5'-cap region (AAQ86656-  
XX 58) of human bcl-2 pre-mRNAs. (Updated on 25-MAR-2003 to correct PN  
XX field.)

SQ Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 2; Length 17;  
Best Local Similarity 93.3%; Pred. No. 4e+02;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGUCCGACGCG 15  
DB 15 AGAGGGTCCGACGCG 1

RESULT 39  
AAV28172/C  
ID AAV28172 standard; DNA; 17 BP.  
XX  
AC AAV28172;  
XX  
XX 08-OCT-1998 (first entry)  
XX  
DE Antisense oligonucleotide to bcl-2 mRNA.  
XX  
XX Purification; oligonucleotide; matrix; affinity unit;  
XX affinity purification; antisense; bcl-2; ss.  
XX  
OS Synthetic.  
XX  
XX WO9827425-A1.  
XX  
XX 25-JUN-1998.  
XX  
XX 18-DEC-1997; 97WO-US023284.  
XX  
XX 19-DEC-1996; 96US-00769951.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Chen D, Srivatsa GS, Cole DL;  
XX  
XX WPI; 1998-362922/31.  
XX  
XX Matrix for selective separation of oligonucleotide - useful for, e.g.  
XX large scale purification of anti-sense agents from their deletion  
XX derivatives formed during synthesis.  
XX  
XX  
XX Disclosure; Page 79; 183pp; English.  
XX  
XX AAV28155-268 represent oligonucleotides which can be purified using the  
XX method of the invention. The specification describes a matrix that  
XX comprises a support and an affinity unit that specifically and reversibly  
XX binds a target oligonucleotide, and comprises a sequence of bases having  
XX the reverse complement of a hybridising portion of the target  
XX oligonucleotide. The matrix is used for affinity purification of  
XX synthetic oligonucleotides, specifically antisense agents, for treatment  
XX of hyperproliferative diseases, for treating a non-pathogen, non-  
XX hyperproliferative disease, e.g. Alzheimer's, for modulating expression  
XX of cell surface proteins, and to inhibit a eukaryotic pathogen,  
XX retrovirus or other viruses  
XX  
XX  
SQ Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 2; Length 17;  
Best Local Similarity 93.3%; Pred. No. 4e+02;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGUCCGACGCG 15  
DB 15 AGAGGGTCCGACGCG 1

RESULT 40  
AAV28172/C  
ID AAV28172 standard; DNA; 17 BP.  
XX

AC AAX18693;  
XX  
XX 10-MAY-1999 (first entry)  
XX  
XX Target bcl-2 antisense oligonucleotide #25.  
XX  
XX Cellular adhesion protein; proliferation; antisense oligonucleotide;  
XX alimentary canal; transport; gastrointestinal mucosa; cancer;  
XX Alzheimer's disease; beta-thalassemia; malaria; viral infection; HIV;  
XX inflammation; ss.  
XX  
XX Synthetic.  
XX  
XX WO9901579-A1.  
XX  
XX 14-JAN-1999.  
XX  
XX 01-JUL-1998; 98WO-US013574.  
XX  
XX 01-JUL-1997; 97US-00868629.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Teng C, Hardee G;  
XX  
XX WPI; 1999-106077/09.  
XX  
XX  
XX Composition comprising nucleic acid and penetration enhancer - used  
XX particularly for delivering therapeutic antisense oligonucleotides across  
XX the gastrointestinal mucosa, provides high bioavailability.  
XX  
XX Example 2; Page 84; 115pp; English.  
XX  
XX A pharmaceutical composition has been developed which comprises a nucleic  
XX acid and at least one penetration enhancer. The compositions are used:  
XX (i) to treat or prevent any disease or disorder that can be treated with  
XX the nucleic acid, e.g. cancer, Alzheimer's disease, beta-thalassemia,  
XX malaria, viral infections (including human immune deficiency virus  
XX (HIV)), inflammation, in human or animal medicine; (ii) to investigate  
XX the role of a gene or gene product in non-human animals; and (iii) to  
XX modulate gene expression in cells, tissues or organs. The compositions  
XX provide bioavailability of at least 15, preferably 17-35%. The  
XX penetration enhancer improves: (i) transport of the nucleic acid across  
XX the mucosa of the alimentary canal and into cells; and (ii) increases  
XX stability of the nucleic acid. Oral administration avoids the  
XX complications and expense of intravenous or other methods of  
XX administration. AAX18693 to AAX18799 and AAX18801 represent antisense  
XX oligonucleotides which can be used as the nucleic acid in the method of  
XX the invention  
XX  
XX  
SQ Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 2; Length 17;  
Best Local Similarity 93.3%; Pred. No. 4e+02;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGUCCGACGCG 15  
DB 15 AGAGGGTCCGACGCG 1

RESULT 41  
AAX23684/C  
ID AAX23684 standard; DNA; 17 BP.  
XX  
XX AAX23684;  
XX  
XX 18-JUN-1999 (first entry)  
XX  
XX Deletion sequence oligonucleotide 137.  
XX  
XX Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;  
XX probe; cellular adhesion modulator; cellular proliferation modulator;  
XX



KM human retrovirus; human immunodeficiency virus; non-human retrovirus;  
 KW HIV; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9911820-A1.  
 XX  
 PD 11-MAR-1999.  
 XX  
 PF 01-SEP-1998; 98WO-US018084.  
 XX  
 PR 02-SEP-1997; 97US-00923771.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Chen D, Srivatsa GS;  
 XX  
 DR WPI; 1999-205198/17.  
 XX  
 PT New compositions comprising sensor arrays made up of unique probe  
 PT oligonucleotides - useful for characterizing a sample of target deletion  
 PT oligonucleotides.  
 XX  
 PS Example 9; Page 149; 163pp; English.  
 XX  
 CC This invention describes a novel composition comprising a number of  
 CC sensor arrays, where each array comprises a unique probe oligonucleotide,  
 CC which is the reverse complement of part of a unique target  
 CC oligonucleotide present in a mixture of target deletion sequence  
 CC oligonucleotides. The compositions form a method for characterizing a  
 CC sample of target deletion oligonucleotides which are labeled and  
 CC hybridize with the probe oligonucleotides of the sensor arrays. Such  
 CC oligonucleotides and their targets are represented in AMX23548-X23709.  
 CC Oligonucleotides characterized by the method form pharmaceutical  
 CC compositions that are useful for modulating cellular adhesion or  
 CC proliferation, and being active against a eukaryotic pathogen, a human  
 CC retrovirus, a human immunodeficiency virus (HIV), or a non-human  
 CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory  
 CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable  
 CC characterization of deletion sequence oligonucleotides having related,  
 CC but different nucleobase sequences, and quantification of different  
 CC species of deletion sequence ("target") oligonucleotides in a mixture.  
 CC Also, if the specificity of the oligonucleotide's nucleobase sequence for  
 CC its reverse complement is not modified, the method may be performed using  
 CC oligodeoxynucleotides  
 CC  
 SQ Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;  
 XX  
 QY Query Match 83.3%; Score 15; DB 2; Length 17;  
 DB Best Local Similarity 93.3%; Pred. No. 4e+02; 0; Indels 0; Gaps 0;  
 Matches 14; Conservative 1; Mismatches 0;  
 1 AGAGGUGCGACGCG 15  
 15 AGAGGCTCCGACGCG 1  
 RESULT 42  
 ABK90271/c  
 ID ABK90271 standard; DNA; 17 BP.  
 XX  
 AC ABK90271;  
 XX  
 DT 21-OCT-2002 (first entry)  
 XX  
 DE Bcl-2-targeting antisense oligonucleotide #8.  
 XX  
 KW Antisense; ss; probe; Bcl-2; cell proliferative disorder; cancer; CRE;  
 KW CAMP response element; bacterial infection; viral infection;  
 KW inflammation; anaphylaxis; allergy; arthritis; asthma; cytostatic;  
 KW autoimmune disorder; parasitic infection; vitruicide; hyperplasia;  
 KW tumorigenesis; hepatitis B infection; human.  
 XX

OS Homo sapiens.  
 XX  
 PN WO200257480-A2.  
 XX  
 PD 25-JUL-2002.  
 XX  
 PF 22-JAN-2002; 2002WO-US001967.  
 XX  
 PR 22-JAN-2001; 2001US-0263244P.  
 XX  
 PA (GENT-) GENTA INC.  
 XX  
 PI Klem RB;  
 XX  
 DR WPI; 2002-590754/63.  
 XX  
 PT Hybrid oligomer comprises a cyclic AMP response element sequence and a  
 PT sequence that hybridizes to the bcl-2 pre-mRNA or mRNA useful for  
 PT preventing or treating cell-proliferative disorders e.g., cancer.  
 XX  
 PS Disclosure; Page 13; 78pp; English.  
 XX  
 CC The invention relates to a hybrid oligomer comprising a cyclic AMP  
 CC response element (CRE) sequence and a sequence that hybridizes to the bcl  
 CC -2 pre-mRNA or mRNA. Also included are: (1) inhibiting the growth of  
 CC cancer cells in vitro, which comprises contacting the cancer cells with a  
 CC hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer;  
 CC (2) treating or preventing cancer in a human, which comprises  
 CC administering a hybrid oligomer or a bcl-2 antisense oligomer and a CRE  
 CC decoy oligomer; and (3) a pharmaceutical composition comprising a hybrid  
 CC oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer and a  
 CC carrier. The pharmaceutical composition of the invention is useful for  
 CC preventing or treating cell-proliferative disorders e.g., cancer,  
 CC hyperplasia or tumorigenesis and also bacterial infection, viral  
 CC infection, inflammation, anaphylaxis, allergy, arthritis, asthma,  
 CC autoimmune disorders and parasitic infection. The CRE decoy oligomer and  
 CC bcl-2 antisense oligomer are also useful for preventing or treating  
 CC hepatitis B virus infection. The hybrid oligomers can also be used for  
 CC screening candidate transcription factors or other molecules e.g., gene  
 CC regulatory proteins or for diagnostic assays. The present sequence is a  
 CC Bcl-2 antisense oligonucleotide  
 CC  
 SQ Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;  
 XX  
 QY Query Match 83.3%; Score 15; DB 6; Length 17;  
 DB Best Local Similarity 93.3%; Pred. No. 4e+02; 0; Indels 0; Gaps 0;  
 Matches 14; Conservative 1; Mismatches 0;  
 1 AGAGGUGCGACGCG 15  
 15 AGAGGCTCCGACGCG 1  
 RESULT 43  
 ABQ78529/c  
 ID ABQ78529 standard; DNA; 17 BP.  
 XX  
 AC ABQ78529;  
 XX  
 DT 25-NOV-2002 (first entry).  
 XX  
 DE Antisense oligodeoxynucleotide of the human bcl-2 gene.  
 XX  
 KW Antisense oligonucleotide; B cell lymphoma/leukemia-2 gene; bcl-2 gene;  
 KW cancer; lymphoma; leukemia; chemotherapeutic agent; bone marrow purging;  
 KW autoimmune disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US641434-B1.  
 XX  
 PD 02-JUL-2002.  
 XX

PF 28-NOV-2000; 2000US-00724426.  
 XX  
 XX 22-DEC-1988; 88US-00288692.  
 PR 21-FEB-1992; 92US-00840716.  
 PR 20-SEP-1993; 93US-00124256.  
 PR 05-JUN-1995; 95US-00465485.  
 PR 18-MAY-1998; 98US-00080285.  
 PR 17-AUG-1999; 99US-00375514.  
 XX  
 PA (UYPE-) UNIV PENNSYLVANIA.  
 XX  
 PI Reed JC;  
 XX  
 XX WPI; 2002-641579/69.  
 DR  
 XX  
 XX Novel antisense oligonucleotide complementary to B cell lymphoma/leukemia  
 PT -2 mRNA, useful for inhibiting cancer cell growth, for treating  
 PT autoimmune disorders, and for ex vivo bone marrow purging.  
 PS  
 XX Example 12; Col 17; 41pp; English.  
 XX  
 XX The present sequence represents an antisense oligonucleotide  
 CC complementary to B cell lymphoma/leukemia-2 (bcl-2) mRNA. The antisense  
 CC oligonucleotide is useful for inhibiting cancer cell (lymphoma or  
 CC leukemia cells) growth, for increasing the sensitivity of cancer cells to  
 CC cancer chemotherapeutic agents, or for inducing cancer cell death alone  
 CC or in combination with any one or more cancer chemotherapeutic agents. It  
 CC is also useful for reducing the bcl-2 gene expression or impairing bcl-2  
 CC protein function, for ex vivo bone marrow purging, for removing residual  
 CC malignant cells from the bone marrow, for inhibiting cancer of neoplastic  
 CC cell growth, and for treating autoimmune disease  
 XX  
 XX Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;  
 SQ  
 Query Match 83.3%; Score 15; DB 6; Length 17;  
 Best Local Similarity 93.3%; Pred. No. 4e+02; Mismatches 0; Gaps 0;  
 Matches 14; Conservative 1; Indels 0; Gaps 0;  
 QY 1 AGAGGGGCGCAGCG 15  
 Db 15 AGAGGGGCGCAGCG 1  
 RESULT 44  
 ID ABL54156/c  
 AC ABL54156 standard; DNA; 17 BP.  
 XX  
 AC ABL54156;  
 XX  
 DT 12-JUL-2002 (first entry)  
 XX  
 DE Bcl-2 antisense oligonucleotide.  
 XX  
 XX B cell lymphoma/leukemia-2; bcl-2; oncogene; antisense; lymphoma;  
 KW leukemia; colon carcinoma; rectal carcinoma; pancreatic cancer;  
 KW breast cancer; ovarian cancer; prostate cancer; renal cell carcinoma;  
 KW hepatoma; bile duct carcinoma; choriocarcinoma; cervical cancer;  
 KW testicular cancer; lung carcinoma; bladder carcinoma; melanoma;  
 KW head and neck cancer; brain cancer; cytostatic; human; gene therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200217852-A2.  
 XX  
 PD 07-MAR-2002.  
 XX  
 XX 23-AUG-2001; 2001WO-US026414.  
 PF  
 XX 25-AUG-2000; 2000US-0227970P.  
 PR 29-SEP-2000; 2000US-0237009P.  
 PR 10-NOV-2000; 2000US-00709170.  
 XX  
 XX (GENT-) GENTA INC.  
 PA

XX  
 PI Warrel RP, Klem RE, Finger H;  
 XX  
 DR WPI; 2002-371796/40.  
 XX  
 XX Treating or preventing cancer, tumors and carcinomas, comprises  
 PT administering B cell lymphoma/leukemia-2 antisense oligonucleotide at  
 PT high doses for short period for time with one or more cancer  
 PT therapeutics.  
 PS  
 XX Disclosure; Page 54; 64pp; English.  
 XX  
 XX The present sequence is that of a B cell lymphoma/leukemia-2 (bcl-2)  
 CC antisense oligonucleotide. The present invention is directed to the use  
 CC of bcl-2 antisense oligomers, particularly G3139 (see ABL54148), to treat  
 CC and prevent bcl-2 related disorders. Administration at high doses results  
 CC in significant therapeutic responses, including low toxicity, high  
 CC tolerance and prolonged survival. Administration at high doses for short  
 CC periods of time (less than 14 days) also provides significant therapeutic  
 CC responses in the treatment of cancer. The bcl-2 antisense oligomer may  
 CC also be used to increase the sensitivity of a subject to cancer  
 CC therapeutics, and in combination with hormone treatment or gene therapy.  
 CC Conditions that may be treated or prevented include cancer of the  
 CC hematopoietic system, skin, bone and soft tissue, reproductive system,  
 CC genitourinary system, breast, endocrine system, brain, central nervous  
 CC system, peripheral nervous system, kidney, lung, respiratory system,  
 CC thorax, gastrointestinal and alimentary canal, lymph nodes, pancreas,  
 CC hepatobiliary system, or cancer of unknown primary site, non-Hodgkin's  
 CC lymphoma, Hodgkin's lymphoma, leukemia, colon carcinoma, rectal  
 CC carcinoma, pancreatic, breast, ovarian, prostate, cervical, testicular,  
 CC head and neck or brain cancer, renal cell carcinoma, hepatoma, bile duct  
 CC carcinoma, choriocarcinoma, lung carcinoma, bladder carcinoma and  
 CC melanoma (all claimed)  
 XX  
 XX Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;  
 SQ  
 Query Match 83.3%; Score 15; DB 6; Length 17;  
 Best Local Similarity 93.3%; Pred. No. 4e+02; Mismatches 0; Gaps 0;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGAGGGGCGCAGCG 15  
 Db 15 AGAGGGGCGCAGCG 1  
 RESULT 45  
 ID ADW13837/c  
 AC ADW13837 standard; DNA; 17 BP.  
 XX  
 AC ADW13837;  
 XX  
 DT 24-MAR-2005 (first entry)  
 XX  
 DE Bcl-2 antisense oligodeoxynucleotide, SEQ ID 8.  
 XX  
 XX cancer; bcl-2; chemotherapy; cytostatic; gene therapy;  
 KW non-hodgkin lymphoma; prostate tumor; breast tumor;  
 KW gastrointestinal tumor; colon tumor; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6841541-B1.  
 XX  
 PD 11-JAN-2005.  
 XX  
 XX 28-NOV-2000; 2000US-00724425.  
 PF  
 XX 21-FEB-1992; 92US-00840716.  
 PR 20-SEP-1993; 93US-00124256.  
 PR 05-JUN-1995; 95US-00465485.  
 PR 18-MAY-1998; 98US-00080285.  
 PR 22-DEC-1998; 98US-00288692.  
 PR 17-AUG-1999; 99US-00375514.  
 XX

XX (UTPR-) UNIT PENNSYLVANIA.  
 XX  
 XX Reed JC;  
 XX  
 XX WPI; 2005-072307/08.  
 XX  
 XX Treating cancer, e.g. non-Hodgkin's lymphoma, prostate cancer, or breast  
 PT cancer, by administering an amount of anticodon oligomer for treating the  
 PT cancer.  
 XX  
 XX Example 12; SEQ ID NO 8; 41pp; English.  
 XX  
 CC The invention relates to a novel method for treating cancer in a human,  
 CC comprising the administration of anticodon oligomers for treating bcl-2  
 CC gene expressing cancer cells. The invention further comprises: a  
 CC pharmaceutical composition comprising an anticodon oligomer, and a  
 CC pharmaceutical carrier; and increasing the sensitivity of a tumor cell to  
 CC chemotherapy. The anticodon oligomers have cytostatic  
 CC activity. The oligomers may be used in gene therapy to treat cancer. The  
 CC method is also useful for increasing the sensitivity of a tumor cell to a  
 CC chemotherapeutic agent. The types of treatable cancer include non-  
 CC Hodgkin's lymphoma, prostate cancer, breast cancer, gastro-intestinal  
 CC cancer, or colon cancer. The anticodon oligomers are useful for inhibiting  
 CC growth of cancer cells or killing tumor cells. This polynucleotide  
 CC sequence represents a bcl-2 oligodeoxynucleotide of the invention.  
 XX  
 XX Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;  
 XX  
 XX Query Match 83.3%; Score 15; DB 14; Length 17;  
 XX Best Local Similarity 93.3%; Pred. No. 4e+02;  
 XX Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1 AGAGGTCGCGACGCG 15  
 DB 15 AGAGGTCGCGACGCG 1  
 XX  
 XX RESULT 46  
 XX AD284115/c  
 XX ID AD284115 standard; DNA; 17 BP.  
 XX  
 XX AD284115;  
 XX  
 XX 14-JUL-2005 (first entry)  
 XX  
 XX Human bcl-2 antisense oligonucleotide, SEQ ID NO:25.  
 XX  
 XX Drug delivery; antisense therapy; antisense oligonucleotide;  
 XX cell proliferation; cancer; tumor; neoplasm; cytostatic; ss.  
 XX  
 XX Homo sapiens.  
 XX  
 XX US6887906-B1.  
 XX  
 XX 03-MAY-2005.  
 XX  
 XX 01-JUL-1998; 98US-00108673.  
 XX  
 XX 01-JUL-1997; 97US-00866829.  
 XX  
 XX (ISIS-) ISIS PHARM INC.  
 XX  
 XX Teng C, Hardee G;  
 XX  
 XX WPI; 2005-321255/33.  
 XX  
 XX Composition useful for enhancing the transport of nucleic acids at  
 PT various sites in the alimentary canal, comprising a modified nucleic acid  
 PT and capric acid and lauric acid or their salts.  
 XX  
 XX Example 2; SEQ ID NO 25; 65pp; English.  
 XX

CC The invention relates to a composition comprising a nucleic acid with a  
 CC modified nucleobase or a modified sugar residue, and capric acid and  
 CC lauric acid or pharmaceutically acceptable salts thereof. The modified  
 CC nucleic acid used in the composition of the invention is especially an  
 CC antisense oligonucleotide which decreases the expression of a cellular  
 CC adhesion protein or the rate of cellular proliferation, and preferably  
 CC contains a 5-methyl-cytosine base or a 2'-methoxyethoxy (2'-MOE) sugar  
 CC modification. Depending on the molecular target of the antisense  
 CC oligonucleotide present in the composition, the compositions can be used  
 CC for the treatment of cancers and tumors, Alzheimer's disease, beta-  
 CC thalassemia, parasite infections and viral (including retroviral)  
 CC infections. The fatty acids capric and lauric acid (and their  
 CC pharmaceutically acceptable salts) serve as penetration enhancers which  
 CC facilitate the transport of the therapeutic nucleic acid across mucous  
 CC membranes such as those of the alimentary canal, thereby increasing their  
 CC alimentary bioavailability. The composition of the invention is therefore  
 CC useful for the oral or rectal delivery of therapeutic nucleic acids such  
 CC as antisense oligonucleotides which to date have required parenteral  
 CC administration. The compositions therefore reduce the complications  
 CC (e.g. the need for sterile procedures and patient hospitalization) and  
 CC the concomitant expense associated with intravenous and other traumatic  
 CC means of administering therapeutic nucleic acids. Sequences AD284098-  
 CC AD284140 and AD284221 represent antisense oligonucleotides that modulate  
 CC cellular proliferation which may be used in compositions of the invention  
 CC for the treatment of tumors.  
 XX  
 XX Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;  
 XX  
 XX Query Match 83.3%; Score 15; DB 14; Length 17;  
 XX Best Local Similarity 93.3%; Pred. No. 4e+02;  
 XX Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 1 AGAGGTCGCGACGCG 15  
 DB 15 AGAGGTCGCGACGCG 1  
 XX  
 XX RESULT 47  
 XX ADM36038/c  
 XX ID ADM36038 standard; DNA; 18 BP.  
 XX  
 XX ADM36038;  
 XX  
 XX 03-JUN-2004 (first entry)  
 XX  
 XX Immunostimulatory CpG/di DNA oligonucleotide #41.  
 XX  
 XX ss; immunostimulatory; deoxyinosine; deoxyuridine; antigenic;  
 XX immune system deficiency; autoimmune disorder;  
 XX systemic lupus erythematosus; SLE; myasthenia gravis;  
 XX immunodeficiency disorder; AIDS; malignant tumor; gastric cancer;  
 XX skin cancer; leukaemia; lymphoma; infectious disease; dermatological;  
 XX immunosuppressive; anti-inflammatory; antibacterial; virucide;  
 XX antiparasitic; cytostatic; antirheumatic; antirheumatic; neuroprotective;  
 XX antimicrobial; antiallergic; immunopharmacological.  
 XX  
 XX Synthetic.  
 XX  
 XX OS  
 XX  
 XX Key Location/Qualifiers  
 XX modified\_base 1..18  
 XX FT /\*tag= a  
 XX FT /mod\_base= OTHER  
 XX FT /note= "OTHER= Any n represents deoxyuridine or  
 XX FT deoxyinosine"  
 XX  
 XX WO2003047602-A1.  
 XX  
 XX 12-JUN-2003.  
 XX  
 XX 05-DEC-2002; 2002WO-EP013791.  
 XX  
 XX 07-DEC-2001; 2001AT-00001924.  
 XX

PA (INTE-) INTERCELL BIOMEDIZINISCHE FORSCHUNGS.  
 XX  
 PI Schmidt W, Schellack C, Eyed A, Lingnan K;  
 XX  
 XX WPI; 2003-569024/53.  
 DR  
 XX  
 XX  
 PT Use of an immunostimulatory oligodeoxynucleic acid molecule in the  
 PT preparation of pharmaceutical composition for treating e.g. systemic  
 PT lupus erythematosus, sepsis or viral infections.  
 XX  
 XX  
 PS Example 14; Page 111; 139pp; English.  
 XX  
 XX This invention relates to a novel use of immunostimulatory  
 CC oligodeoxynucleic acid molecules (ODNs) that contain deoxyinosine (di) or  
 CC deoxyuridine (du). Specifically, it refers to ODN molecules that encode  
 CC antigenic proteins, yet do not induce the systemic production of pro-  
 CC inflammatory cytokines such as TNF-alpha and interleukin-6 (IL-6), thus  
 CC reducing the induction of potential harmful side effects. The present  
 CC invention describes compositions that are useful for preparing a  
 CC pharmaceutical composition that can activate dendritic cells, B cells,  
 CC natural killer cells and hence treat an immune system deficiency.  
 CC Furthermore, they can be used to treat various diseases including  
 CC autoimmune disorders such as systemic lupus erythematosus (SLE) and  
 CC myasthenia gravis, immunodeficiency disorders such as AIDS, malignant  
 CC tumours that cause gastric and skin cancer as well as leukaemia and  
 CC lymphoma, and various infectious diseases for example from bacteria,  
 CC viruses and protozoa. Accordingly, such compositions exhibit  
 CC dermatological, immunosuppressive, antiinflammatory, antibacterial,  
 CC virucide, antiparasitic, cytostatic, antineoplastic, antiahrthritic,  
 CC neuroprotective, antineurobiol and antiallergic activities. These  
 CC oligodeoxynucleotides have immunopharmacological activity and induce a  
 CC synergistic antigen specific immune response of an immunopotentiating  
 CC cytokine. This oligonucleotide sequence is a immunostimulatory di/du  
 CC containing ODN taken from table 1 of the invention.  
 XX  
 SQ Sequence 18 BP; 2 A; 8 C; 1 G; 4 T; 0 U; 3 Other;  
 Query Match 83.3%; Score 15; DB 11; Length 18;  
 Best Local Similarity 72.2%; Pred. No. 4e+02;  
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 AGAGGCGCGACCGCGUA 18  
 Db 18 AGAGGCGTGCANGCGTA 1  
 RESULT 48  
 ADM35932/C  
 ID ADM35932 standard; DNA; 18 BP.  
 XX  
 AC ADM35932;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 XX DNA oligo #3 useful for induction of natural killer lytic activity.  
 DE  
 XX  
 XX ss; immunostimulatory; deoxyinosine; deoxyuridine; antigenic;  
 KW immune system deficiency; autoimmune disorder;  
 KW systemic lupus erythematosus; SLE; myasthenia gravis;  
 KW immunodeficiency disorder; AIDS; malignant tumour; gastric cancer;  
 KW skin cancer; leukaemia; lymphoma; infectious disease; dermatological;  
 KW immunosuppressive; antineoplastic; antibacterial; virucide;  
 KW antiparasitic; cytostatic; antineoplastic; antiahrthritic; neuroprotective;  
 KW antineurobiol; antiallergic; immunopharmacological.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..18  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "OTHER= Any n represents deoxyuridine or  
 FT deoxyinosine"

XX  
 PN WO2003047602-A1.  
 XX  
 PD 12-JUN-2003.  
 XX  
 XX  
 PF 05-DEC-2002; 2002WO-EP013791.  
 XX  
 XX 07-DEC-2001; 2001AT-00001924.  
 PR  
 XX  
 XX (INTE-) INTERCELL BIOMEDIZINISCHE FORSCHUNGS.  
 PA  
 PI Schmidt W, Schellack C, Eyed A, Lingnan K;  
 XX  
 XX WPI; 2003-569024/53.  
 DR  
 XX  
 XX  
 PT Use of an immunostimulatory oligodeoxynucleic acid molecule in the  
 PT preparation of pharmaceutical composition for treating e.g. systemic  
 PT lupus erythematosus, sepsis or viral infections.  
 XX  
 XX  
 PS Example 14; Page 107; 139pp; English.  
 XX  
 XX This invention relates to a novel use of immunostimulatory  
 CC oligodeoxynucleic acid molecules (ODNs) that contain deoxyinosine (di) or  
 CC deoxyuridine (du). Specifically, it refers to ODN molecules that encode  
 CC antigenic proteins, yet do not induce the systemic production of pro-  
 CC inflammatory cytokines such as TNF-alpha and interleukin-6 (IL-6), thus  
 CC reducing the induction of potential harmful side effects. The present  
 CC invention describes compositions that are useful for preparing a  
 CC pharmaceutical composition that can activate dendritic cells, B cells,  
 CC natural killer cells and hence treat an immune system deficiency.  
 CC Furthermore, they can be used to treat various diseases including  
 CC autoimmune disorders such as systemic lupus erythematosus (SLE) and  
 CC myasthenia gravis, immunodeficiency disorders such as AIDS, malignant  
 CC tumours that cause gastric and skin cancer as well as leukaemia and  
 CC lymphoma, and various infectious diseases for example from bacteria,  
 CC viruses and protozoa. Accordingly, such compositions exhibit  
 CC dermatological, immunosuppressive, antiinflammatory, antibacterial,  
 CC virucide, antiparasitic, cytostatic, antineoplastic, antiahrthritic,  
 CC neuroprotective, antineurobiol and antiallergic activities. These  
 CC oligodeoxynucleotides have immunopharmacological activity and induce a  
 CC synergistic antigen specific immune response of an immunopotentiating  
 CC cytokine. This oligonucleotide sequence is an immunostimulatory di/du  
 CC containing ODN of the invention.  
 XX  
 SQ Sequence 18 BP; 2 A; 8 C; 1 G; 4 T; 0 U; 3 Other;  
 Query Match 83.3%; Score 15; DB 11; Length 18;  
 Best Local Similarity 72.2%; Pred. No. 4e+02;  
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 AGAGGCGCGACCGCGUA 18  
 Db 18 AGAGGCGTGCANGCGTA 1  
 RESULT 49  
 ADQ17851  
 ID ADQ17851 standard; DNA; 337 BP.  
 XX  
 AC ADQ17851;  
 XX  
 DT 26-AUG-2004 (first entry)  
 XX  
 XX Human soft tissue sarcoma-upregulated DNA - SEQ ID 668.  
 DE  
 XX  
 XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;  
 KW ds.  
 KW  
 OS Homo sapiens.  
 XX  
 XX  
 PN WO2004048938-A2.  
 XX  
 PD 10-JUN-2004.

```

XX 26-NOV-2003; 2003MO-US038193.
PR
XX
XX 26-NOV-2002; 2002US-0429739P.
PR
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Aziz N, Ginsburg WM, Zlotnick A;
PI WPI; 2004-441208/41.
DR
XX WPI; 2004-441208/41.
PT
XX Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
XX Example 2; SEQ ID NO 668; 210bp; English.
PS
XX The invention relates to a novel method for detecting soft tissue sarcoma
XX which comprises obtaining a first soft tissue sample from an individual
XX and a normal soft tissue sample from the same or different individual,
XX determining the expression of a gene in both samples and comparing the
XX expression of the gene in both soft tissue samples, where a higher level
XX of protein expression in the first soft tissue sample indicates the
XX presence of soft tissue sarcoma. The method of the invention has
XX cytostatic applications and may be useful for detecting soft tissue
XX sarcoma, possibly via gene therapy or vaccine production. The nucleic
XX acid sequences may be useful in diagnostic and screening applications.
XX The current sequence is that of a human soft tissue sarcoma-upregulated
XX DNA of the invention. The current sequence is not shown within the
XX specification per se but was submitted in CD format by the inventor.
SQ
XX Sequence 337 BP; 55 A; 98 C; 107 G; 77 T; 0 U; 0 Other;
SQ
Query Match      83.3%; Score 15; DB 12; Length 337;
Best Local Similarity 93.3%; Pred. No. 4.3e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY      2 GAGGGUCCGACGCCGG 16
DB      128 GAGGGUCCGACGCCGG 142

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DR WPI; 2001-514838/56.
DR P-PSDB; AAO12046.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
XX
XX Claim 1; SEQ ID NO 12037; 1399bp + Sequence Listing; English.
PS
XX The invention relates to human polynucleotides (AA179941-AA193441) and
XX the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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XX Sequence 381 BP; 87 A; 91 C; 108 G; 95 T; 0 U; 0 Other;
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Query Match      83.3%; Score 15; DB 4; Length 381;
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Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DB      20 GAGGGUCCGACGCCGG 34

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Search completed: March 18, 2006, 18:53:35  
Job time : 423.731 secs

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RESULT 50
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XX
XX AA191977;
AC
XX
XX 06-NOV-2001 (first entry)
DT
XX
XX Human polynucleotide SEQ ID NO 12037.
DB
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XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorders; arthritis; inflammation; ss.
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XX Homo sapiens.
OS
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XX WO200164835-A2.
PN
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XX 07-SEP-2001.
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XX 26-FEB-2001; 2001MO-US004927.
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XX 28-FEB-2000; 2000US-00515126.
PR
XX 18-MAY-2000; 2000US-00577409.
XX
XX (HYSE-) HYSEQ INC.
PA
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XX Tang YT, Liu C, Drmanac RT;
PI
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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

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Searched: 8023312 seqs, 1165852854 residues

Total number of hits satisfying chosen parameters: 16046624

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Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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7	13	92.9	2055	US-10-932-182A-1393	Sequence 1393, A
8	13	92.9	3002	US-11-136-527-2658	Sequence 2658, A
9	13	92.9	12514	US-11-124-367A-5111	Sequence 5111, A
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13	12.6	90.0	321019	US-10-995-561-13387	Sequence 13387, A
14	12.6	88.6	19	US-11-101-244-868490	Sequence 868490, A
15	12.4	88.6	19	US-11-083-784-868490	Sequence 868490, A
16	12.4	88.6	25	US-10-933-982-90062	Sequence 90062, A
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20	12.4	88.6	600	US-10-750-623-2691	Sequence 2691, A

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C 136	11.4	81.4	19	11	US-11-083-784-729727	Sequence 729727, A	C 209	11.4	81.4	523	6	US-09-925-065A-558558	Sequence 558558,
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C 142	11.4	81.4	20	7	US-10-831-286A-22449	Sequence 22449, A	C 215	11.4	81.4	533	6	US-09-925-065A-392824	Sequence 392824,
C 143	11.4	81.4	20	7	US-10-831-286A-22896	Sequence 22896, A	C 216	11.4	81.4	537	6	US-09-925-065A-593536	Sequence 593536,
C 144	11.4	81.4	20	12	US-11-226-943-7	Sequence 7, App1	C 217	11.4	81.4	542	9	US-11-116-881A-616	Sequence 616, App
C 145	11.4	81.4	20	12	US-11-226-943-18	Sequence 18, App1	C 218	11.4	81.4	545	6	US-09-925-065A-42076	Sequence 42076, A
C 146	11.4	81.4	24	8	US-10-310-914A-753884	Sequence 753884, A	C 219	11.4	81.4	545	6	US-09-925-065A-939369	Sequence 939369, A
C 147	11.4	81.4	24	8	US-10-310-914A-883471	Sequence 883471, A	C 220	11.4	81.4	548	6	US-09-925-065A-12538	Sequence 12538, A
C 148	11.4	81.4	25	7	US-10-932-182A-28325	Sequence 28325, A	C 221	11.4	81.4	548	6	US-09-925-065A-42462	Sequence 42462, A
C 149	11.4	81.4	25	7	US-10-932-182A-68934	Sequence 68934, A	C 222	11.4	81.4	551	6	US-09-925-065A-768235	Sequence 768235,
C 150	11.4	81.4	25	7	US-10-932-182A-68937	Sequence 68937, A	C 223	11.4	81.4	551	6	US-09-925-065A-790930	Sequence 790930,
C 151	11.4	81.4	25	7	US-10-932-182A-68938	Sequence 68938, A	C 224	11.4	81.4	551	6	US-09-925-065A-790930	Sequence 790930,
C 152	11.4	81.4	25	7	US-10-932-182A-68939	Sequence 68939, A	C 225	11.4	81.4	553	6	US-09-925-065A-552124	Sequence 552124,
C 153	11.4	81.4	25	7	US-10-932-182A-90577	Sequence 90577, A	C 226	11.4	81.4	553	6	US-09-925-065A-153267	Sequence 153267,
C 154	11.4	81.4	25	7	US-10-932-182A-115957	Sequence 115957, A	C 227	11.4	81.4	555	6	US-09-925-065A-789150	Sequence 789150,
C 155	11.4	81.4	25	7	US-10-932-182A-149045	Sequence 149045, A	C 228	11.4	81.4	555	6	US-09-925-065A-263542	Sequence 263542,
C 156	11.4	81.4	25	7	US-10-932-182A-28325	Sequence 28325, A	C 229	11.4	81.4	559	6	US-09-925-065A-263542	Sequence 263542,
C 157	11.4	81.4	25	7	US-10-932-182A-68937	Sequence 68937, A	C 230	11.4	81.4	561	6	US-09-925-065A-119415	Sequence 119415,
C 158	11.4	81.4	25	7	US-10-932-182A-68937	Sequence 68937, A	C 231	11.4	81.4	561	6	US-09-925-065A-119415	Sequence 119415,
C 159	11.4	81.4	25	7	US-10-932-182A-68938	Sequence 68938, A	C 232	11.4	81.4	565	6	US-09-925-065A-149751	Sequence 149751,
C 160	11.4	81.4	25	7	US-10-932-182A-68938	Sequence 68939, A	C 233	11.4	81.4	565	6	US-09-925-065A-149752	Sequence 149752,
C 161	11.4	81.4	25	7	US-10-932-182A-90577	Sequence 90577, A	C 234	11.4	81.4	565	6	US-09-925-065A-291745	Sequence 291745,
C 162	11.4	81.4	25	7	US-10-932-182A-115957	Sequence 115957, A	C 235	11.4	81.4	565	6	US-09-925-065A-291745	Sequence 291745,
C 163	11.4	81.4	25	7	US-10-932-182A-149045	Sequence 149045, A	C 236	11.4	81.4	566	6	US-09-925-065A-355603	Sequence 355603,
C 164	11.4	81.4	25	7	US-10-933-982-39124	Sequence 39124, A	C 237	11.4	81.4	566	6	US-09-925-065A-355604	Sequence 355604,
C 165	11.4	81.4	25	7	US-10-933-982-62646	Sequence 62646, A	C 238	11.4	81.4	568	6	US-09-925-065A-271433	Sequence 271433,
C 166	11.4	81.4	25	7	US-10-933-982-101441	Sequence 101441, A	C 239	11.4	81.4	568	6	US-09-925-065A-271434	Sequence 271434,

C 240	11.4	81.4	568	6	US-09-925-065A-421457	Sequence 421457,	C 313	11.4	81.4	653	6	US-09-925-065A-840013	Sequence 840013,
C 241	11.4	81.4	569	6	US-09-925-065A-490760	Sequence 490760,	C 314	11.4	81.4	660	6	US-09-925-065A-354747	Sequence 354747,
C 242	11.4	81.4	573	6	US-09-925-065A-402205	Sequence 402205,	C 315	11.4	81.4	660	6	US-09-925-065A-354748	Sequence 354748,
C 243	11.4	81.4	573	6	US-09-925-065A-412582	Sequence 412582,	C 316	11.4	81.4	660	6	US-09-925-065A-906681	Sequence 906681,
C 244	11.4	81.4	576	6	US-09-925-065A-412583	Sequence 412583,	C 317	11.4	81.4	668	12	US-11-136-527-1493	Sequence 1493, Ap
C 245	11.4	81.4	576	6	US-09-925-065A-106712	Sequence 106712,	C 318	11.4	81.4	683	6	US-09-925-065A-908737	Sequence 908737,
C 246	11.4	81.4	580	6	US-09-925-065A-144982	Sequence 144982,	C 319	11.4	81.4	708	6	US-09-925-065A-847600	Sequence 847600,
C 247	11.4	81.4	580	6	US-09-925-065A-148748	Sequence 148748,	C 320	11.4	81.4	708	6	US-09-925-065A-847601	Sequence 847601,
C 248	11.4	81.4	581	6	US-09-925-065A-419877	Sequence 419877,	C 321	11.4	81.4	732	7	US-10-932-182A-2479	Sequence 2479, Ap
C 249	11.4	81.4	581	6	US-09-925-065A-419878	Sequence 419878,	C 322	11.4	81.4	732	7	US-10-932-182A-2479	Sequence 2479, Ap
C 250	11.4	81.4	581	6	US-09-925-065A-119879	Sequence 419879,	C 323	11.4	81.4	750	7	US-10-932-182A-4661	Sequence 4661, Ap
C 251	11.4	81.4	582	6	US-09-925-065A-477973	Sequence 477973,	C 324	11.4	81.4	750	7	US-10-932-182A-4661	Sequence 4661, Ap
C 252	11.4	81.4	582	6	US-09-925-065A-116860	Sequence 116860,	C 325	11.4	81.4	756	7	US-10-510-959-2	Sequence 2, Appl1
C 253	11.4	81.4	583	6	US-09-925-065A-116861	Sequence 116861,	C 326	11.4	81.4	759	8	US-10-750-623-50114	Sequence 50114, A
C 254	11.4	81.4	583	6	US-09-925-065A-116862	Sequence 116862,	C 327	11.4	81.4	759	8	US-10-750-623-50114	Sequence 50114, A
C 255	11.4	81.4	583	6	US-09-925-065A-116863	Sequence 116863,	C 328	11.4	81.4	783	8	US-10-467-657-599	Sequence 399, App
C 256	11.4	81.4	584	6	US-09-925-065A-168782	Sequence 168782,	C 329	11.4	81.4	793	8	US-10-750-185-59353	Sequence 59353, A
C 257	11.4	81.4	587	6	US-09-925-065A-529457	Sequence 529457,	C 330	11.4	81.4	793	8	US-10-750-623-59353	Sequence 59353, A
C 258	11.4	81.4	587	6	US-09-925-065A-529458	Sequence 529458,	C 331	11.4	81.4	825	8	US-10-467-657-2241	Sequence 2241, Ap
C 259	11.4	81.4	587	6	US-09-925-065A-529459	Sequence 529459,	C 332	11.4	81.4	832	6	US-09-925-065A-679848	Sequence 679848,
C 260	11.4	81.4	588	6	US-09-925-065A-477972	Sequence 477972,	C 333	11.4	81.4	834	8	US-10-750-185-49368	Sequence 49368, A
C 261	11.4	81.4	589	6	US-09-925-065A-291182	Sequence 291182,	C 334	11.4	81.4	834	8	US-10-750-623-49368	Sequence 49368, A
C 262	11.4	81.4	589	6	US-09-925-065A-537680	Sequence 537680,	C 335	11.4	81.4	856	9	US-11-096-568A-4928	Sequence 4928, Ap
C 263	11.4	81.4	591	6	US-09-925-065A-538282	Sequence 538282,	C 336	11.4	81.4	886	9	US-11-096-568A-20682	Sequence 20682, A
C 264	11.4	81.4	591	6	US-09-925-065A-538283	Sequence 538283,	C 337	11.4	81.4	891	7	US-10-932-182A-2025	Sequence 2025, Ap
C 265	11.4	81.4	591	6	US-09-925-065A-556162	Sequence 556162,	C 338	11.4	81.4	891	7	US-10-932-182A-2025	Sequence 2025, Ap
C 266	11.4	81.4	595	6	US-09-925-065A-556162	Sequence 556162,	C 339	11.4	81.4	916	6	US-09-925-065A-42170	Sequence 42170, A
C 267	11.4	81.4	596	6	US-09-925-065A-126154	Sequence 126154,	C 340	11.4	81.4	969	7	US-10-932-182A-2129	Sequence 2129, Ap
C 268	11.4	81.4	600	6	US-09-925-065A-168975	Sequence 168975,	C 341	11.4	81.4	969	7	US-10-932-182A-2129	Sequence 2129, Ap
C 269	11.4	81.4	600	8	US-10-750-185-235	Sequence 235, App	C 342	11.4	81.4	994	12	US-11-024-959-183	Sequence 183, App
C 270	11.4	81.4	600	8	US-10-750-185-1663	Sequence 1663, Ap	C 343	11.4	81.4	1014	7	US-10-931-793-53	Sequence 53, Appl1
C 271	11.4	81.4	600	8	US-10-750-623-235	Sequence 235, App	C 344	11.4	81.4	1014	7	US-10-931-198-53	Sequence 53, Appl1
C 272	11.4	81.4	600	8	US-10-750-623-1663	Sequence 1663, App	C 345	11.4	81.4	1026	7	US-10-932-182A-1112	Sequence 1112, Ap
C 273	11.4	81.4	600	12	US-11-136-527-5589	Sequence 5589, Ap	C 346	11.4	81.4	1026	7	US-10-932-182A-1112	Sequence 1112, Ap
C 274	11.4	81.4	603	6	US-09-925-065A-468902	Sequence 468902,	C 347	11.4	81.4	1030	8	US-10-775-169-343	Sequence 343, App
C 275	11.4	81.4	603	6	US-09-925-065A-468903	Sequence 468903,	C 348	11.4	81.4	1040	6	US-09-925-065A-75840	Sequence 75840, A
C 276	11.4	81.4	603	6	US-09-925-065A-468904	Sequence 468904,	C 349	11.4	81.4	1093	6	US-09-925-065A-80603	Sequence 80603, A
C 277	11.4	81.4	603	6	US-09-925-065A-468905	Sequence 468905,	C 350	11.4	81.4	1093	6	US-09-925-065A-80603	Sequence 80603, A
C 278	11.4	81.4	603	6	US-09-925-065A-470416	Sequence 470416,	C 351	11.4	81.4	1107	7	US-10-932-182A-75407	Sequence 75407, A
C 279	11.4	81.4	608	12	US-11-112-908-490	Sequence 490, App	C 352	11.4	81.4	1107	7	US-10-932-182A-75407	Sequence 75407, A
C 280	11.4	81.4	609	8	US-10-467-657-7495	Sequence 7495, Ap	C 353	11.4	81.4	1116	6	US-09-925-065A-699915	Sequence 699915,
C 281	11.4	81.4	611	6	US-09-925-065A-718946	Sequence 718946,	C 354	11.4	81.4	1128	6	US-10-793-626-1171	Sequence 626, Ap
C 282	11.4	81.4	611	6	US-09-925-065A-718947	Sequence 718947,	C 355	11.4	81.4	1138	6	US-09-925-065A-692849	Sequence 692849,
C 283	11.4	81.4	611	6	US-09-925-065A-718948	Sequence 718948,	C 356	11.4	81.4	1138	6	US-09-925-065A-692850	Sequence 692850,
C 284	11.4	81.4	611	6	US-09-925-065A-718949	Sequence 718949,	C 357	11.4	81.4	1175	6	US-09-925-065A-93708	Sequence 93708, A
C 285	11.4	81.4	611	6	US-09-925-065A-824936	Sequence 824936,	C 358	11.4	81.4	1175	6	US-09-925-065A-93709	Sequence 93709, A
C 286	11.4	81.4	612	6	US-09-925-065A-137044	Sequence 137044,	C 359	11.4	81.4	1182	7	US-10-932-182A-76041	Sequence 76041, A
C 287	11.4	81.4	612	6	US-09-925-065A-137045	Sequence 137045,	C 360	11.4	81.4	1182	7	US-10-932-182A-76041	Sequence 76041, A
C 288	11.4	81.4	614	6	US-09-925-065A-523513	Sequence 523513,	C 361	11.4	81.4	1182	7	US-10-932-182A-76041	Sequence 76041, A
C 289	11.4	81.4	616	6	US-09-925-065A-461824	Sequence 461824,	C 362	11.4	81.4	1182	12	US-11-144-236-7	Sequence 7, Appl1
C 290	11.4	81.4	616	6	US-09-925-065A-461825	Sequence 461825,	C 363	11.4	81.4	1196	8	US-10-750-185-58400	Sequence 58400, A
C 291	11.4	81.4	618	6	US-09-925-065A-938880	Sequence 938880,	C 364	11.4	81.4	1196	8	US-10-750-623-58400	Sequence 58400, A
C 292	11.4	81.4	618	6	US-09-925-065A-954572	Sequence 954572,	C 365	11.4	81.4	1235	9	US-10-770-726-4	Sequence 4, Appl1
C 293	11.4	81.4	621	6	US-09-925-065A-525353	Sequence 525353,	C 366	11.4	81.4	1252	9	US-11-096-568A-7048	Sequence 7048, Ap
C 294	11.4	81.4	621	6	US-09-925-065A-820790	Sequence 820790,	C 367	11.4	81.4	1290	8	US-10-750-185-40140	Sequence 40140, A
C 295	11.4	81.4	622	6	US-09-925-065A-213345	Sequence 213345,	C 368	11.4	81.4	1290	8	US-10-750-623-40140	Sequence 40140, A
C 296	11.4	81.4	622	6	US-09-925-065A-421458	Sequence 421458,	C 369	11.4	81.4	1306	8	US-10-750-185-34631	Sequence 34631, A
C 297	11.4	81.4	622	6	US-09-925-065A-886865	Sequence 886865,	C 370	11.4	81.4	1329	8	US-10-750-623-34631	Sequence 34631, A
C 298	11.4	81.4	623	6	US-09-925-065A-54104	Sequence 54104, A	C 371	11.4	81.4	1329	7	US-10-932-182A-75773	Sequence 75773, A
C 299	11.4	81.4	624	6	US-09-925-065A-460178	Sequence 460178,	C 372	11.4	81.4	1349	9	US-10-932-182A-75773	Sequence 75773, A
C 300	11.4	81.4	632	6	US-09-925-065A-460178	Sequence 460178,	C 373	11.4	81.4	1349	9	US-11-096-568A-21697	Sequence 21697, A
C 301	11.4	81.4	632	6	US-09-925-065A-469646	Sequence 469646,	C 374	11.4	81.4	1353	8	US-10-750-185-60402	Sequence 60402, A
C 302	11.4	81.4	632	6	US-09-925-065A-687225	Sequence 687225,	C 375	11.4	81.4	1353	8	US-10-750-623-60402	Sequence 60402, A
C 303	11.4	81.4	632	6	US-09-925-065A-903405	Sequence 903405,	C 376	11.4	81.4	1356	8	US-10-510-876-3	Sequence 3, Appl1
C 304	11.4	81.4	635	6	US-09-925-065A-488298	Sequence 488298,	C 377	11.4	81.4	1372	8	US-10-750-185-44630	Sequence 44630, A
C 305	11.4	81.4	636	6	US-09-925-065A-284166	Sequence 284166,	C 378	11.4	81.4	1372	8	US-10-750-623-44630	Sequence 44630, A
C 306	11.4	81.4	636	6	US-09-925-065A-284167	Sequence 284167,	C 379	11.4	81.4	1386	8	US-10-750-185-61595	Sequence 61595, A
C 307	11.4	81.4	640	6	US-09-925-065A-908935	Sequence 908935,	C 380	11.4	81.4	1386	9	US-10-750-623-61595	Sequence 61595, A
C 308	11.4	81.4	644	6	US-09-925-065A-131661	Sequence 131661,	C 381	11.4	81.4	1391	9	US-11-096-568A-10024	Sequence 10024, A
C 309	11.4	81.4	644	6	US-09-925-065A-131662	Sequence 131662,	C 382	11.4	81.4	1396	8	US-10-750-185-30337	Sequence 30337, A
C 310	11.4	81.4	644	6	US-09-925-065A-131663	Sequence 131663,	C 383	11.4	81.4	1396	8	US-10-750-623-30337	Sequence 30337, A
C 311	11.4	81.4	645	6	US-09-925-065A-753018	Sequence 753018,	C 384	11.4	81.4	1399	5	US-09-978-360A-395	Sequence 395, App
C 312	11.4	81.4	645	6	US-09-925-065A-824428	Sequence 824428,	C 385	11.4	81.4	1430	8	US-10-750-185-61160	Sequence 61160, A

C 386	11.4	81.4	1430	8	US-10-750-623-61160	Sequence 61160, A
C 387	11.4	81.4	1431	12	US-11-169-041-103	Sequence 185, App
C 388	11.4	81.4	1474	8	US-10-821-234-185	Sequence 185, App
C 389	11.4	81.4	1488	6	US-09-925-065A-51174	Sequence 51174, A
C 390	11.4	81.4	1488	6	US-09-925-065A-51175	Sequence 51175, A
C 391	11.4	81.4	1488	6	US-09-925-065A-51176	Sequence 51176, A
C 392	11.4	81.4	1490	7	US-10-510-959-1	Sequence 1, App1
C 393	11.4	81.4	1504	8	US-10-750-185-37779	Sequence 37779, A
C 394	11.4	81.4	1504	8	US-10-750-623-37779	Sequence 37779, A
C 395	11.4	81.4	1506	7	US-10-932-182A-81259	Sequence 81259, A
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C 397	11.4	81.4	1620	9	US-11-232-406A-31	Sequence 31, App1
C 398	11.4	81.4	1636	8	US-10-981-029-6	Sequence 6, App1
C 399	11.4	81.4	1665	7	US-10-932-182A-78311	Sequence 78311, A
C 400	11.4	81.4	1665	7	US-10-932-182A-78311	Sequence 78311, A
C 401	11.4	81.4	1710	8	US-11-096-568A-12694	Sequence 12694, A
C 402	11.4	81.4	1710	8	US-10-750-185-43905	Sequence 43905, A
C 403	11.4	81.4	1770	8	US-10-750-623-43905	Sequence 43905, A
C 404	11.4	81.4	1779	7	US-10-932-182A-78831	Sequence 78831, A
C 405	11.4	81.4	1779	7	US-10-932-182A-78831	Sequence 78831, A
C 406	11.4	81.4	1783	9	US-11-096-568A-15986	Sequence 15986, A
C 407	11.4	81.4	1854	6	US-09-925-065A-551308	Sequence 551308, A
C 408	11.4	81.4	1885	9	US-11-096-568A-26579	Sequence 26579, A
C 409	11.4	81.4	1962	12	US-11-055-882-109	Sequence 109, App
C 410	11.4	81.4	1967	12	US-11-091-883-125	Sequence 125, App
C 411	11.4	81.4	1972	7	US-10-501-035-89	Sequence 89, App1
C 412	11.4	81.4	1972	8	US-10-955-054A-153	Sequence 153, App
C 413	11.4	81.4	2010	6	US-09-925-065A-700416	Sequence 700416, A
C 414	11.4	81.4	2010	6	US-09-925-065A-700417	Sequence 700417, A
C 415	11.4	81.4	2010	6	US-09-925-065A-700418	Sequence 700418, A
C 416	11.4	81.4	2037	9	US-11-086-568A-22288	Sequence 22288, A
C 417	11.4	81.4	2070	8	US-10-750-185-32492	Sequence 32492, A
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C 420	11.4	81.4	2071	8	US-10-750-623-56138	Sequence 56138, A
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C 424	11.4	81.4	2140	9	US-11-072-512-283	Sequence 283, App
C 425	11.4	81.4	2180	9	US-11-096-568A-2081	Sequence 2081, App
C 426	11.4	81.4	2181	7	US-10-932-182A-2825	Sequence 2825, App
C 427	11.4	81.4	2181	7	US-10-932-182A-2825	Sequence 2825, App
C 428	11.4	81.4	2196	12	US-11-080-991-91	Sequence 91, App1
C 429	11.4	81.4	2244	7	US-10-932-182A-3372	Sequence 3372, App
C 430	11.4	81.4	2244	7	US-10-932-182A-3372	Sequence 3372, App
C 431	11.4	81.4	2271	6	US-09-925-065A-682918	Sequence 682918, A
C 432	11.4	81.4	2271	6	US-09-925-065A-682919	Sequence 682919, A
C 433	11.4	81.4	2291	7	US-10-921-793-51	Sequence 51, App1
C 434	11.4	81.4	2291	7	US-10-931-198-51	Sequence 51, App1
C 435	11.4	81.4	2351	6	US-09-925-065A	

532	11	78.6	22	8	US-10-453-372-1326	Sequence 1326, Ap	c 605	11	78.6	454	6	US-09-925-065A-161559	Sequence 161559,
533	11	78.6	23	8	US-10-310-914A-1263522	Sequence 883522, A	c 606	11	78.6	456	6	US-09-925-065A-456544	Sequence 456544,
534	11	78.6	23	8	US-10-310-914A-1262763	Sequence 1262763, A	c 607	11	78.6	470	6	US-09-925-065A-293778	Sequence 293778,
535	11	78.6	24	8	US-10-310-914A-657805	Sequence 657805, A	c 608	11	78.6	471	6	US-09-925-065A-223240	Sequence 223240,
536	11	78.6	24	8	US-10-310-914A-1351031	Sequence 1351031, A	c 609	11	78.6	472	8	US-10-750-185-35119	Sequence 35119, A
537	11	78.6	25	7	US-10-932-182A-12922	Sequence 12922, A	c 610	11	78.6	473	6	US-09-925-065A-223134	Sequence 223134,
538	11	78.6	25	7	US-10-932-182A-149601	Sequence 149601, A	c 611	11	78.6	476	6	US-09-925-065A-765073	Sequence 765073,
539	11	78.6	25	7	US-10-932-182A-12922	Sequence 12922, A	c 612	11	78.6	475	6	US-09-925-065A-832074	Sequence 832074,
540	11	78.6	25	7	US-10-932-182A-149601	Sequence 149601, A	c 613	11	78.6	476	6	US-09-925-065A-514488	Sequence 514488,
541	11	78.6	25	7	US-10-933-982-45415	Sequence 45415, A	c 614	11	78.6	479	6	US-09-925-065A-239591	Sequence 239591,
542	11	78.6	25	7	US-10-933-982-60683	Sequence 60683, A	c 615	11	78.6	481	6	US-09-925-065A-345103	Sequence 345103,
543	11	78.6	25	7	US-10-933-982-150739	Sequence 150739, A	c 616	11	78.6	481	6	US-09-925-065A-345104	Sequence 345104,
544	11	78.6	25	7	US-10-933-982-194520	Sequence 194520, A	c 617	11	78.6	481	6	US-09-925-065A-345105	Sequence 345105,
545	11	78.6	25	7	US-10-934-046A-88459	Sequence 88459, A	c 618	11	78.6	488	6	US-09-925-065A-530338	Sequence 530338,
546	11	78.6	25	12	US-11-121-849-57845	Sequence 57845, A	c 619	11	78.6	488	6	US-09-925-065A-835549	Sequence 835549,
547	11	78.6	25	12	US-11-121-849-163110	Sequence 163110, A	c 620	11	78.6	488	6	US-09-925-065A-293896	Sequence 293896,
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550	11	78.6	25	12	US-11-121-849-199701	Sequence 199701, A	c 623	11	78.6	491	6	US-09-925-065A-293899	Sequence 293899,
551	11	78.6	25	12	US-11-121-849-199702	Sequence 199702, A	c 624	11	78.6	499	6	US-09-925-065A-484388	Sequence 484388,
552	11	78.6	25	12	US-11-121-849-386995	Sequence 386995, A	c 625	11	78.6	499	6	US-09-925-065A-532826	Sequence 532826,
553	11	78.6	25	12	US-11-121-849-570131	Sequence 570131, A	c 626	11	78.6	494	6	US-09-925-065A-487017	Sequence 487017,
554	11	78.6	25	12	US-11-121-849-656037	Sequence 656037, A	c 627	11	78.6	494	6	US-09-925-065A-943013	Sequence 943013,
555	11	78.6	25	12	US-11-136-527-218773	Sequence 218773, A	c 628	11	78.6	498	6	US-09-925-065A-308452	Sequence 308452,
556	11	78.6	25	12	US-11-136-527-218776	Sequence 218776, A	c 629	11	78.6	499	6	US-09-925-065A-397538	Sequence 397538,
557	11	78.6	25	12	US-11-136-527-218782	Sequence 218782, A	c 630	11	78.6	499	6	US-09-925-065A-484388	Sequence 484388,
558	11	78.6	25	12	US-11-136-527-218783	Sequence 218783, A	c 631	11	78.6	499	6	US-09-925-065A-532826	Sequence 532826,
559	11	78.6	25	12	US-11-136-527-218791	Sequence 218791, A	c 632	11	78.6	500	6	US-09-925-065A-447038	Sequence 447038,
560	11	78.6	25	12	US-11-136-527-218813	Sequence 218813, A	c 633	11	78.6	504	6	US-09-925-065A-724047	Sequence 724047,
561	11	78.6	47	9	US-11-204-311-674	Sequence 674, App	c 634	11	78.6	505	6	US-09-925-065A-738440	Sequence 738440,
562	11	78.6	50	12	US-11-175-859-55295	Sequence 55295, A	c 635	11	78.6	505	6	US-09-925-065A-829964	Sequence 829964,
563	11	78.6	50	12	US-11-175-859-56213	Sequence 56213, A	c 636	11	78.6	507	6	US-09-925-065A-407145	Sequence 407145,
564	11	78.6	50	12	US-11-175-859-57260	Sequence 57260, A	c 637	11	78.6	509	6	US-09-925-065A-407146	Sequence 407146,
565	11	78.6	50	12	US-11-175-859-593731	Sequence 593731, A	c 638	11	78.6	509	6	US-09-925-065A-843332	Sequence 843332,
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567	11	78.6	195	12	US-11-124-367A-3127	Sequence 3127, App	c 640	11	78.6	513	6	US-09-925-065A-520317	Sequence 520317,
568	11	78.6	201	8	US-10-995-561-81111	Sequence 81111, A	c 641	11	78.6	513	6	US-09-925-065A-834105	Sequence 834105,
569	11	78.6	201	12	US-11-124-368A-14287	Sequence 14287, A	c 642	11	78.6	520	6	US-09-925-065A-639740	Sequence 639740,
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571	11	78.6	201	12	US-11-124-368A-14366	Sequence 14366, A	c 644	11	78.6	520	6	US-09-925-065A-639742	Sequence 639742,
572	11	78.6	201	12	US-11-124-368A-14367	Sequence 14367, A	c 645	11	78.6	521	6	US-09-925-065A-127237	Sequence 127237,
573	11	78.6	201	12	US-11-124-367A-3039	Sequence 3039, App	c 646	11	78.6	521	6	US-11-128-061-621	Sequence 621, App
574	11	78.6	201	12	US-11-124-367A-3050	Sequence 3050, App	c 647	11	78.6	521	12	US-11-128-061-4263	Sequence 4263, App
575	11	78.6	201	12	US-11-124-367A-3082	Sequence 3082, App	c 648	11	78.6	521	12	US-11-128-049-621	Sequence 621, App
576	11	78.6	201	12	US-11-124-367A-3126	Sequence 3126, App	c 649	11	78.6	521	12	US-11-128-049-621	Sequence 621, App
577	11	78.6	201	12	US-11-124-367A-5732	Sequence 5732, App	c 650	11	78.6	521	12	US-11-128-049-621	Sequence 621, App
578	11	78.6	201	12	US-11-124-367A-5733	Sequence 5733, App	c 651	11	78.6	528	6	US-09-925-065A-525158	Sequence 525158,
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580	11	78.6	201	12	US-11-124-367A-6634	Sequence 6634, App	c 653	11	78.6	529	6	US-09-925-065A-497803	Sequence 497803,
581	11	78.6	201	12	US-11-124-367A-6994	Sequence 6994, App	c 654	11	78.6	529	6	US-09-925-065A-497804	Sequence 497804,
582	11	78.6	201	12	US-11-124-367A-20446	Sequence 20446, A	c 655	11	78.6	531	6	US-09-925-065A-554859	Sequence 554859,
583	11	78.6	201	12	US-11-124-367A-21067	Sequence 21067, A	c 656	11	78.6	531	6	US-09-925-065A-816629	Sequence 816629, A
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585	11	78.6	276	7	US-10-932-182A-81310	Sequence 81310, A	c 658	11	78.6	546	12	US-11-074-176-217	Sequence 217, App
586	11	78.6	301	12	US-11-234-786-381	Sequence 281, App	c 659	11	78.6	546	6	US-09-925-065A-576020	Sequence 576020,
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589	11	78.6	363	6	US-10-993-543-9	Sequence 9, App11	c 662	11	78.6	551	6	US-09-925-065A-241065	Sequence 241065,
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593	11	78.6	387	7	US-10-932-182A-75776	Sequence 75776, A	c 666	11	78.6	555	6	US-09-925-065A-650341	Sequence 650341,
594	11	78.6	389	6	US-09-925-065A-438101	Sequence 438101, A	c 667	11	78.6	556	6	US-09-925-065A-236778	Sequence 236778,
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597	11	78.6	418	6	US-09-925-065A-410430	Sequence 410430, A	c 670	11	78.6	557	6	US-09-925-065A-309274	Sequence 309274,
598	11	78.6	420	6	US-09-925-065A-290399	Sequence 290399, A	c 671	11	78.6	557	6	US-09-925-065A-771515	Sequence 771515,
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602	11	78.6	448	6	US-09-925-065A-377392	Sequence 377392, A	c 675	11	78.6	560	6	US-09-925-065A-380633	Sequence 380633,
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687	-11	78.6	565	6	US-09-925-065A-830730	Sequence 830730,	760	11	78.6	616	6	US-09-925-065A-208848	Sequence 208848,
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694	-11	78.6	573	6	US-09-925-065A-504165	Sequence 504165,	767	11	78.6	627	6	US-09-925-065A-344670	Sequence 344670,
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703	-11	78.6	581	6	US-09-925-065A-528508	Sequence 528508,	776	11	78.6	644	6	US-09-925-065A-793114	Sequence 793114,
704	-11	78.6	582	6	US-09-925-065A-760994	Sequence 760994,	777	11	78.6	644	6	US-09-925-065A-815835	Sequence 815835,
705	-11	78.6	585	6	US-09-925-065A-303871	Sequence 303871,	778	11	78.6	644	6	US-09-925-065A-912069	Sequence 912069,
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714	-11	78.6	592	6	US-09-925-065A-456751	Sequence 456751,	787	11	78.6	671	6	US-09-925-065A-690637	Sequence 690637,
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718	-11	78.6	594	7	US-10-932-182A-1796	Sequence 1796, Ap	791	11	78.6	705	8	US-10-453-372-421	Sequence 421, App
719	-11	78.6	598	6	US-09-925-065A-44516	Sequence 44516,	792	11	78.6	724	6	US-09-925-065A-950285	Sequence 950285,
720	-11	78.6	598	6	US-09-925-065A-44516	Sequence 44516,	793	11	78.6	744	6	US-09-925-065A-34377	Sequence 34377, A
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## ALIGNMENTS

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; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108927.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
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; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
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RESULT 3
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; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 162449
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-162449

```

```

Query Match      92.9%; Score 13; DB 7; Length 25;
Best Local Similarity 76.9%; Pred. No. 43;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 GUACGCAACTCG 14
DB      17 GTACTGCAACTCG 5

```

```

RESULT 4
US-10-932-182A-82453/C
; Sequence 82453, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO

```



```
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: 030685-043
/ CURRENT APPLICATION NUMBER: US/10/932,182A
/ CURRENT FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 82453
/ LENGTH: 1017
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-10-932-182A-82453

Query Match          92.9%; Score 13; DB 7; Length 1017;
Best Local Similarity 76.9%; Pred. No. 92;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GUACUGCAACUCG 14
DB      477 GTACTGCAACTCG 465

RESULT 5
US-10-932-182A-82453/c
/ Sequence 82453, Application US/10932182A
/ Publication No. US20060046253A1
/ GENERAL INFORMATION:
/ APPLICANT: NAKAO, YOSHIHIRO
/ APPLICANT: NAKAMURA, NORIHISA
/ APPLICANT: KODAMA, YUKIKO
/ APPLICANT: FUJIMURA, TOMOKO
/ APPLICANT: ASHIKARI, TOSHIHIKO
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: 030685-043
/ CURRENT APPLICATION NUMBER: US/10/932,182A
/ CURRENT FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 82453
/ LENGTH: 1017
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-10-932-182A-82453

Query Match          92.9%; Score 13; DB 7; Length 1017;
Best Local Similarity 76.9%; Pred. No. 92;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GUACUGCAACUCG 14
DB      477 GTACTGCAACTCG 465

RESULT 6
US-10-932-182A-1393/c
/ Sequence 1393, Application US/10932182A
/ Publication No. US20060046253A1
/ GENERAL INFORMATION:
/ APPLICANT: NAKAO, YOSHIHIRO
/ APPLICANT: NAKAMURA, NORIHISA
/ APPLICANT: KODAMA, YUKIKO
/ APPLICANT: FUJIMURA, TOMOKO
/ APPLICANT: ASHIKARI, TOSHIHIKO
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: 030685-043
/ CURRENT APPLICATION NUMBER: US/10/932,182A
/ CURRENT FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1393
/ LENGTH: 2055
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-10-932-182A-1393
```

```
Query Match          92.9%; Score 13; DB 7; Length 2055;
Best Local Similarity 76.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GUACUGCAACUCG 14
DB      1095 GTACTGCAACTCG 1083

RESULT 7
US-10-932-182A-1393/c
/ Sequence 1393, Application US/10932182A
/ Publication No. US20060046253A1
/ GENERAL INFORMATION:
/ APPLICANT: NAKAO, YOSHIHIRO
/ APPLICANT: NAKAMURA, NORIHISA
/ APPLICANT: KODAMA, YUKIKO
/ APPLICANT: FUJIMURA, TOMOKO
/ APPLICANT: ASHIKARI, TOSHIHIKO
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: 030685-043
/ CURRENT APPLICATION NUMBER: US/10/932,182A
/ CURRENT FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1393
/ LENGTH: 2055
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-10-932-182A-1393

Query Match          92.9%; Score 13; DB 7; Length 2055;
Best Local Similarity 76.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GUACUGCAACUCG 14
DB      1095 GTACTGCAACTCG 1083
```

```
RESULT 8
US-11-136-527-2658
/ Sequence 2658, Application US/11136527
/ Publication No. US20050287570A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Mounts, William M
/ TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
/ FILE REFERENCE: 031896-041000 (AM101086)
/ CURRENT APPLICATION NUMBER: US/11/136,527
/ CURRENT FILING DATE: 2005-05-25
/ PRIOR APPLICATION NUMBER: US 60/574,294
/ PRIOR FILING DATE: 2005-05-26
/ NUMBER OF SEQ ID NOS: 362830
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 2658
/ LENGTH: 3002
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
/ FEATURES:
/ NAME/KEY: misc feature
/ LOCATION: (2885)..(2885)
/ OTHER INFORMATION: n is a, c, g, or t
US-11-136-527-2658

Query Match          92.9%; Score 13; DB 12; Length 3002;
Best Local Similarity 76.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GUACUGCAACUCG 14
DB      1472 GTACTGCAACTCG 1484
```

```

RESULT 9
US-11-124-367A-5111
; Sequence 5111, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5111
; LENGTH: 12514
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-5111

```

```

Query Match          92.9%; Score 13; DB 12; Length 12514;
Best Local Similarity 76.9%; Pred. No. 1.5e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 GUACUGCAACUC 14
||:|||||:|
Db      6306 GTACTGCAACTCG 6318

```

```

RESULT 10
US-10-995-561-16849
; Sequence 16849, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16849
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-16849

```

```

Query Match          90.0%; Score 12.6; DB 8; Length 201;
Best Local Similarity 76.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 CGUACUGCAACUC 13
||:|||||:|
Db      99 CGYACTGCAACTC 111

```

```

RESULT 11
US-10-995-561-66965/c
; Sequence 66965, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

```

```

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66965
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-66965

```

```

Query Match          90.0%; Score 12.6; DB 8; Length 201;
Best Local Similarity 76.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 CGUACUGCAACUC 13
||:|||||:|
Db      103 CGYACTGCAACTC 91

```

```

RESULT 12
US-10-995-561-13387/c
; Sequence 13387, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13387
; LENGTH: 29871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(29871)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13387

```

```

Query Match          90.0%; Score 12.6; DB 8; Length 29871;
Best Local Similarity 76.9%; Pred. No. 3.5e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 CGUACUGCAACUC 13
||:|||||:|
Db      14198 CGYACTGCAACTC 14186

```

```

RESULT 13
US-10-995-561-13204
; Sequence 13204, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13204
; LENGTH: 32109
; TYPE: DNA
; ORGANISM: Homo sapiens

```

FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(321019)  
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-  
US-10-995-561-13204

Query Match 90.0%; Score 12.6; DB 8; Length 321019;  
Best Local Similarity 76.9%; Pred. No. 5.5e+02;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13  
||:|:|:|:|:|:|:  
DB 16112 CGTACTCGAATCG 16124

RESULT 14  
US-11-101-244-868490/c  
Sequence 868490, Application US/11101244  
Publication No. US20050246794A1  
GENERAL INFORMATION:  
APPLICANT: Dharmoon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/101,244  
CURRENT FILING DATE: 2005-04-07  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911  
SOFTWARE: Proprietary  
SEQ ID NO 868490  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-101-244-868490

Query Match 88.6%; Score 12.4; DB 10; Length 19;  
Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 14  
||:|:|:|:|:|:|:  
DB 18 CGTACTCGAATCG 5

RESULT 15  
US-11-083-784-868490/c  
Sequence 868490, Application US/11083784  
Publication No. US20050245475A1  
GENERAL INFORMATION:  
APPLICANT: Dharmoon, Inc.  
APPLICANT: Khvorova, Anastasia  
APPLICANT: Reynolds, Angela  
APPLICANT: Leake, Devin  
APPLICANT: Marshall, William  
APPLICANT: Scaringe, Stephen  
TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
FILE REFERENCE: 13499US  
CURRENT APPLICATION NUMBER: US/11/083,784  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US/10/714,333  
PRIOR FILING DATE: 2003-11-14  
PRIOR APPLICATION NUMBER: 60/502,050  
PRIOR FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: 60/426,137  
PRIOR FILING DATE: 2002-11-14  
NUMBER OF SEQ ID NOS: 1591911

SOFTWARE: Proprietary  
SEQ ID NO 868490  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-083-784-868490

Query Match 88.6%; Score 12.4; DB 11; Length 19;  
Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 14  
||:|:|:|:|:|:|:  
DB 18 CGTACTCGAATCG 5

RESULT 16  
US-10-933-982-90062/c  
Sequence 90062, Application US/10933982  
Publication No. US20060051769A1  
GENERAL INFORMATION:  
APPLICANT: Barts, Jennifer  
TITLE OF INVENTION: Methods of Genetic Analysis of E. coli  
FILE REFERENCE: 3700  
CURRENT APPLICATION NUMBER: US/10/933,982  
CURRENT FILING DATE: 2004-09-03  
NUMBER OF SEQ ID NOS: 224976  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 90062  
LENGTH: 25  
TYPE: DNA  
ORGANISM: E. coli  
US-10-933-982-90062

Query Match 88.6%; Score 12.4; DB 7; Length 25;  
Best Local Similarity 78.6%; Pred. No. 1.1e+02;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 14  
||:|:|:|:|:|:|:  
DB 23 CGTACTCGAATCG 10

RESULT 17  
US-09-925-065A-138336  
Sequence 138336, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
Nucleotide Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 138336  
LENGTH: 499  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-138336

Query Match 88.6%; Score 12.4; DB 6; Length 499;

Best Local Similarity 71.4%; Pred. No. 2.1e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14  
|:|:|:|:|:|:|:  
Db 247 CTTACTGCACTCG 260

## RESULT 18

US-11-096-568A-11706/c  
; Sequence 11706, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; PRIOR FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 11706  
; LENGTH: 575  
; TYPE: DNA  
; ORGANISM: Triticum aestivum  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)..(575)  
; OTHER INFORMATION: Ceres Seq. ID no. 13656404  
US-11-096-568A-11706

Query Match 88.6%; Score 12.4; DB 9; Length 575;  
Best Local Similarity 71.4%; Pred. No. 2.2e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14  
|:|:|:|:|:|:|:  
Db 558 CTTCTGCACTCG 545

## RESULT 19

US-10-750-185-2691  
; Sequence 2691, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM11100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; PRIOR FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2691  
; LENGTH: 600  
; TYPE: DNA  
; ORGANISM: Bovine  
US-10-750-185-2691

Query Match 88.6%; Score 12.4; DB 8; Length 600;  
Best Local Similarity 71.4%; Pred. No. 2.2e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14  
|:|:|:|:|:|:|:  
Db 31 CCGCTGCACTCG 44

## RESULT 20

US-10-750-623-2691  
; Sequence 2691, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM11100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; PRIOR FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2691  
; LENGTH: 600  
; TYPE: DNA  
; ORGANISM: Bovine  
US-10-750-623-2691

Query Match 88.6%; Score 12.4; DB 8; Length 600;  
Best Local Similarity 71.4%; Pred. No. 2.2e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14  
|:|:|:|:|:|:|:  
Db 31 CCGCTGCACTCG 44

## RESULT 21

US-11-096-568A-20227  
; Sequence 20227, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; PRIOR FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 20227  
; LENGTH: 847  
; TYPE: DNA  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)..(847)  
; OTHER INFORMATION: Ceres Seq. ID no. 12379704  
US-11-096-568A-20227

Query Match 88.6%; Score 12.4; DB 9; Length 847;  
Best Local Similarity 78.6%; Pred. No. 2.3e+02;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14  
|:|:|:|:|:|:|:  
Db 511 CCGCTGCACTCG 524

## RESULT 22

US-10-467-657-4195/c  
; Sequence 4195, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA

APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASIGNANI Vega  
APPLICANT: MONACI Elisabetta  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
CURRENT FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8  
PRIOR FILING DATE: 2001-02-12  
NUMBER OF SEQ ID NOS: 9218  
SOFTWARE: SeqWin99, version 1.04  
SEQ ID NO 4195  
LENGTH: 1080  
TYPE: DNA  
ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-4195

Query Match 88.6%; Score 12.4; DB 8; Length 1080;  
Best Local Similarity 71.4%; Pred. No. 2.5e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUCG 14  
||:|||||:  
Db 763 CGTCTGCACTCG 750

RESULT 23  
US-10-750-185-56170/c  
Sequence 56170, Application US/10750185  
Publication No. US20050260603A1  
GENERAL INFORMATION:  
APPLICANT: MMI GENOMICS, INC.  
APPLICANT: DENISE, Sue K.  
APPLICANT: KERR, Richard  
APPLICANT: ROSENFELD, David  
APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen  
APPLICANT: FANTIN, Dennis  
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
FILE REFERENCE: MM1100-2  
CURRENT APPLICATION NUMBER: US/10/750,185  
CURRENT FILING DATE: 2003-12-31  
PRIOR APPLICATION NUMBER: US 60/437,482  
PRIOR FILING DATE: 2002-12-31  
NUMBER OF SEQ ID NOS: 64922  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 56170  
LENGTH: 1223  
TYPE: DNA  
ORGANISM: Bovine 19866880790313  
US-10-750-185-56170

Query Match 88.6%; Score 12.4; DB 8; Length 1223;  
Best Local Similarity 78.6%; Pred. No. 2.5e+02;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUCG 14  
||:|||||:  
Db 765 CGTACGCACTCG 772

RESULT 24  
US-10-750-623-56170/c  
Sequence 56170, Application US/10750623  
Publication No. US20050287531A1  
GENERAL INFORMATION:  
APPLICANT: MMI GENOMICS, INC.  
APPLICANT: DENISE, Sue K.  
APPLICANT: KERR, Richard  
APPLICANT: ROSENFELD, David  
APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen

APPLICANT: FANTIN, Dennis  
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
FILE REFERENCE: MM1100-1  
CURRENT APPLICATION NUMBER: US/10/750,623  
CURRENT FILING DATE: 2003-12-31  
PRIOR APPLICATION NUMBER: US 60/437,482  
PRIOR FILING DATE: 2002-12-31  
NUMBER OF SEQ ID NOS: 64922  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 56170  
LENGTH: 1223  
TYPE: DNA  
ORGANISM: Bovine 19866880790313  
US-10-750-623-56170

Query Match 88.6%; Score 12.4; DB 8; Length 1223;  
Best Local Similarity 78.6%; Pred. No. 2.5e+02;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUCG 14  
||:|||||:  
Db 785 CGTACGCACTCG 772

RESULT 25  
US-11-096-568A-19170  
Sequence 19170, Application US/11096568A  
Publication No. US20060048240A1  
GENERAL INFORMATION:  
APPLICANT: Alexandrov, Nickolai et al.  
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
FILE REFERENCE: 2750-1592PUS2  
CURRENT APPLICATION NUMBER: US/11/096,568A  
CURRENT FILING DATE: 2005-04-01  
NUMBER OF SEQ ID NOS: 34471  
SEQ ID NO 19170  
LENGTH: 1733  
TYPE: DNA  
ORGANISM: Zea mays subsp. mays  
FEATURES:  
NAME/KEY: misc feature  
LOCATION: (1)\_(1733)  
OTHER INFORMATION: Ceres Seq. ID no. 12369271  
US-11-096-568A-19170

Query Match 88.6%; Score 12.4; DB 9; Length 1733;  
Best Local Similarity 78.6%; Pred. No. 2.7e+02;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUCG 14  
||:|||||:  
Db 1054 CGTACGCACTCG 1067

RESULT 26  
US-10-504-034B-1/c  
Sequence 1, Application US/10504034B  
Publication No. US20060040343A1  
GENERAL INFORMATION:  
APPLICANT: Van Der Geize, Robert  
APPLICANT: Van Der Weijden, Peter  
APPLICANT: Hesseels, Gerda  
APPLICANT: Dijkhuizen, Lubbert  
TITLE OF INVENTION: Microbial delta-1-dehydrogenation of steroids  
FILE REFERENCE: 2002.716US  
CURRENT APPLICATION NUMBER: US/10/504,034B  
CURRENT FILING DATE: 2004-08-05  
PRIOR APPLICATION NUMBER: PCT/EP03/50025  
PRIOR FILING DATE: 2003-02-19  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn ver. 3.3  
SEQ ID NO 1

```
; LENGTH: 1770
; TYPE: DNA
; ORGANISM: Rhodococcus erythropolis SQU
US-10-504-034B-1
```

Query Match	88.6%	Score 12.4;	DB 7;	Length 1770;
Best Local Similarity	78.6%;	Pred. No. 2.7e+02;		
Matches	11; Conservative	2; Mismatches	1; Indels	0; Gaps

Qy	1	CGUACUGCAACUCG	14
		:	
Db	1354	CGTACTGCAACACG	1341

```

RESULT 27
US-10-750-185-29862/c
; Sequence 29862, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Denis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29862
; LENGTH: 3250
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-29862 19866880972249

```

Query Match	88.6%	Score 12.4	DB 8	Length 3250
Best Local Similarity	71.4%	Pred. No. 3.1e+08		
Matches 10	Conservative 3	Mismatches 1	Indels 0	Gaps 0
QY	1 CGUACGCAACUCG 14			
	: : : : :			
Db	335 CTTACTGCAACTCG 322			

```

RESULT 28
US-10-750-623-29862/c
Sequence 29862, Application US/10750623
Publication NO. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29862
LENGTH: 3250
TYPE: DNA
ORGANISM: Bovine 1986680972249

```

US-10-750-623-29862

Query Match	88.6%;	Score 12.4;	DB 8;	Length 3250;
Best Local Similarity	71.4%;	Pred. No. 3.1e+02;		
Matches 10;	Conservative 3;	Mismatches 1;	Indels 0;	Gaps 0;

QY	1	CGUACUGCAACTUCG	14
		:   :         :	
Db	335	CTTACTGCAACTCG	322

```

RESULT 29
US-10-750-185-29967
; Sequence 29967, Application US/10750185
; Publication No. US200502603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MW11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29967
; LENGTH: 3661
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-29967
19866880504081

```

Query Match	88.6%	Score 12.4	DB 8	Length 3661
Best Local Similarity	71.4%	Pred. No. 3.2e+02		
Matches	10	Conservative	3	Mismatches 1
				Indels 0
				Gaps 0
QY	1	CGUACUGCAACTUC	14	
		:: :     ::		
Db	1322	CGCTCTGCAACTCG	1335	

```

RESULT 30
US-10-750-623-29967
; Sequence 29967, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OR INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; PRIORITY APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 29967
; LENGTH: 3661
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-623-29967
Query Match      88.6%; Score 12.4; DB 8; Length 3661;

```

Best Local Similarity 71.4%; Pred. No. 3.2e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACGCACTCG 14  
Db 1322 CGTCTGCAACTCG 1335

## RESULT 31

US-11-082-154A-18/c  
; Sequence 18, Application US/11082154A  
; Publication No. US20060024820A1  
; GENERAL INFORMATION:  
; APPLICANT: Perkins, Edward  
; APPLICANT: Perez, Carl  
; APPLICANT: Lindenbaum, Michael  
; APPLICANT: Greene, Amy  
; APPLICANT: Leung, Josephine  
; APPLICANT: Fleming, Elena  
; APPLICANT: Stewart, Sandra  
; APPLICANT: Shellard, Joan  
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS  
; FILE REFERENCE: 17084-022003 (420C)  
; CURRENT APPLICATION NUMBER: US/11/082,154A  
; PRIOR FILING DATE: 2005-03-15  
; PRIOR APPLICATION NUMBER: 60/294,758  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: 60/366,891  
; PRIOR FILING DATE: 2002-03-21  
; PRIOR APPLICATION NUMBER: US 10/161,403  
; PRIOR FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 129  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 22118  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: GenBank X82564  
; DATABASE ENTRY DATE: 1996-04-09  
US-11-082-154A-18

Query Match 88.6%; Score 12.4; DB 12; Length 22118;  
Best Local Similarity 78.6%; Pred. No. 4.6e+02;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACGCACTCG 14  
Db 3661 CGTACGCAACTCG 3648

## RESULT 32

US-11-101-244-1009794/c  
; Sequence 1009794, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmoon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 1349905  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; PRIOR FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1009794

LENGTH: 19  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-11-101-244-1009794

Query Match 85.7%; Score 12; DB 10; Length 19;  
Best Local Similarity 75.0%; Pred. No. 2e+02;  
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACGCACTCG 12  
Db 18 GTACTGCAACTC 7

## RESULT 33

US-11-101-244-1239747/c  
; Sequence 1239747, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmoon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 1349905  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; PRIOR FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 1239747  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-1239747

Query Match 85.7%; Score 12; DB 10; Length 19;  
Best Local Similarity 75.0%; Pred. No. 2e+02;  
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GUACGCACTCG 13  
Db 18 GTACTGCAACTC 7

## RESULT 34

US-11-083-784-1009794/c  
; Sequence 1009794, Application US/11083784  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmoon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 1349905  
; CURRENT APPLICATION NUMBER: US/11/083,784  
; PRIOR FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary



```

; SEQ ID NO 1009794
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1009794

Query Match      85.7%; Score 12; DB 11; Length 19;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGUACUGCAACU 12
      |||:|||||:
DB      18 GACTGCAACT 7

RESULT 35
US-11-083-784-1239747/c
; Sequence 1239747, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1239747
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1239747

Query Match      85.7%; Score 12; DB 11; Length 19;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GUACUGCAACUC 13
      |||:|||||:
DB      18 GACTGCAACT 7

RESULT 36
US-10-310-914A-573268
; Sequence 573268, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 573268
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-573268
```

```

Query Match      85.7%; Score 12; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GUACUGCAACUC 13
      |||:|||||:
DB      6 GUACUGCAACUC 17

RESULT 37
US-10-521-162-30
; Sequence 30, Application US/10521162
; Publication No. US20050287529A1
; GENERAL INFORMATION:
; APPLICANT: Brandt, Kevin S.
; TITLE OF INVENTION: FLEA AND TICK OCTOPAMINE RECEPTOR NUCLEIC ACID MOLECULES,
; FILE REFERENCE: FC-11-PCT
; CURRENT FILING DATE: 2005-01-13
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 60/319,402
; PRIOR FILING DATE: 2003-11-15
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 102
; TYPE: DNA
; ORGANISM: Rhipicephalus sanguineus
; NAME/KEY: CDS
; LOCATION: (1)..(102)
US-10-521-162-30

Query Match      85.7%; Score 12; DB 8; Length 102;
Best Local Similarity 75.0%; Pred. No. 2.9e+02;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 UACUGCAACUCG 14
      |||:|||||:
DB      76 TACTGCACTCG 87

RESULT 38
US-10-521-162-32/c
; Sequence 32, Application US/10521162
; Publication No. US20050287529A1
; GENERAL INFORMATION:
; APPLICANT: Brandt, Kevin S.
; TITLE OF INVENTION: FLEA AND TICK OCTOPAMINE RECEPTOR NUCLEIC ACID MOLECULES,
; FILE REFERENCE: FC-11-PCT
; CURRENT FILING DATE: 2005-01-13
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 60/426,601
; PRIOR FILING DATE: 2003-11-15
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 102
; TYPE: DNA
; ORGANISM: Rhipicephalus sanguineus
US-10-521-162-32

Query Match      85.7%; Score 12; DB 8; Length 102;
Best Local Similarity 75.0%; Pred. No. 2.9e+02;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 UACUGCAACUCG 14
      |||:|||||:
DB      76 TACTGCACTCG 87
```

Db 27 TACTGCACTCG 16

## RESULT 39

US-10-995-561-81304/c  
; Sequence 81304, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 81304  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-995-561-81304

Query Match 85.7%; Score 12; DB 8; Length 201;  
Best Local Similarity 75.0%; Pred. No. 3.3e+02;  
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GUACUGCAACUC 13

Db 125 GTACTGCACTC 114

## RESULT 40

US-10-995-561-81478/c  
; Sequence 81478, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 81478  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-995-561-81478

Query Match 85.7%; Score 12; DB 8; Length 201;  
Best Local Similarity 75.0%; Pred. No. 3.3e+02;  
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GUACUGCAACUC 13

Db 128 GTACTGCACTC 117

## RESULT 41

US-10-932-182A-637/c  
; Sequence 637, Application US/10932182A  
; Publication No. US20060046253A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: 030685-043

CURRENT APPLICATION NUMBER: US/10/932,182A

CURRENT FILING DATE: 2004-09-02

NUMBER OF SEQ ID NOS: 197023

SOFTWARE: Patentin version 3.3

SEQ ID NO 637

LENGTH: 444

TYPE: DNA

ORGANISM: Saccharomyces pastorianus

US-10-932-182A-637

Query Match 85.7%; Score 12; DB 7; Length 444;  
Best Local Similarity 75.0%; Pred. No. 3.9e+02;  
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GUACUGCAACUC 13

Db 285 GTACTGCACTC 274

## RESULT 42

US-10-932-182A-637/c  
; Sequence 637, Application US/10932182A  
; Publication No. US20060046253A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: 030685-043  
; CURRENT APPLICATION NUMBER: US/10/932,182A  
; CURRENT FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 637  
; LENGTH: 444  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-10-932-182A-637

Query Match 85.7%; Score 12; DB 7; Length 444;  
Best Local Similarity 75.0%; Pred. No. 3.9e+02;  
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GUACUGCAACUC 13

Db 285 GTACTGCACTC 274

## RESULT 43

US-09-925-065A-746961/c  
; Sequence 746961, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 746961  
 LENGTH: 445  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-925-065A-746961

Query Match 85.7%; Score 12; DB 6; Length 445;  
 Best Local Similarity 75.0%; Pred. No. 3.9e+02;  
 Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GUACUGCACTCG 13  
 Db 292 GTACTGCACTCG 281

RESULT 44  
 US-10-521-162-33  
 Sequence 33, Application US/10521162  
 Publication No. US20050287529A1  
 GENERAL INFORMATION:

APPLICANT: Brandt, Kevin S.  
 TITLE OF INVENTION: FLEA AND TICK OCTOPAMINE RECEPTOR NUCLEIC ACID MOLECULES,  
 TITLE OF INVENTION: PROTEINS AND USES THEREOF  
 FILE REFERENCE: FC-11-PCT

CURRENT APPLICATION NUMBER: US/10/521,162  
 CURRENT FILING DATE: 2005-01-13  
 PRIOR APPLICATION NUMBER: 60/319,402  
 PRIOR FILING DATE: 2003-07-17  
 PRIOR APPLICATION NUMBER: 60/426,601  
 PRIOR FILING DATE: 2003-11-15  
 NUMBER OF SEQ ID NOS: 50  
 SOFTWARE: PatentIn version 3.2

SEQ ID NO 33  
 LENGTH: 499  
 TYPE: DNA  
 ORGANISM: Rhhipicephalus sanguineus

FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (3)..(278)

FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (8)..(8)  
 OTHER INFORMATION: n = unknown  
 OTHER INFORMATION: Xaa at location 2 = Tyr  
 US-10-521-162-33

Query Match 85.7%; Score 12; DB 8; Length 499;  
 Best Local Similarity 75.0%; Pred. No. 4e+02;  
 Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 UACUGCACTCG 14  
 Db 99 TACTGCACTCG 110

RESULT 45  
 US-10-521-162-35/c

Sequence 35, Application US/10521162  
 Publication No. US20050287529A1  
 GENERAL INFORMATION:

APPLICANT: Brandt, Kevin S.  
 TITLE OF INVENTION: FLEA AND TICK OCTOPAMINE RECEPTOR NUCLEIC ACID MOLECULES,  
 TITLE OF INVENTION: PROTEINS AND USES THEREOF  
 FILE REFERENCE: FC-11-PCT

CURRENT APPLICATION NUMBER: US/10/521,162  
 CURRENT FILING DATE: 2005-01-13  
 PRIOR APPLICATION NUMBER: 60/319,402  
 PRIOR FILING DATE: 2003-07-17  
 PRIOR APPLICATION NUMBER: 60/426,601  
 PRIOR FILING DATE: 2003-11-15  
 NUMBER OF SEQ ID NOS: 50  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 35

LENGTH: 499  
 TYPE: DNA  
 ORGANISM: Rhhipicephalus sanguineus  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (492)..(492)  
 OTHER INFORMATION: n = unknown  
 US-10-521-162-35

Query Match 85.7%; Score 12; DB 8; Length 499;  
 Best Local Similarity 75.0%; Pred. No. 4e+02;  
 Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 UACUGCACTCG 14  
 Db 401 TACTGCACTCG 390

RESULT 46  
 US-09-925-065A-313926/c

Sequence 313926, Application US/09925065A  
 Publication No. US20040181048A1  
 GENERAL INFORMATION:

APPLICANT: Wang, David G.  
 TITLE OF INVENTION: Identification and Mapping of Single  
 TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
 FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A  
 CURRENT FILING DATE: 2001-08-08  
 PRIOR APPLICATION NUMBER: US 60/243,096  
 PRIOR FILING DATE: 2000-10-24  
 PRIOR APPLICATION NUMBER: US 60/252,147  
 PRIOR FILING DATE: 2000-11-20  
 PRIOR APPLICATION NUMBER: US 60/250,092  
 PRIOR FILING DATE: 2000-11-30  
 PRIOR APPLICATION NUMBER: US 60/261,766  
 PRIOR FILING DATE: 2001-01-16  
 PRIOR APPLICATION NUMBER: US 60/289,846  
 PRIOR FILING DATE: 2001-05-09  
 NUMBER OF SEQ ID NOS: 957086  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 313926  
 LENGTH: 542  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-925-065A-313926

Query Match 85.7%; Score 12; DB 6; Length 542;  
 Best Local Similarity 75.0%; Pred. No. 4.1e+02;  
 Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GUACUGCACTCG 13  
 Db 22 GTACTGCACTCG 11

RESULT 47  
 US-09-925-065A-53948

Sequence 53948, Application US/09925065A  
 Publication No. US20040181048A1  
 GENERAL INFORMATION:

APPLICANT: Wang, David G.  
 TITLE OF INVENTION: Identification and Mapping of Single  
 TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
 FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A  
 CURRENT FILING DATE: 2001-08-08  
 PRIOR APPLICATION NUMBER: US 60/243,096  
 PRIOR FILING DATE: 2000-10-24  
 PRIOR APPLICATION NUMBER: US 60/252,147  
 PRIOR FILING DATE: 2000-11-20  
 PRIOR APPLICATION NUMBER: US 60/250,092  
 PRIOR FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 53948  
LENGTH: 549  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-53948

Query Match 85.7%; Score 12; DB 6; Length 549;  
Best Local Similarity 75.0%; Pred. No. 4.1e+02;  
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCAACUC 13  
DB 337 GTACTGCAACTC 348

RESULT 48  
US-09-925-065A-940341/c  
Sequence 940341, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 940341  
LENGTH: 554  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-940341

Query Match 85.7%; Score 12; DB 6; Length 554;  
Best Local Similarity 75.0%; Pred. No. 4.1e+02;  
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCAACUC 13  
DB 421 GTACTGCAACTC 410

RESULT 49  
US-09-925-065A-940300  
Sequence 940300, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 940300  
LENGTH: 557  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-940300

Query Match 85.7%; Score 12; DB 6; Length 557;  
Best Local Similarity 75.0%; Pred. No. 4.1e+02;  
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCAACUC 13  
DB 134 GTACTGCAACTC 145

RESULT 50  
US-09-925-065A-922392/c  
Sequence 922392, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 922392  
LENGTH: 558  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-922392

Query Match 85.7%; Score 12; DB 6; Length 558;  
Best Local Similarity 75.0%; Pred. No. 4.1e+02;  
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCAACUC 13  
DB 425 GTACTGCAACTC 414

Search completed: March 19, 2006, 05:42:31  
Job time: 939.923 secs

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OM nucleic - nucleic search, using sw model1

Run on: March 18, 2006, 18:35:47, Search time 2096.77 Seconds  
(without alignments)  
55.214 Million cell updates/sec

Title: US-10-800-926-2

Perfect score: 14

Sequence: 14

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

19587084

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications NA Main:\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	100.0	14	US-10-800-926-2	Sequence 2, Appl1
2	14	100.0	542	US-09-925-065A-30493	Sequence 30493, A
3	14	100.0	1786	US-10-369-493-36408	Sequence 36408, A
4	14	100.0	1981	US-10-369-493-38056	Sequence 38056, A
5	14	100.0	1986	US-10-282-122A-12964	Sequence 12964, A
6	14	100.0	2080	US-10-369-493-30810	Sequence 30810, A
7	14	100.0	2460	US-10-282-122A-33109	Sequence 33109, A
8	14	100.0	6024	US-10-437-963-61758	Sequence 61758, A
9	14	100.0	6808	US-10-437-963-87284	Sequence 87284, A
10	13	92.9	65	US-09-908-975-33753	Sequence 33753, A
11	13	92.9	196	US-10-437-963-5526	Sequence 5526, A
12	13	92.9	472	US-10-425-115-6477	Sequence 46477, A
13	13	92.9	600	US-10-972-079-46310	Sequence 46310, A
14	13	92.9	653	US-10-425-115-161649	Sequence 161649, A
15	13	92.9	838	US-10-437-963-98896	Sequence 98896, A
16	13	92.9	1042	US-10-437-963-84553	Sequence 84553, A
17	13	92.9	1239	US-10-156-761-4883	Sequence 4883, A
18	13	92.9	1306	US-10-369-493-29486	Sequence 29486, A
19	13	92.9	1359	US-10-450-763-8883	Sequence 8883, A
20	13	92.9	1473	US-10-957-828-11	Sequence 11, Appl1
21	13	92.9	1647	US-09-815-242-6126	Sequence 6126, A
22	13	92.9	1647	US-10-282-122A-20432	Sequence 20432, A
23	13	92.9	1720	US-09-801-042-1	Sequence 1, Appl1

24	13	92.9	1732	US-10-450-763-28629	Sequence 28629, A
25	13	92.9	1919	US-10-450-763-25885	Sequence 25885, A
26	13	92.9	1945	US-09-864-761-4533	Sequence 4533, A
27	13	92.9	2133	US-10-450-763-23995	Sequence 23995, A
28	13	92.9	2559	US-10-156-761-2636	Sequence 2636, A
29	13	92.9	3222	US-10-450-763-25886	Sequence 25886, A
30	13	92.9	51657	US-10-057-475H-10475	Sequence 10475, A
31	13	92.9	51657	US-10-154-8848-10475	Sequence 10475, A
32	13	92.9	83493	US-10-331-053-61	Sequence 61, Appl1
33	13	92.9	684707	US-10-398-221-9	Sequence 9, Appl1
34	13	92.9	3011208	US-10-398-221-2058	Sequence 2058, A
35	13	92.9	9025608	US-10-156-761-1	Sequence 1, Appl1
36	13	92.9	9025608	US-10-156-761-1	Sequence 1, Appl1
37	12.4	88.6	25	US-10-843-527-74919	Sequence 74919, A
38	12.4	88.6	25	US-10-843-527-74933	Sequence 74933, A
39	12.4	88.6	25	US-10-843-527-163184	Sequence 163184, A
40	12.4	88.6	25	US-10-843-527-164158	Sequence 164158, A
41	12.4	88.6	110	US-10-767-701-28070	Sequence 28070, A
42	12.4	88.6	219	US-10-425-115-49773	Sequence 49773, A
43	12.4	88.6	229	US-10-424-599-53399	Sequence 53399, A
44	12.4	88.6	228	US-10-424-599-133643	Sequence 133643, A
45	12.4	88.6	285	US-10-425-115-2960	Sequence 2960, A
46	12.4	88.6	308	US-10-424-599-106360	Sequence 106360, A
47	12.4	88.6	312	US-10-425-115-86279	Sequence 86279, A
48	12.4	88.6	332	US-10-425-115-161997	Sequence 161997, A
49	12.4	88.6	331	US-10-424-599-139244	Sequence 139244, A
50	12.4	88.6	333	US-10-424-599-139244	Sequence 139244, A
51	12.4	88.6	335	US-09-732-627A-1293	Sequence 1293, A
52	12.4	88.6	371	US-10-425-115-40014	Sequence 40014, A
53	12.4	88.6	373	US-09-563-817-673	Sequence 673, A
54	12.4	88.6	387	US-10-424-599-159801	Sequence 159801, A
55	12.4	88.6	389	US-10-425-115-181715	Sequence 181715, A
56	12.4	88.6	406	US-10-425-115-51320	Sequence 51320, A
57	12.4	88.6	446	US-09-860-432-20	Sequence 20, Appl1
58	12.4	88.6	446	US-10-425-115-14596	Sequence 14596, A
59	12.4	88.6	455	US-10-424-599-120244	Sequence 120244, A
60	12.4	88.6	478	US-09-918-995-28991	Sequence 28991, A
61	12.4	88.6	489	US-10-767-701-16475	Sequence 16475, A
62	12.4	88.6	499	US-09-925-065A-18336	Sequence 18336, A
63	12.4	88.6	500	US-10-424-599-40913	Sequence 40913, A
64	12.4	88.6	503	US-10-425-115-94418	Sequence 94418, A
65	12.4	88.6	515	US-10-425-115-2601	Sequence 2601, A
66	12.4	88.6	521	US-10-425-115-156043	Sequence 156043, A
67	12.4	88.6	558	US-09-815-242-5946	Sequence 5946, A
68	12.4	88.6	558	US-10-282-122A-20240	Sequence 20240, A
69	12.4	88.6	563	US-10-437-963-49186	Sequence 49186, A
70	12.4	88.6	570	US-10-363-345A-33709	Sequence 33709, A
71	12.4	88.6	570	US-10-363-345A-33710	Sequence 33710, A
72	12.4	88.6	570	US-10-363-483A-33709	Sequence 33709, A
73	12.4	88.6	570	US-10-363-483A-33710	Sequence 33710, A
74	12.4	88.6	582	US-10-437-963-35382	Sequence 35382, A
75	12.4	88.6	582	US-10-425-115-145338	Sequence 145338, A
76	12.4	88.6	594	US-10-363-345A-1517	Sequence 1517, A
77	12.4	88.6	594	US-10-363-345A-1518	Sequence 1518, A
78	12.4	88.6	594	US-10-363-483A-1517	Sequence 1517, A
79	12.4	88.6	604	US-10-363-483A-1518	Sequence 1518, A
80	12.4	88.6	630	US-10-425-115-171874	Sequence 171874, A
81	12.4	88.6	630	US-10-282-122A-30630	Sequence 30630, A
82	12.4	88.6	659	US-10-437-963-23809	Sequence 23809, A
83	12.4	88.6	659	US-11-097-143-18683	Sequence 18683, A
84	12.4	88.6	706	US-10-424-599-133766	Sequence 133766, A
85	12.4	88.6	711	US-10-156-761-5594	Sequence 5594, A
86	12.4	88.6	712	US-10-437-963-109	Sequence 109, A
87	12.4	88.6	772	US-10-767-701-11773	Sequence 11773, A
88	12.4	88.6	793	US-10-450-763-14177	Sequence 14177, A
89	12.4	88.6	819	US-10-437-963-40318	Sequence 40318, A
90	12.4	88.6	831	US-10-437-963-56117	Sequence 56117, A
91	12.4	88.6	842	US-10-027-632-160164	Sequence 160164, A
92	12.4	88.6	842	US-10-027-632-160164	Sequence 160164, A
93	12.4	88.6	855	US-10-425-115-83584	Sequence 83584, A
94	12.4	88.6	879	US-10-369-493-39691	Sequence 39691, A
95	12.4	88.6	879	US-10-369-493-40043	Sequence 40043, A
96	12.4	88.6	889	US-10-398-221-1272	Sequence 1272, A

C 97	12.4	88.6	915	6	US-10-369-493-35220	Sequence 35220, A	170	12.4	88.6	1959	6	US-10-369-493-27811	Sequence 27811, A
C 98	12.4	88.6	915	6	US-10-369-493-38130	Sequence 38130, A	171	12.4	88.6	2066	8	US-10-425-115-16562	Sequence 16562, A
C 99	12.4	88.6	915	6	US-10-369-493-38451	Sequence 38451, A	C 172	12.4	88.6	2022	8	US-10-425-115-11743	Sequence 11743, A
C 100	12.4	88.6	915	6	US-10-369-493-38931	Sequence 38931, A	173	12.4	88.6	2132	7	US-10-437-963-56684	Sequence 56684, A
C 101	12.4	88.6	927	6	US-10-369-493-39316	Sequence 39316, A	174	12.4	88.6	2253	3	US-09-765-231A-6	Sequence 6, Appl1
C 102	12.4	88.6	960	8	US-10-425-115-18223	Sequence 18223, A	175	12.4	88.6	2302	5	US-10-106-698-2091	Sequence 2091, Ap
C 103	12.4	88.6	1028	10	US-11-097-143-9890	Sequence 9890, Ap	176	12.4	88.6	2308	6	US-10-786-148-74	Sequence 74, Appl
C 104	12.4	88.6	1068	10	US-11-097-143-35978	Sequence 35978, A	177	12.4	88.6	2406	6	US-10-216-817-32	Sequence 32, Appl
C 105	12.4	88.6	1032	6	US-10-084-846A-47	Sequence 47, Appl	178	12.4	88.6	2406	3	US-10-777-131A-32	Sequence 32, Appl
C 106	12.4	88.6	1035	6	US-10-107-431-82	Sequence 82, Appl	179	12.4	88.6	2409	3	US-09-855-604-618	Sequence 618, Ap
C 107	12.4	88.6	1065	9	US-10-450-763-14128	Sequence 14128, A	180	12.4	88.6	2409	3	US-09-855-604-618	Sequence 618, Ap
C 108	12.4	88.6	1092	8	US-10-414-588-7	Sequence 7, Appl1	181	12.4	88.6	2448	9	US-10-756-149-3651	Sequence 3651, Ap
C 109	12.4	88.6	1137	6	US-10-156-761-3714	Sequence 3714, Ap	182	12.4	88.6	2451	3	US-09-855-604-620	Sequence 620, Ap
C 110	12.4	88.6	1144	8	US-10-216-817-20	Sequence 20, Appl	183	12.4	88.6	2451	3	US-10-037-270-272	Sequence 272, Ap
C 111	12.4	88.6	1152	7	US-10-777-131A-20	Sequence 20, Appl	184	12.4	88.6	2455	5	US-10-037-270-272	Sequence 272, Ap
C 112	12.4	88.6	1152	7	US-10-283-122A-28882	Sequence 28882, A	C 185	12.4	88.6	2495	6	US-10-117-722-272	Sequence 272, Ap
C 113	12.4	88.6	1182	7	US-10-437-963-20085	Sequence 20085, A	C 186	12.4	88.6	2495	6	US-10-122-851-272	Sequence 272, Ap
C 114	12.4	88.6	1185	3	US-09-815-242-7909	Sequence 7909, Ap	187	12.4	88.6	2502	9	US-10-450-763-18340	Sequence 18340, A
C 115	12.4	88.6	1185	3	US-10-283-122A-30463	Sequence 30463, A	188	12.4	88.6	2508	7	US-10-282-122A-33100	Sequence 33100, A
C 116	12.4	88.6	1195	7	US-10-495-300-29	Sequence 29, Appl	C 189	12.4	88.6	2553	6	US-10-369-493-37353	Sequence 37353, A
C 117	12.4	88.6	1206	3	US-09-996-008B-1	Sequence 1, Appl1	C 190	12.4	88.6	2556	7	US-10-398-221-3606	Sequence 3606, Ap
C 118	12.4	88.6	1206	9	US-10-491-958-3	Sequence 3, Appl1	C 191	12.4	88.6	2571	7	US-10-282-122A-23256	Sequence 23256, A
C 119	12.4	88.6	1215	6	US-10-156-761-2315	Sequence 2315, Ap	C 192	12.4	88.6	2595	7	US-10-282-122A-14528	Sequence 14528, A
C 120	12.4	88.6	1225	7	US-10-437-963-24070	Sequence 24070, A	C 193	12.4	88.6	2595	7	US-10-282-122A-14532	Sequence 14532, A
C 121	12.4	88.6	1254	7	US-10-425-114-473	Sequence 473, Ap	C 194	12.4	88.6	2634	6	US-10-369-493-41519	Sequence 41519, A
C 122	12.4	88.6	1264	9	US-10-491-958-2	Sequence 2, Appl1	C 195	12.4	88.6	2645	9	US-10-840-060-193	Sequence 193, Ap
C 123	12.4	88.6	1266	6	US-10-156-761-4878	Sequence 4878, Ap	C 196	12.4	88.6	2645	10	US-11-097-143-5480	Sequence 5480, Ap
C 124	12.4	88.6	1278	7	US-10-425-114-33084	Sequence 33084, A	C 197	12.4	88.6	2697	7	US-10-437-963-48159	Sequence 48159, A
C 125	12.4	88.6	1285	7	US-10-425-114-3185	Sequence 3185, Ap	C 198	12.4	88.6	2721	6	US-10-369-493-44876	Sequence 44876, A
C 126	12.4	88.6	1287	3	US-09-815-242-7768	Sequence 7768, Ap	C 199	12.4	88.6	2757	7	US-10-437-963-53102	Sequence 53102, A
C 127	12.4	88.6	1287	9	US-10-283-122A-30181	Sequence 30181, Ap	C 200	12.4	88.6	2806	6	US-10-216-817-22	Sequence 22, Appl
C 128	12.4	88.6	1287	9	US-10-953-901-292	Sequence 292, App	C 201	12.4	88.6	2806	8	US-10-777-131A-22	Sequence 22, Appl
C 129	12.4	88.6	1290	7	US-10-437-963-44218	Sequence 44218, A	C 202	12.4	88.6	2841	8	US-10-764-330-2	Sequence 3, Appl1
C 130	12.4	88.6	1300	7	US-10-425-114-3282	Sequence 3282, Ap	C 203	12.4	88.6	2852	10	US-11-097-143-18682	Sequence 18682, A
C 131	12.4	88.6	1300	7	US-10-156-761-5076	Sequence 5076, Ap	C 204	12.4	88.6	2854	10	US-11-097-143-20080	Sequence 20080, A
C 132	12.4	88.6	1320	6	US-10-425-114-4236	Sequence 4236, Ap	C 205	12.4	88.6	2874	10	US-11-097-143-13994	Sequence 13994, A
C 133	12.4	88.6	1324	7	US-10-425-114-4236	Sequence 4236, Ap	C 206	12.4	88.6	3148	10	US-11-097-143-35377	Sequence 35377, A
C 134	12.4	88.6	1326	7	US-10-283-122A-11720	Sequence 11720, A	C 207	12.4	88.6	3244	10	US-11-097-143-9889	Sequence 9889, Ap
C 135	12.4	88.6	1349	7	US-10-424-599-115311	Sequence 115311, A	C 208	12.4	88.6	3398	10	US-11-097-143-6187	Sequence 6187, Ap
C 136	12.4	88.6	1349	7	US-10-437-963-41186	Sequence 41186, A	C 209	12.4	88.6	3468	9	US-10-450-763-30051	Sequence 30051, A
C 137	12.4	88.6	1363	7	US-10-425-114-17757	Sequence 17757, A	C 210	12.4	88.6	3472	10	US-11-097-143-8680	Sequence 8680, Ap
C 138	12.4	88.6	1365	6	US-10-369-493-40125	Sequence 40125, A	C 211	12.4	88.6	3507	10	US-11-097-143-17789	Sequence 17789, A
C 139	12.4	88.6	1374	7	US-10-425-114-6260	Sequence 6260, Ap	C 212	12.4	88.6	3710	10	US-11-097-143-17030	Sequence 17030, A
C 140	12.4	88.6	1397	7	US-10-283-122A-12951	Sequence 12951, A	C 213	12.4	88.6	3773	10	US-11-097-143-8063	Sequence 8063, Ap
C 141	12.4	88.6	1397	7	US-10-425-114-22792	Sequence 22792, A	C 214	12.4	88.6	3812	10	US-10-450-763-29192	Sequence 29192, A
C 142	12.4	88.6	1406	7	US-10-424-599-122464	Sequence 122464, A	C 215	12.4	88.6	3846	8	US-10-425-115-69524	Sequence 69524, A
C 143	12.4	88.6	1411	7	US-10-425-114-24493	Sequence 24493, A	C 216	12.4	88.6	3939	7	US-10-168-582-17	Sequence 17, Appl
C 144	12.4	88.6	1443	7	US-10-424-599-139711	Sequence 139711, A	C 217	12.4	88.6	4029	7	US-10-282-122A-38904	Sequence 38904, A
C 145	12.4	88.6	1489	7	US-10-437-963-22814	Sequence 22814, A	C 218	12.4	88.6	4143	3	US-09-815-242-9945	Sequence 9945, Ap
C 146	12.4	88.6	1498	7	US-10-425-114-3307	Sequence 3307, Ap	C 219	12.4	88.6	4251	9	US-10-450-763-25459	Sequence 25459, A
C 147	12.4	88.6	1541	7	US-10-425-114-4160	Sequence 4160, Ap	C 220	12.4	88.6	4285	5	US-10-128-714-343	Sequence 343, App
C 148	12.4	88.6	1557	9	US-10-760-493-66	Sequence 7620, Ap	C 221	12.4	88.6	4357	5	US-10-259-194A-185	Sequence 185, App
C 149	12.4	88.6	1572	3	US-09-815-242-7820	Sequence 30297, Ap	C 222	12.4	88.6	4651	5	US-10-128-714-5343	Sequence 5343, Ap
C 150	12.4	88.6	1572	3	US-10-282-122A-30287	Sequence 29, Appl	C 223	12.4	88.6	4859	5	US-09-764-891-6624	Sequence 6624, Ap
C 151	12.4	88.6	1583	7	US-10-425-114-6364	Sequence 6364, Ap	C 224	12.4	88.6	4859	5	US-10-091-572-188	Sequence 4824, Ap
C 152	12.4	88.6	1584	6	US-10-045-612A-29	Sequence 47186, A	C 225	12.4	88.6	5188	10	US-11-097-143-13993	Sequence 13993, A
C 153	12.4	88.6	1593	8	US-10-425-115-47186	Sequence 2690, Ap	C 226	12.4	88.6	6157	7	US-10-437-963-193717	Sequence 63717, A
C 154	12.4	88.6	1593	8	US-10-156-761-2690	Sequence 47164, A	C 227	12.4	88.6	6239	5	US-10-082-830-159	Sequence 159, App
C 155	12.4	88.6	1603	8	US-10-425-115-47164	Sequence 148597, A	C 228	12.4	88.6	6465	7	US-10-282-122A-30511	Sequence 30511, A
C 156	12.4	88.6	1624	7	US-10-425-115-18597	Sequence 3392, Ap	C 229	12.4	88.6	6986	7	US-10-437-963-99770	Sequence 99770, A
C 157	12.4	88.6	1624	8	US-10-425-114-3392	Sequence 3446, Ap	C 230	12.4	88.6	7114	10	US-11-097-143-8062	Sequence 8062, Ap
C 158	12.4	88.6	1627	7	US-10-425-114-3446	Sequence 36141, A	C 231	12.4	88.6	7365	10	US-11-097-143-15166	Sequence 15166, A
C 159	12.4	88.6	1645	6	US-10-369-493-36141	Sequence 4898, Ap	C 232	12.4	88.6	8544	10	US-11-097-143-17972	Sequence 17972, Ap
C 160	12.4	88.6	1690	9	US-10-956-157-4898	Sequence 4898, Ap	C 233	12.4	88.6	8802	10	US-11-097-143-17788	Sequence 17788, A
C 161	12.4	88.6	1703	7	US-10-437-963-54978	Sequence 54978, A	C 234	12.4	88.6	10387	3	US-09-754-468-15	Sequence 15, Appl
C 162	12.4	88.6	1707	7	US-10-282-122A-13869	Sequence 13869, A	C 235	12.4	88.6	11204	9	US-10-893-671-30	Sequence 30, Appl
C 163	12.4	88.6	1743	7	US-10-282-122A-24153	Sequence 24153, A	C 236	12.4	88.6	14283	9	US-11-097-143-5479	Sequence 5479, Appl
C 164	12.4	88.6	1795	7	US-10-424-599-130899	Sequence 130899, A	C 237	12.4	88.6	15042	10	US-11-097-143-36010	Sequence 36010, A
C 165	12.4	88.6	1823	8	US-10-425-115-147697	Sequence 147697, A	C 238	12.4	88.6	15711	10	US-11-097-143-33409	Sequence 3409, A
C 166	12.4	88.6	1878	7	US-10-437-963-41189	Sequence 41189, A	C 239	12.4	88.6	16499	10	US-11-097-143-17029	Sequence 17029, A
C 167	12.4	88.6	1926	9	US-10-450-763-15831	Sequence 15831, A	C 240	12.4	88.6	22118	10	US-09-799-462A-16	Sequence 16, Appl
C 168	12.4	88.6	1938	7	US-10-424-599-34488	Sequence 34488, A	C 241	12.4	88.6	22118	3	US-09-815-981-5	Sequence 5, Appl1
C 169	12.4	88.6	1954	8	US-10-425-115-117144	Sequence 117144, A	C 242	12.4	88.6	22118	3	US-09-815-981-5	Sequence 5, Appl1



C 243	12.4	88.6	22118	3	US-09-836-911A-16	Sequence 16, Appl	C 316	12	85.7	476	5	US-10-040-862-3499	Sequence 3499, Ap
C 244	12.4	88.6	22118	3	US-09-815-979-5	Sequence 5, Appl	C 317	12	85.7	476	6	US-10-057-4758-3499	Sequence 3499, Ap
C 245	12.4	88.6	22118	5	US-10-125-767-16	Sequence 16, Appl	C 318	12	85.7	476	6	US-10-154-8848-3499	Sequence 3499, Ap
C 246	12.4	88.6	22118	5	US-10-151-081-16	Sequence 16, Appl	C 319	12	85.7	476	8	US-10-764-324-3499	Sequence 3499, Ap
C 247	12.4	88.6	22118	5	US-10-287-313-16	Sequence 16, Appl	C 320	12	85.7	477	7	US-10-424-599-43792	Sequence 43792, A
C 248	12.4	88.6	22118	5	US-10-219-694-16	Sequence 16, Appl	C 321	12	85.7	477	7	US-10-642-277-30	Sequence 30, Appl
C 249	12.4	88.6	22118	5	US-10-235-119-5	Sequence 5, Appl	C 322	12	85.7	481	8	US-10-647-625A-143	Sequence 143, App
C 250	12.4	88.6	22118	6	US-10-161-403-18	Sequence 18, Appl	C 323	12	85.7	488	7	US-10-260-238-2687	Sequence 2687, Ap
C 251	12.4	88.6	22118	6	US-10-086-745-5	Sequence 5, Appl	C 324	12	85.7	501	5	US-09-796-692-5809	Sequence 5809, Ap
C 252	12.4	88.6	22118	6	US-10-428-653-5	Sequence 5, Appl	C 325	12	85.7	501	5	US-10-040-862-5809	Sequence 5809, Ap
C 253	12.4	88.6	22118	7	US-10-808-689-46	Sequence 16, Appl	C 326	12	85.7	501	6	US-10-057-4758-5809	Sequence 5809, Ap
C 254	12.4	88.6	22118	9	US-10-976-394-5	Sequence 5, Appl	C 327	12	85.7	501	6	US-10-154-8848-5809	Sequence 5809, Ap
C 255	12.4	88.6	22118	9	US-10-151-078A-16	Sequence 16, Appl	C 328	12	85.7	501	8	US-10-764-324-5809	Sequence 5809, Ap
C 256	12.4	88.6	22118	10	US-11-006-076-18	Sequence 18, Appl	C 329	12	85.7	539	7	US-09-918-995-29429	Sequence 29429, A
C 257	12.4	88.6	22432	10	US-11-037-143-4756	Sequence 4756, Ap	C 330	12	85.7	539	7	US-10-152-319A-485	Sequence 485, App
C 258	12.4	88.6	45055	6	US-10-107-431-277	Sequence 277, App	C 331	12	85.7	542	4	US-09-925-065A-313926	Sequence 313926, A
C 259	12.4	88.6	59816	6	US-10-084-846A-1	Sequence 1, Appl	C 332	12	85.7	544	3	US-09-918-995-26616	Sequence 26616, A
C 260	12.4	88.6	59816	6	US-10-084-846A-2	Sequence 2, Appl	C 333	12	85.7	546	4	US-09-925-065A-53948	Sequence 53948, A
C 261	12.4	88.6	60872	9	US-10-915-740A-17	Sequence 17, Appl	C 334	12	85.7	554	4	US-09-925-065A-940341	Sequence 940341, A
C 262	12.4	88.6	64482	9	US-10-323-696-151	Sequence 151, App	C 335	12	85.7	557	4	US-09-925-065A-940300	Sequence 940300, A
C 263	12.4	88.6	164051	9	US-10-760-493-18	Sequence 18, Appl	C 336	12	85.7	558	4	US-09-925-065A-9923392	Sequence 9923392, A
C 264	12.4	88.6	326002	9	US-10-461-862-56	Sequence 56, Appl	C 337	12	85.7	566	9	US-10-756-149-4554	Sequence 4554, Ap
C 265	12.4	88.6	561515	8	US-10-741-601-5682	Sequence 5682, Ap	C 338	12	85.7	573	4	US-09-925-065A-831424	Sequence 831424, A
C 266	12.4	88.6	561515	8	US-10-741-600-17730	Sequence 17730, A	C 339	12	85.7	574	7	US-10-767-701-27715	Sequence 27715, A
C 267	12.4	88.6	713059	6	US-10-027-632-174581	Sequence 174581, A	C 340	12	85.7	582	4	US-09-925-065A-563409	Sequence 563409, A
C 268	12.4	88.6	2242715	9	US-10-027-632-174581	Sequence 174581, A	C 341	12	85.7	582	4	US-09-925-065A-865611	Sequence 862611, A
C 269	12.4	88.6	2242715	9	US-10-470-565-1	Sequence 1068, Ap	C 342	12	85.7	584	4	US-09-925-065A-484572	Sequence 484572, A
C 270	12.4	88.6	2256646	7	US-10-470-565-1	Sequence 1, Appl	C 343	12	85.7	584	4	US-09-925-065A-484572	Sequence 484572, A
C 271	12.4	88.6	2256646	7	US-10-037-632-174763	Sequence 174763, A	C 344	12	85.7	594	4	US-09-925-065A-415302	Sequence 415302, A
C 272	12.4	88.6	2940917	5	US-10-037-632-174763	Sequence 174763, A	C 345	12	85.7	595	4	US-09-925-065A-747987	Sequence 747987, A
C 273	12.4	88.6	2940917	6	US-10-098-263B-15548	Sequence 15548, A	C 346	12	85.7	600	9	US-10-972-079-18197	Sequence 18197, A
C 274	12.4	88.6	2940917	5	US-10-719-956-269836	Sequence 269836, A	C 347	12	85.7	600	9	US-10-972-079-18197	Sequence 18197, A
C 275	12.4	88.6	2940917	5	US-10-719-900-464545	Sequence 464545, A	C 348	12	85.7	601	5	US-10-027-632-116332	Sequence 116332, A
C 276	12.4	88.6	2940917	5	US-10-719-900-464545	Sequence 464545, A	C 349	12	85.7	601	6	US-10-027-632-116332	Sequence 116332, A
C 277	12.4	88.6	2940917	5	US-10-956-157-160850	Sequence 160850, A	C 350	12	85.7	612	4	US-09-925-065A-294218	Sequence 294218, A
C 278	12.4	88.6	2940917	5	US-10-956-157-160850	Sequence 160850, A	C 351	12	85.7	615	8	US-10-486-924A-111	Sequence 111, App
C 279	12.4	88.6	2940917	5	US-10-843-527-55580	Sequence 55580, A	C 352	12	85.7	616	5	US-10-027-632-295520	Sequence 295520, A
C 280	12.4	88.6	2940917	5	US-10-843-527-55580	Sequence 55580, A	C 353	12	85.7	616	6	US-10-027-632-295520	Sequence 295520, A
C 281	12.4	88.6	2940917	5	US-11-036-317-173791	Sequence 173791, A	C 354	12	85.7	622	7	US-10-021-323-8848	Sequence 8848, Ap
C 282	12.4	88.6	2940917	5	US-11-036-317-173791	Sequence 173791, A	C 355	12	85.7	627	4	US-09-925-065A-287925	Sequence 287925, A
C 283	12.4	88.6	2940917	5	US-11-036-317-191115	Sequence 191115, A	C 356	12	85.7	634	4	US-09-925-065A-831444	Sequence 831444, A
C 284	12.4	88.6	2940917	5	US-11-036-317-191115	Sequence 191115, A	C 357	12	85.7	640	4	US-09-925-065A-857309	Sequence 857309, A
C 285	12.4	88.6	2940917	5	US-11-036-317-226894	Sequence 226894, A	C 358	12	85.7	645	4	US-09-925-065A-425511	Sequence 425511, A
C 286	12.4	88.6	2940917	5	US-11-036-317-300460	Sequence 300460, A	C 359	12	85.7	645	4	US-09-925-065A-425511	Sequence 425511, A
C 287	12.4	88.6	2940917	5	US-11-036-317-386301	Sequence 386301, A	C 360	12	85.7	645	4	US-10-021-323-8876	Sequence 8876, Ap
C 288	12.4	88.6	2940917	5	US-08-860-844-59	Sequence 59, Appl	C 361	12	85.7	663	4	US-09-925-065A-542867	Sequence 542867, A
C 289	12.4	88.6	2940917	5	US-10-407-543-59	Sequence 59, Appl	C 362	12	85.7	663	4	US-09-925-065A-542867	Sequence 542867, A
C 290	12.4	88.6	2940917	5	US-09-728-445-662	Sequence 662, App	C 363	12	85.7	664	8	US-10-425-115-143889	Sequence 143889, A
C 291	12.4	88.6	2940917	5	US-10-964-549-662	Sequence 662, App	C 364	12	85.7	675	6	US-10-156-761-2804	Sequence 2804, Ap
C 292	12.4	88.6	2940917	5	US-10-741-601-20202	Sequence 20202, A	C 365	12	85.7	675	6	US-09-925-065A-542862	Sequence 542862, A
C 293	12.4	88.6	2940917	5	US-10-741-601-20373	Sequence 20373, A	C 366	12	85.7	678	6	US-10-369-493-32637	Sequence 32637, A
C 294	12.4	88.6	2940917	5	US-10-741-600-21042	Sequence 21042, A	C 367	12	85.7	693	3	US-10-424-599-85723	Sequence 85723, A
C 295	12.4	88.6	2940917	5	US-10-741-600-55687	Sequence 55687, A	C 368	12	85.7	703	8	US-10-653-047-6348	Sequence 6348, Ap
C 296	12.4	88.6	2940917	5	US-10-741-600-55856	Sequence 55856, A	C 369	12	85.7	722	8	US-10-425-115-175820	Sequence 175820, A
C 297	12.4	88.6	2940917	5	US-10-767-701-23254	Sequence 23254, A	C 370	12	85.7	722	8	US-10-425-115-175820	Sequence 175820, A
C 298	12.4	88.6	2940917	5	US-09-923-876-2619	Sequence 2619, Ap	C 371	12	85.7	728	7	US-10-424-599-15852	Sequence 15852, A
C 299	12.4	88.6	2940917	5	US-09-923-876-2619	Sequence 2619, Ap	C 372	12	85.7	738	7	US-10-425-114-21632	Sequence 21632, A
C 300	12.4	88.6	2940917	5	US-09-928-457-92	Sequence 92, Appl	C 373	12	85.7	739	7	US-10-424-599-58433	Sequence 58433, A
C 301	12.4	88.6	2940917	5	US-09-928-457-92	Sequence 92, Appl	C 374	12	85.7	744	3	US-09-912-787-1	Sequence 106870, A
C 302	12.4	88.6	2940917	5	US-10-424-599-35699	Sequence 35699, A	C 375	12	85.7	744	3	US-09-912-787-1	Sequence 106870, A
C 303	12.4	88.6	2940917	5	US-09-864-761-20454	Sequence 20454, A	C 376	12	85.7	744	3	US-09-912-787-1	Sequence 106870, A
C 304	12.4	88.6	2940917	5	US-10-424-599-118867	Sequence 118867, A	C 377	12	85.7	744	5	US-10-014-326-40	Sequence 40, Appl
C 305	12.4	88.6	2940917	5	US-10-437-963-38416	Sequence 38416, A	C 378	12	85.7	744	5	US-10-014-326-40	Sequence 40, Appl
C 306	12.4	88.6	2940917	5	US-10-767-701-30176	Sequence 30176, A	C 379	12	85.7	745	9	US-10-956-157-3941	Sequence 3941, Ap
C 307	12.4	88.6	2940917	5	US-10-424-599-58463	Sequence 58463, A	C 380	12	85.7	745	9	US-10-956-157-3941	Sequence 3941, Ap
C 308	12.4	88.6	2940917	5	US-10-357-930-58918	Sequence 58918, A	C 381	12	85.7	765	7	US-10-437-963-36022	Sequence 36022, Ap
C 309	12.4	88.6	2940917	5	US-10-424-599-113119	Sequence 113119, A	C 382	12	85.7	777	8	US-10-425-115-46229	Sequence 46229, A
C 310	12.4	88.6	2940917	5	US-10-425-115-136113	Sequence 136113, A	C 383	12	85.7	778	8	US-10-425-115-106516	Sequence 106516, A
C 311	12.4	88.6	2940917	5	US-10-437-963-91271	Sequence 91271, A	C 384	12	85.7	811	9	US-10-487-901-59891	Sequence 59891, Ap
C 312	12.4	88.6	2940917	5	US-09-925-065A-746961	Sequence 746961, A	C 385	12	85.7	812	8	US-10-425-115-181101	Sequence 181101, A
C 313	12.4	88.6	2940917	5	US-10-424-599-123597	Sequence 123597, A	C 386	12	85.7	816	8	US-10-282-122A-40311	Sequence 40311, A
C 314	12.4	88.6	2940917	5	US-10-425-115-53505	Sequence 53505, A	C 387	12	85.7	825	7	US-10-282-122A-20553	Sequence 20553, A
C 315	12.4	88.6	2940917	5	US-09-796-692-3499	Sequence 3499, Ap	C 388	12	85.7	843	7	US-10-437-963-65019	Sequence 65019, A

C 389	12	85.7	845	5	US-10-027-632-160028	Sequence 160028,	462	12	85.7	1867	4	US-09-925-065A-82062	Sequence 82062, A
C 330	12	85.7	845	5	US-10-027-632-160029	Sequence 160029,	463	12	85.7	1867	4	US-09-925-065A-82063	Sequence 82063, A
C 331	12	85.7	845	6	US-10-027-632-160028	Sequence 160028,	464	12	85.7	1872	7	US-10-287-226-307	Sequence 307, App
C 332	12	85.7	845	6	US-10-027-632-160029	Sequence 160029,	465	12	85.7	1887	5	US-10-083-620A-18	Sequence 18, Appl
C 333	12	85.7	870	6	US-10-369-423-42174	Sequence 42174, A	466	12	85.7	1887	5	US-10-034-015-18	Sequence 18, Appl
C 334	12	85.7	882	4	US-09-925-065A-65741	Sequence 65741, A	467	12	85.7	1887	8	US-10-842-965-18	Sequence 18, Appl
C 335	12	85.7	882	4	US-09-925-065A-65742	Sequence 65742, A	468	12	85.7	1887	8	US-10-842-965-18	Sequence 18, Appl
C 336	12	85.7	882	4	US-09-925-065A-65743	Sequence 65743, A	469	12	85.7	1892	9	US-10-078-929-105	Sequence 105, App
C 337	12	85.7	882	4	US-09-925-065A-65743	Sequence 65743, A	470	12	85.7	1929	9	US-10-764-420-2402	Sequence 2402, App
C 338	12	85.7	896	10	US-11-042-988-59	Sequence 59, Appl	471	12	85.7	1967	5	US-10-425-114-35681	Sequence 35681, A
C 339	12	85.7	896	10	US-10-437-963-65012	Sequence 65012, A	472	12	85.7	1967	5	US-10-083-620A-20	Sequence 20, Appl
C 400	12	85.7	929	7	US-10-424-559-11516	Sequence 11516, A	473	12	85.7	1967	6	US-10-034-015-20	Sequence 20, Appl
C 401	12	85.7	932	4	US-09-925-065A-25984	Sequence 25984, A	474	12	85.7	1967	6	US-10-842-965-20	Sequence 20, Appl
C 402	12	85.7	932	4	US-09-925-065A-25985	Sequence 25985, A	475	12	85.7	1967	6	US-10-341-834-1	Sequence 1, Appl1
C 403	12	85.7	932	4	US-09-925-065A-25986	Sequence 25986, A	476	12	85.7	1991	6	US-10-341-834-146	Sequence 146, App
C 404	12	85.7	932	4	US-09-925-065A-25987	Sequence 25987, A	477	12	85.7	1991	6	US-10-341-834-146	Sequence 146, App
C 405	12	85.7	935	5	US-10-027-632-30966	Sequence 30966, A	478	12	85.7	2005	8	US-09-802-741A-2	Sequence 2, Appl1
C 406	12	85.7	935	5	US-10-027-632-30967	Sequence 30967, A	479	12	85.7	2005	8	US-10-425-115-93679	Sequence 93679, A
C 407	12	85.7	935	6	US-10-027-632-30966	Sequence 30966, A	480	12	85.7	2025	8	US-10-424-559-15860	Sequence 15850, A
C 408	12	85.7	935	6	US-10-027-632-30967	Sequence 30967, A	481	12	85.7	2025	8	US-10-474-792-631	Sequence 631, App
C 409	12	85.7	968	4	US-09-925-065A-676660	Sequence 676660, A	482	12	85.7	2076	7	US-10-437-963-47582	Sequence 47582, A
C 410	12	85.7	1009	7	US-10-424-559-84710	Sequence 84710, A	483	12	85.7	2148	4	US-09-925-065A-65016	Sequence 65016, A
C 411	12	85.7	1036	8	US-10-425-115-129837	Sequence 129837, A	484	12	85.7	2148	4	US-10-437-963-65016	Sequence 65016, A
C 412	12	85.7	1039	7	US-10-424-559-121717	Sequence 121717, A	485	12	85.7	2166	6	US-10-032-585-6729	Sequence 6729, App
C 413	12	85.7	1039	7	US-10-425-114-6130	Sequence 6130, App	486	12	85.7	2166	6	US-10-437-963-87429	Sequence 87429, A
C 414	12	85.7	1047	5	US-10-194-163-59	Sequence 59, Appl	487	12	85.7	2169	8	US-10-425-115-90209	Sequence 90209, A
C 415	12	85.7	1092	7	US-10-424-559-58457	Sequence 58457, A	488	12	85.7	2207	6	US-10-310-630-6	Sequence 6, Appl1
C 416	12	85.7	1112	7	US-10-767-701-12406	Sequence 12406, A	489	12	85.7	2207	6	US-10-310-630-6	Sequence 6, Appl1
C 417	12	85.7	1136	8	US-10-425-115-48970	Sequence 48970, A	490	12	85.7	2237	8	US-10-841-798-1	Sequence 1, Appl1
C 418	12	85.7	1146	7	US-10-283-112A-25699	Sequence 25699, A	491	12	85.7	2255	7	US-10-437-963-87250	Sequence 87250, A
C 419	12	85.7	1168	8	US-10-425-114-21067	Sequence 21067, A	492	12	85.7	2283	7	US-10-437-963-87250	Sequence 87250, A
C 420	12	85.7	1168	8	US-10-425-115-33637	Sequence 33337, A	493	12	85.7	2288	10	US-11-097-143-37859	Sequence 37859, A
C 421	12	85.7	1179	10	US-11-097-143-33637	Sequence 33337, A	494	12	85.7	2289	7	US-10-312-554-66	Sequence 66, Appl
C 422	12	85.7	1254	6	US-10-027-632-212626	Sequence 212626, A	495	12	85.7	2311	7	US-10-437-963-87220	Sequence 87220, A
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C 424	12	85.7	1267	4	US-09-925-065A-65260	Sequence 65260, A	497	12	85.7	2346	7	US-10-437-963-87328	Sequence 87328, A
C 425	12	85.7	1267	4	US-09-925-065A-65261	Sequence 65261, A	498	12	85.7	2409	6	US-10-437-963-87315	Sequence 87315, A
C 426	12	85.7	1267	4	US-09-925-065A-65262	Sequence 65262, A	499	12	85.7	2419	6	US-10-170-385-202	Sequence 202, App
C 427	12	85.7	1293	6	US-10-238-075-401	Sequence 401, App	500	12	85.7	2419	9	US-10-956-157-2225	Sequence 2225, App
C 428	12	85.7	1356	7	US-10-425-114-32758	Sequence 32758, A	501	12	85.7	2445	7	US-10-425-114-32460	Sequence 32460, A
C 429	12	85.7	1361	4	US-09-925-065A-68140	Sequence 68140, A	502	12	85.7	2457	7	US-10-437-963-87260	Sequence 87260, A
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C 431	12	85.7	1361	7	US-10-424-559-74954	Sequence 74954, A	504	12	85.7	2551	7	US-10-391-068-29	Sequence 391, Appl
C 432	12	85.7	1361	7	US-10-424-559-74954	Sequence 74954, A	505	12	85.7	2557	7	US-10-391-068-29	Sequence 391, Appl
C 433	12	85.7	1368	5	US-10-114-170-199	Sequence 199, App	506	12	85.7	2564	7	US-10-425-114-867	Sequence 867, App
C 434	12	85.7	1368	5	US-10-114-170-199	Sequence 199, App	507	12	85.7	2694	7	US-10-437-963-87318	Sequence 87318, A
C 435	12	85.7	1378	6	US-10-238-075-400	Sequence 400, App	508	12	85.7	2724	9	US-10-450-763-14241	Sequence 14241, App
C 436	12	85.7	1391	4	US-09-925-065A-9326	Sequence 9326, App	509	12	85.7	2724	9	US-10-450-763-14241	Sequence 14241, App
C 437	12	85.7	1422	7	US-10-437-963-36803	Sequence 36803, A	510	12	85.7	2728	7	US-10-437-963-87438	Sequence 87438, A
C 438	12	85.7	1453	5	US-10-044-090-157	Sequence 157, App	511	12	85.7	2728	7	US-10-437-963-87438	Sequence 87438, A
C 439	12	85.7	1457	5	US-10-083-620A-22	Sequence 22, Appl	512	12	85.7	2728	7	US-10-437-963-87438	Sequence 87438, A
C 440	12	85.7	1457	6	US-10-034-015-22	Sequence 22, Appl	513	12	85.7	2728	7	US-10-437-963-87438	Sequence 87438, A
C 441	12	85.7	1457	6	US-10-034-015-22	Sequence 22, Appl	514	12	85.7	2728	7	US-10-437-963-87438	Sequence 87438, A
C 442	12	85.7	1497	4	US-09-925-065A-68482	Sequence 68482, A	515	12	85.7	2728	7	US-10-437-963-87438	Sequence 87438, A
C 443	12	85.7	1523	6	US-10-083-959-174	Sequence 174, App	516	12	85.7	2728	7	US-10-437-963-87438	Sequence 87438, A
C 444	12	85.7	1537	5	US-10-037-270-561	Sequence 561, App	517	12	85.7	2728	7	US-10-437-963-87438	Sequence 87438, A
C 445	12	85.7	1537	6	US-10-117-722-561	Sequence 561, App	518	12	85.7	2728	7	US-10-437-963-87438	Sequence 87438, A
C 446	12	85.7	1537	6	US-10-117-722-561	Sequence 561, App	519	12	85.7	2728	7	US-10-437-963-87438	Sequence 87438, A
C 447	12	85.7	1554	8	US-10-425-115-109915	Sequence 109915, A	520	12	85.7	3060	8	US-10-425-115-177044	Sequence 177044, A
C 448	12	85.7	1560	7	US-10-479-334-23	Sequence 23, Appl	521	12	85.7	3060	8	US-10-425-115-177044	Sequence 177044, A
C 449	12	85.7	1568	7	US-10-437-963-3504	Sequence 3504, A	522	12	85.7	3060	8	US-10-425-115-177044	Sequence 177044, A
C 450	12	85.7	1636	6	US-10-097-065-16	Sequence 16, Appl	523	12	85.7	3060	8	US-10-425-115-177044	Sequence 177044, A
C 451	12	85.7	1636	6	US-10-372-876-16	Sequence 16, Appl	524	12	85.7	3060	8	US-10-425-115-177044	Sequence 177044, A
C 452	12	85.7	1653	8	US-10-428-226-309	Sequence 309, App	525	12	85.7	3060	8	US-10-425-115-177044	Sequence 177044, A
C 453	12	85.7	1653	8	US-10-428-226-309	Sequence 309, App	526	12	85.7	3060	8	US-10-425-115-177044	Sequence 177044, A
C 454	12	85.7	1713	7	US-10-767-701-12371	Sequence 12371, A	527	12	85.7	3060	8	US-10-425-115-177044	Sequence 177044, A
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C 457	12	85.7	1770	6	US-10-097-065-121	Sequence 121, App	530	12	85.7	3060	8	US-10-425-115-177044	Sequence 177044, A
C 458	12	85.7	1788	7	US-10-372-876-121	Sequence 121, App	531	12	85.7	3060	8	US-10-425-115-177044	Sequence 177044, A
C 459	12	85.7	1803	7	US-10-437-963-23584	Sequence 23584, A	532	12	85.7	3060	8	US-10-425-115-177044	Sequence 177044, A
C 460	12	85.7	1803	7	US-10-437-963-23584	Sequence 23584, A	533	12	85.7	3060	8	US-10-425-115-177044	Sequence 177044, A
C 461	12	85.7	1834	7	US-10-424-559-113736	Sequence 113736, A	534	12	85.7	3060	8	US-10-425-115-177044	Sequence 177044, A

C 535	12	85.7	3812	8	US-10-425-115-134479	Sequence 134479,	608	11.6	82.9	600	9	US-10-972-079-11514	Sequence 11514, A
C 536	12	85.7	3828	6	US-10-021-660-21	Sequence 21, Appl	609	11.6	82.9	600	3	US-10-972-079-11515	Sequence 11515, A
C 537	12	85.7	3828	7	US-10-211-462-39	Sequence 29, Appl	610	11.4	81.4	20	3	US-09-873-873-7	Sequence 7, Appl
C 538	12	85.7	4089	7	US-10-437-963-56240	Sequence 56240, A	611	11.4	81.4	20	3	US-09-873-873-18	Sequence 18, Appl
C 539	12	85.7	4121	5	US-10-091-333-4	Sequence 4, Appl1	612	11.4	81.4	20	3	US-09-916-956-7	Sequence 7, Appl
C 540	12	85.7	4121	6	US-10-325-878-4	Sequence 4, Appl1	613	11.4	81.4	20	3	US-09-916-956-18	Sequence 18, Appl
C 541	12	85.7	4125	7	US-10-437-963-87187	Sequence 87187, A	614	11.4	81.4	20	3	US-09-997-914-7	Sequence 7, Appl
C 542	12	85.7	4128	7	US-10-437-963-28616	Sequence 28616, A	615	11.4	81.4	20	3	US-09-997-914-18	Sequence 18, Appl
C 543	12	85.7	4181	8	US-10-425-115-106997	Sequence 106997, A	616	11.4	81.4	20	6	US-10-365-645-7	Sequence 7, Appl
C 544	12	85.7	4203	7	US-10-437-963-56192	Sequence 56192, A	617	11.4	81.4	20	6	US-10-365-645-18	Sequence 18, Appl
C 545	12	85.7	4290	10	US-11-097-143-31753	Sequence 31753, A	618	11.4	81.4	20	7	US-10-612-163-7	Sequence 7, Appl
C 546	12	85.7	4323	7	US-10-437-963-87253	Sequence 87253, A	619	11.4	81.4	20	7	US-10-612-163-18	Sequence 18, Appl
C 547	12	85.7	4343	10	US-11-097-143-3384	Sequence 2384, Ap	620	11.4	81.4	20	7	US-10-739-482-7	Sequence 7, Appl
C 548	12	85.7	4369	6	US-10-108-260A-1401	Sequence 1401, Ap	621	11.4	81.4	20	7	US-10-739-482-18	Sequence 18, Appl
C 549	12	85.7	4405	7	US-10-437-963-9786	Sequence 9786, Ap	622	11.4	81.4	20	7	US-10-817-182-7	Sequence 7, Appl
C 550	12	85.7	4455	7	US-10-437-963-87217	Sequence 87217, A	623	11.4	81.4	20	7	US-10-817-182-18	Sequence 18, Appl
C 551	12	85.7	4482	10	US-11-097-143-42700	Sequence 42700, A	624	11.4	81.4	24	3	US-09-940-185-682	Sequence 682, Ap
C 552	12	85.7	4513	10	US-11-097-143-39436	Sequence 39436, A	625	11.4	81.4	25	3	US-09-940-185-4648	Sequence 4648, Ap
C 553	12	85.7	4562	8	US-10-775-920-121	Sequence 121, App	626	11.4	81.4	25	5	US-10-215-112-5836	Sequence 5836, Ap
C 554	12	85.7	4562	8	US-10-775-920-123	Sequence 123, App	627	11.4	81.4	25	7	US-10-719-956-142027	Sequence 142027,
C 555	12	85.7	4767	7	US-10-437-963-87258	Sequence 87258, A	628	11.4	81.4	25	7	US-10-719-956-197006	Sequence 197006,
C 556	12	85.7	4860	7	US-10-437-963-12409	Sequence 12409, A	629	11.4	81.4	25	7	US-10-719-956-270637	Sequence 270637,
C 557	12	85.7	4900	5	US-10-270-333-142	Sequence 142, App	630	11.4	81.4	25	7	US-10-719-956-425273	Sequence 425273,
C 558	12	85.7	4900	10	US-11-097-143-30523	Sequence 30523, A	631	11.4	81.4	25	7	US-10-719-956-455986	Sequence 455986,
C 559	12	85.7	5076	7	US-10-437-963-56202	Sequence 56202, A	632	11.4	81.4	25	7	US-10-719-956-480082	Sequence 480082,
C 560	12	85.7	5242	9	US-10-934-998-4	Sequence 4, Appl1	633	11.4	81.4	25	7	US-10-719-956-604683	Sequence 604683,
C 561	12	85.7	5589	10	US-11-097-143-9905	Sequence 9905, Ap	634	11.4	81.4	25	7	US-10-719-956-634660	Sequence 634660,
C 562	12	85.7	5736	10	US-11-097-143-9905	Sequence 2383, Ap	635	11.4	81.4	25	7	US-10-719-956-637939	Sequence 637939,
C 563	12	85.7	7040	10	US-11-097-143-2383	Sequence 31753, A	636	11.4	81.4	25	8	US-10-719-900-11471	Sequence 11471, A
C 564	12	85.7	7176	10	US-10-437-963-87441	Sequence 87441, A	637	11.4	81.4	25	8	US-10-719-900-100601	Sequence 100601,
C 565	12	85.7	7443	7	US-11-097-143-27880	Sequence 27880, A	638	11.4	81.4	25	8	US-10-719-900-101816	Sequence 101816,
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C 567	12	85.7	9577	10	US-11-097-143-9904	Sequence 118, App	640	11.4	81.4	25	8	US-10-719-900-276069	Sequence 276069,
C 568	12	85.7	9870	6	US-10-115-831-118	Sequence 7438, Ap	641	11.4	81.4	25	8	US-10-719-900-402953	Sequence 402953,
C 569	12	85.7	10486	10	US-11-097-143-7438	Sequence 23788, A	642	11.4	81.4	25	8	US-10-719-900-580170	Sequence 580170,
C 570	12	85.7	13227	10	US-11-097-143-23788	Sequence 7615, Ap	643	11.4	81.4	25	8	US-10-719-900-752648	Sequence 752648,
C 571	12	85.7	15762	10	US-11-097-143-7615	Sequence 861, App	644	11.4	81.4	25	8	US-10-719-900-762012	Sequence 762012,
C 572	12	85.7	17379	3	US-09-764-860-861	Sequence 861, App	645	11.4	81.4	25	8	US-10-719-900-773677	Sequence 773677,
C 573	12	85.7	17379	5	US-10-212-872-861	Sequence 861, App	646	11.4	81.4	25	8	US-10-719-900-807162	Sequence 807162,
C 574	12	85.7	17379	6	US-09-754-468-37	Sequence 37, Appl	647	11.4	81.4	25	8	US-10-719-900-836594	Sequence 836594,
C 575	12	85.7	21570	6	US-10-132-134-13	Sequence 13, Appl	648	11.4	81.4	25	8	US-10-719-900-856654	Sequence 856654,
C 576	12	85.7	24081	6	US-10-242-355-693	Sequence 693, App	649	11.4	81.4	25	8	US-10-719-900-861184	Sequence 861184,
C 577	12	85.7	26190	8	US-10-741-600-17577	Sequence 1, Appl1	650	11.4	81.4	25	8	US-10-809-189-6531	Sequence 6531, Ap
C 578	12	85.7	30553	8	US-10-132-134-1	Sequence 80, Appl	651	11.4	81.4	25	9	US-10-809-189-87490	Sequence 87490, A
C 579	12	85.7	52101	6	US-10-737-318-80	Sequence 5696, Ap	652	11.4	81.4	25	9	US-10-809-189-109332	Sequence 109332,
C 580	12	85.7	7409	7	US-10-741-601-5696	Sequence 17771, A	653	11.4	81.4	25	9	US-10-809-189-109333	Sequence 109333,
C 581	12	85.7	84409	8	US-10-741-601-5696	Sequence 18, Appl	654	11.4	81.4	25	9	US-10-809-189-109334	Sequence 109334,
C 582	12	85.7	84409	8	US-10-417-375-18	Sequence 677, App	655	11.4	81.4	25	9	US-10-809-189-109335	Sequence 109335,
C 583	12	85.7	113486	5	US-10-087-192-673	Sequence 33, Appl	656	11.4	81.4	25	9	US-10-809-189-109336	Sequence 109336,
C 584	12	85.7	115284	5	US-10-737-082-33	Sequence 33, Appl	657	11.4	81.4	25	9	US-10-809-189-109337	Sequence 109337,
C 585	12	85.7	122673	9	US-10-765-790-33	Sequence 15, Appl	658	11.4	81.4	25	9	US-10-809-189-109338	Sequence 109338,
C 586	12	85.7	122673	9	US-10-765-790-33	Sequence 15, Appl	659	11.4	81.4	25	9	US-10-809-189-109339	Sequence 109339,
C 587	12	85.7	143899	3	US-09-972-546-15	Sequence 55, Appl	660	11.4	81.4	25	9	US-10-809-189-109340	Sequence 109340,
C 588	12	85.7	143899	3	US-10-735-256-15	Sequence 95, Appl	661	11.4	81.4	25	9	US-10-809-189-109341	Sequence 109341,
C 589	12	85.7	150275	9	US-10-981-277-55	Sequence 95, App	662	11.4	81.4	25	9	US-10-809-189-109342	Sequence 109342,
C 590	12	85.7	168325	5	US-10-087-192-955	Sequence 43, Appl	663	11.4	81.4	25	9	US-10-809-189-109343	Sequence 109343,
C 591	12	85.7	193074	9	US-10-981-277-43	Sequence 43, Appl	664	11.4	81.4	25	9	US-10-809-189-109344	Sequence 109344,
C 592	12	85.7	230101	8	US-10-719-993-6829	Sequence 6829, Ap	665	11.4	81.4	25	10	US-11-036-317-125881	Sequence 125881,
C 593	12	85.7	235070	8	US-10-087-192-1990	Sequence 1990, Ap	666	11.4	81.4	25	10	US-11-036-317-125882	Sequence 125882,
C 594	12	85.7	301692	6	US-10-428-487-11	Sequence 11, Appl	667	11.4	81.4	25	10	US-11-036-317-125883	Sequence 125883,
C 595	12	85.7	310268	6	US-10-367-094-195	Sequence 195, App	668	11.4	81.4	25	10	US-11-036-317-125884	Sequence 125884,
C 596	12	85.7	653122	5	US-10-087-192-226	Sequence 226, App	669	11.4	81.4	25	10	US-11-036-317-125885	Sequence 125885,
C 597	12	85.7	1223197	5	US-10-027-632-179264	Sequence 179264, Sequence 179264, A	670	11.4	81.4	25	10	US-11-036-317-125886	Sequence 125886,
C 598	12	85.7	1223197	6	US-10-027-632-179264	Sequence 179264, A	671	11.4	81.4	25	10	US-11-036-317-125887	Sequence 125887,
C 599	12	85.7	2731748	7	US-10-297-465A-1	Sequence 1, Appl1	672	11.4	81.4	25	10	US-11-036-317-125888	Sequence 125888,
C 600	11.6	82.9	552	5	US-10-027-632-146814	Sequence 146814, A	673	11.4	81.4	25	10	US-11-036-317-125889	Sequence 125889,
C 601	11.6	82.9	552	5	US-10-027-632-146815	Sequence 146815, A	674	11.4	81.4	25	10	US-11-036-317-125890	Sequence 125890,
C 602	11.6	82.9	552	6	US-10-027-632-146816	Sequence 146816, A	675	11.4	81.4	25	10	US-11-036-317-125891	Sequence 125891,
C 603	11.6	82.9	552	6	US-10-027-632-146817	Sequence 146817, A	676	11.4	81.4	25	10	US-11-036-317-125892	Sequence 125892,
C 604	11.6	82.9	600	6	US-10-972-079-10987	Sequence 10987, A	677	11.4	81.4	25	10	US-11-036-317-125893	Sequence 125893,
C 605	11.6	82.9	600	9	US-10-972-079-11511	Sequence 11511, A	678	11.4	81.4	25	10	US-11-036-317-125894	Sequence 125894,
C 606	11.6	82.9	600	9	US-10-972-079-11512	Sequence 11512, A	679	11.4	81.4	25	10	US-11-036-317-125895	Sequence 125895,
C 607	11.6	82.9	600	9	US-10-972-079-11513	Sequence 11513, A	680	11.4	81.4	25	10	US-11-036-317-125896	Sequence 125896,

C 661	11.4	81.4	25	10	US-11-060-756-146834	Sequence 146834,	C 754	11.4	81.4	256	3	US-09-294-093B-2838	Sequence 2838, Ap
662	11.4	81.4	25	10	US-11-060-756-156140	Sequence 156140,	755	11.4	81.4	259	3	US-09-783-590-664	Sequence 664, App
C 663	11.4	81.4	25	10	US-11-060-756-156141	Sequence 156141,	756	11.4	81.4	300	8	US-10-425-115-118130	Sequence 118130,
C 664	11.4	81.4	25	10	US-11-060-756-217029	Sequence 217029,	C 757	11.4	81.4	305	3	US-09-728-445-32	Sequence 32, App1
665	11.4	81.4	25	10	US-11-060-756-227686	Sequence 227686,	C 758	11.4	81.4	305	9	US-10-964-549-93	Sequence 32, App1
666	11.4	81.4	25	10	US-11-060-756-237269	Sequence 237269,	C 759	11.4	81.4	307	8	US-10-425-115-121120	Sequence 121120,
667	11.4	81.4	25	10	US-11-060-756-248267	Sequence 248267,	760	11.4	81.4	310	3	US-09-796-692-6500	Sequence 6500, Ap
C 668	11.4	81.4	50	3	US-09-389-782-29	Sequence 29, App1	761	11.4	81.4	310	3	US-10-040-862-6500	Sequence 6500, Ap
C 669	11.4	81.4	60	3	US-09-908-975-10521	Sequence 10521, A	762	11.4	81.4	310	6	US-10-057-478B-6500	Sequence 6500, Ap
C 670	11.4	81.4	60	3	US-09-908-975-15073	Sequence 15073, A	763	11.4	81.4	310	6	US-10-154-884B-6500	Sequence 6500, Ap
C 671	11.4	81.4	60	3	US-09-908-975-22492	Sequence 22492, A	764	11.4	81.4	310	7	US-10-242-535A-52001	Sequence 52001, A
C 672	11.4	81.4	60	5	US-10-021-723A-55	Sequence 55, App1	765	11.4	81.4	310	8	US-10-085-783A-52001	Sequence 52001, A
C 673	11.4	81.4	65	3	US-09-908-975-1225	Sequence 1225, Ap	766	11.4	81.4	310	8	US-10-764-324-6500	Sequence 6500, Ap
C 674	11.4	81.4	67	5	US-10-021-723A-30	Sequence 30, App1	767	11.4	81.4	316	8	US-10-425-115-2445	Sequence 2445, Ap
C 675	11.4	81.4	110	3	US-09-844-653-35	Sequence 35, App1	C 768	11.4	81.4	316	3	US-09-783-590-2380	Sequence 2380, Ap
C 676	11.4	81.4	117	8	US-10-425-115-65825	Sequence 65825, A	769	11.4	81.4	316	7	US-10-437-963-23251	Sequence 23251, A
C 677	11.4	81.4	117	8	US-09-783-590-8202	Sequence 8202, Ap	C 770	11.4	81.4	320	7	US-10-242-535A-4436	Sequence 4436, Ap
C 678	11.4	81.4	139	8	US-10-425-115-5003	Sequence 5003, Ap	C 771	11.4	81.4	320	7	US-10-085-783A-4436	Sequence 4436, Ap
C 679	11.4	81.4	147	6	US-10-084-846A-23	Sequence 23, App1	C 772	11.4	81.4	321	3	US-09-062-113-99	Sequence 99, App1
C 700	11.4	81.4	156	3	US-09-923-876-1642	Sequence 1642, Ap	C 773	11.4	81.4	321	6	US-10-232-858-99	Sequence 99, App1
C 701	11.4	81.4	156	3	US-09-923-876-1642	Sequence 1642, Ap	C 774	11.4	81.4	321	7	US-10-663-244-82	Sequence 82, App1
C 702	11.4	81.4	159	3	US-09-864-761-31331	Sequence 31331, A	C 775	11.4	81.4	321	7	US-10-785-109-99	Sequence 99, App1
C 703	11.4	81.4	162	3	US-09-864-761-22190	Sequence 22190, A	C 776	11.4	81.4	321	7	US-10-785-114-99	Sequence 99, App1
C 704	11.4	81.4	165	8	US-10-425-115-8054	Sequence 8054, Ap	C 777	11.4	81.4	321	8	US-10-929-958-99	Sequence 99, App1
C 705	11.4	81.4	165	8	US-10-425-115-162709	Sequence 162709, A	C 778	11.4	81.4	321	8	US-10-929-748-99	Sequence 99, App1
C 706	11.4	81.4	173	3	US-09-864-761-26899	Sequence 26899, A	C 779	11.4	81.4	321	9	US-10-979-303-99	Sequence 99, App1
C 707	11.4	81.4	175	7	US-10-424-559-72659	Sequence 72659, A	C 780	11.4	81.4	321	9	US-10-979-654-99	Sequence 99, App1
C 708	11.4	81.4	177	10	US-11-097-143-34304	Sequence 34304, A	781	11.4	81.4	324	7	US-10-424-559-142496	Sequence 142496, A
C 709	11.4	81.4	180	6	US-10-395-740-13	Sequence 13, App1	C 782	11.4	81.4	324	7	US-10-424-559-142496	Sequence 142496, A
C 710	11.4	81.4	180	7	US-10-437-963-94631	Sequence 94631, A	C 783	11.4	81.4	324	7	US-10-437-963-17072	Sequence 17072, A
C 711	11.4	81.4	189	7	US-10-282-122A-13288	Sequence 13288, A	784	11.4	81.4	324	3	US-09-918-995-29929	Sequence 29929, A
C 712	11.4	81.4	190	7	US-10-437-963-94533	Sequence 94533, A	C 785	11.4	81.4	348	8	US-10-425-115-33067	Sequence 33067, A
C 713	11.4	81.4	191	3	US-09-864-761-24983	Sequence 24983, A	786	11.4	81.4	352	6	US-10-029-386-26631	Sequence 26631, A
C 714	11.4	81.4	191	8	US-10-425-115-125439	Sequence 125439, A	787	11.4	81.4	354	7	US-10-424-559-120746	Sequence 120746, A
C 715	11.4	81.4	195	5	US-10-106-698-2331	Sequence 2331, Ap	788	11.4	81.4	354	7	US-10-437-963-37632	Sequence 37632, A
C 716	11.4	81.4	198	3	US-09-864-408A-3381	Sequence 3381, Ap	789	11.4	81.4	358	8	US-09-770-791-582	Sequence 582, App
C 717	11.4	81.4	199	6	US-10-029-386-16252	Sequence 16252, Ap	C 790	11.4	81.4	369	8	US-10-425-115-83408	Sequence 83408, A
C 718	11.4	81.4	201	7	US-10-741-601-16990	Sequence 16990, A	791	11.4	81.4	373	7	US-10-424-559-124569	Sequence 124569
C 719	11.4	81.4	201	8	US-10-719-993-9101	Sequence 9101, Ap	C 792	11.4	81.4	378	6	US-10-395-740-17	Sequence 17, App1
C 720	11.4	81.4	201	8	US-10-741-600-21912	Sequence 21912, A	C 793	11.4	81.4	381	3	US-09-918-995-34114	Sequence 34114, A
C 721	11.4	81.4	201	8	US-10-741-600-50717	Sequence 50717, A	794	11.4	81.4	383	7	US-10-424-559-60501	Sequence 60501, A
C 722	11.4	81.4	203	3	US-09-923-876-1846	Sequence 1846, Ap	795	11.4	81.4	385	3	US-10-424-559-92386	Sequence 92386, A
C 723	11.4	81.4	203	7	US-09-923-876-1846	Sequence 1846, Ap	C 796	11.4	81.4	388	3	US-09-918-995-6867	Sequence 6867, Ap
C 724	11.4	81.4	209	7	US-10-424-559-65475	Sequence 65475, A	797	11.4	81.4	392	8	US-10-425-115-155397	Sequence 155397, A
C 725	11.4	81.4	211	8	US-10-425-115-160936	Sequence 160936, A	C 798	11.4	81.4	395	7	US-10-425-115-122879	Sequence 122879, A
C 726	11.4	81.4	216	9	US-10-756-149-1508	Sequence 1508, Ap	C 799	11.4	81.4	396	8	US-10-424-559-131073	Sequence 131073, A
C 727	11.4	81.4	221	8	US-10-674-124A-19400	Sequence 19400, A	800	11.4	81.4	397	8	US-10-425-115-116176	Sequence 116176, A
C 728	11.4	81.4	222	7	US-10-437-963-52698	Sequence 52698, A	C 801	11.4	81.4	398	3	US-09-960-352-1749	Sequence 1749, Ap
C 729	11.4	81.4	224	8	US-10-425-115-22979	Sequence 22979, A	C 802	11.4	81.4	398	3	US-10-485-508B-6	Sequence 6, App1
C 730	11.4	81.4	237	6	US-10-369-493-29045	Sequence 29045, A	803	11.4	81.4	402	8	US-10-425-115-115151	Sequence 115151, A
C 731	11.4	81.4	237	7	US-10-437-963-24899	Sequence 24899, A	804	11.4	81.4	403	3	US-09-864-761-16708	Sequence 16708, A
C 732	11.4	81.4	237	9	US-10-450-763-7640	Sequence 7640, Ap	C 805	11.4	81.4	405	6	US-10-287-274-444	Sequence 274, App
C 733	11.4	81.4	238	8	US-10-425-115-3093	Sequence 3093, Ap	C 806	11.4	81.4	405	6	US-10-029-386-16555	Sequence 16555, A
C 734	11.4	81.4	244	3	US-09-987-899-2188	Sequence 2188, Ap	C 807	11.4	81.4	405	7	US-10-282-122A-6507	Sequence 6507, Ap
C 735	11.4	81.4	244	3	US-10-437-963-27310	Sequence 27310, A	C 808	11.4	81.4	405	8	US-10-767-795-2639	Sequence 2639, Ap
C 736	11.4	81.4	250	6	US-10-238-075-77	Sequence 77, App1	C 809	11.4	81.4	405	9	US-10-779-543-12743	Sequence 12743, A
C 737	11.4	81.4	252	3	US-09-783-590-6711	Sequence 6711, Ap	C 810	11.4	81.4	406	3	US-09-918-995-16397	Sequence 16397, A
C 738	11.4	81.4	262	7	US-10-437-963-41790	Sequence 41790, A	811	11.4	81.4	406	8	US-10-425-115-13533	Sequence 35393, A
C 739	11.4	81.4	263	8	US-10-425-115-22937	Sequence 22937, A	C 812	11.4	81.4	408	3	US-09-960-352-2750	Sequence 2654, Ap
C 740	11.4	81.4	264	3	US-09-738-626-1658	Sequence 1658, Ap	C 813	11.4	81.4	412	3	US-09-960-352-2750	Sequence 2750, App
C 741	11.4	81.4	264	8	US-10-425-115-105548	Sequence 105548, A	814	11.4	81.4	413	7	US-10-469-285-112	Sequence 512, App
C 742	11.4	81.4	266	3	US-09-987-899-5286	Sequence 5286, Ap	C 815	11.4	81.4	414	7	US-10-242-535A-26405	Sequence 26405, A
C 743	11.4	81.4	279	3	US-09-294-093B-4114	Sequence 4114, Ap	C 816	11.4	81.4	414	7	US-10-085-783A-26405	Sequence 26405, A
C 744	11.4	81.4	284	8	US-10-425-115-162584	Sequence 162584, A	817	11.4	81.4	415	3	US-09-724-569-11	Sequence 7, App1
C 745	11.4	81.4	284	8	US-10-425-115-43501	Sequence 43501, A	818	11.4	81.4	415	8	US-10-425-115-10986	Sequence 30986, A
C 746	11.4	81.4	291	3	US-09-736-457-832	Sequence 832, App	C 819	11.4	81.4	417	3	US-09-983-965-5753	Sequence 5753, Ap
C 747	11.4	81.4	291	3	US-09-902-941-832	Sequence 832, App	C 820	11.4	81.4	417	4	US-09-925-065A-483092	Sequence 483092, A
C 748	11.4	81.4	291	3	US-09-849-626-832	Sequence 832, App	821	11.4	81.4	419	7	US-10-437-963-23609	Sequence 23609, A
C 749	11.4	81.4	291	5	US-10-017-754-832	Sequence 832, App	822	11.4	81.4	420	8	US-10-357-930-16283	Sequence 16283, A
C 750	11.4	81.4	291	5	US-10-113-872-832	Sequence 832, App	C 823	11.4	81.4	421	3	US-09-867-550-1849	Sequence 1849, Ap
C 751	11.4	81.4	291	6	US-10-283-017-832	Sequence 832, App	824	11.4	81.4	421	9	US-10-424-559-48144	Sequence 48144, A
C 752	11.4	81.4	293	3	US-09-987-899-5824	Sequence 5824, Ap	825	11.4	81.4	421	9	US-10-779-543-13255	Sequence 13255, A
C 753	11.4	81.4	294	8	US-10-425-115-181462	Sequence 181462, A	C 826	11.4	81.4	422	4	US-09-925-065A-392821	Sequence 392821, A

C 827	11.4	81.4	422	4	US-09-925-065A-392823	Sequence 392823,	C 900	11.4	81.4	465	9	US-10-979-654-12	Sequence 12, Appl
828	11.4	81.4	422	5	US-10-027-632-140713	Sequence 140713,	C 901	11.4	81.4	469	3	US-09-918-995-743	Sequence 743, App
829	11.4	81.4	422	5	US-10-027-632-140714	Sequence 140714,	C 902	11.4	81.4	470	7	US-10-424-599-117455	Sequence 117455,
830	11.4	81.4	422	6	US-10-027-632-140713	Sequence 140713,	C 903	11.4	81.4	473	7	US-10-424-599-926	Sequence 926, App
831	11.4	81.4	422	6	US-10-027-632-140714	Sequence 140714,	C 904	11.4	81.4	476	5	US-10-027-632-94159	Sequence 94159, A
C 832	11.4	81.4	422	6	US-09-925-065A-207157	Sequence 207157,	C 905	11.4	81.4	476	6	US-10-027-632-94159	Sequence 94159, A
833	11.4	81.4	429	3	US-09-960-352-1407	Sequence 140715,	C 906	11.4	81.4	476	6	US-10-424-599-24036	Sequence 24036, A
C 834	11.4	81.4	430	8	US-10-425-115-116451	Sequence 116451,	C 907	11.4	81.4	477	8	US-10-674-1294-16019	Sequence 16019, A
835	11.4	81.4	431	7	US-10-242-535A-5420	Sequence 5420, Ap	C 908	11.4	81.4	480	7	US-10-342-535A-2211	Sequence 2211, Ap
836	11.4	81.4	431	7	US-10-085-763A-5420	Sequence 5420, Ap	C 909	11.4	81.4	480	7	US-10-085-763A-2211	Sequence 2211, Ap
837	11.4	81.4	431	8	US-10-425-115-52209	Sequence 52209, A	C 910	11.4	81.4	483	3	US-09-918-995-970	Sequence 970, App
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C 839	11.4	81.4	432	3	US-09-917-800A-810	Sequence 810, App	C 912	11.4	81.4	486	4	US-09-925-065A-489817	Sequence 489817,
C 840	11.4	81.4	432	6	US-10-232-858-98	Sequence 98, Appl	C 913	11.4	81.4	480	3	US-09-918-995-20602	Sequence 20602, A
C 841	11.4	81.4	432	7	US-10-785-109-98	Sequence 98, Appl	C 914	11.4	81.4	480	3	US-10-425-114-25294	Sequence 25294, A
C 842	11.4	81.4	432	7	US-10-785-114-98	Sequence 98, Appl	C 915	11.4	81.4	486	7	US-10-021-323-5479	Sequence 5479, Ap
C 843	11.4	81.4	432	8	US-10-425-115-93490	Sequence 93490, A	C 916	11.4	81.4	486	7	US-10-021-323-5479	Sequence 5479, Ap
C 844	11.4	81.4	432	8	US-10-929-958-98	Sequence 98, Appl	C 917	11.4	81.4	497	7	US-10-021-323-5565	Sequence 5565, Ap
C 845	11.4	81.4	432	8	US-10-929-958-98	Sequence 98, Appl	C 918	11.4	81.4	497	7	US-10-767-701-17377	Sequence 17377, A
C 846	11.4	81.4	432	9	US-10-979-303-98	Sequence 98, Appl	C 919	11.4	81.4	498	3	US-09-919-580-794	Sequence 794, App
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C 848	11.4	81.4	433	5	US-10-027-632-288751	Sequence 288751,	C 921	11.4	81.4	500	6	US-10-029-386-10429	Sequence 10429, A
C 849	11.4	81.4	433	6	US-10-027-632-288751	Sequence 288751,	C 922	11.4	81.4	500	7	US-10-424-599-9034	Sequence 9034, Ap
850	11.4	81.4	435	8	US-10-424-599-59884	Sequence 59884, A	C 923	11.4	81.4	501	3	US-09-864-761-8239	Sequence 8249, Ap
C 851	11.4	81.4	435	8	US-10-425-115-135104	Sequence 135104,	C 924	11.4	81.4	503	4	US-09-925-065A-208087	Sequence 208087,
852	11.4	81.4	436	8	US-10-425-115-108720	Sequence 108720,	C 925	11.4	81.4	503	4	US-09-925-065A-355321	Sequence 355321,
C 853	11.4	81.4	438	3	US-09-062-113-14	Sequence 14, Appl	C 926	11.4	81.4	504	4	US-09-925-065A-355321	Sequence 355321,
C 854	11.4	81.4	438	6	US-10-232-858-14	Sequence 14, Appl	C 927	11.4	81.4	504	7	US-10-437-963-13115	Sequence 13115, A
C 855	11.4	81.4	438	7	US-10-785-109-14	Sequence 14, Appl	C 928	11.4	81.4	504	9	US-10-487-901-31390	Sequence 3390, Ap
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C 857	11.4	81.4	438	8	US-10-357-930-18605	Sequence 18605, A	C 930	11.4	81.4	505	6	US-10-341-961A-1178	Sequence 1178, App
C 858	11.4	81.4	438	8	US-10-929-958-14	Sequence 14, Appl	C 931	11.4	81.4	506	4	US-09-925-065A-654825	Sequence 64825,
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C 860	11.4	81.4	438	9	US-10-979-303-14	Sequence 14, Appl	C 933	11.4	81.4	507	5	US-10-027-632-211603	Sequence 211603,
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C 862	11.4	81.4	439	7	US-10-424-599-16229	Sequence 16229, A	C 935	11.4	81.4	507	6	US-10-437-963-15343	Sequence 15343, A
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C 865	11.4	81.4	443	9	US-10-450-763-4620	Sequence 4620, Ap	C 938	11.4	81.4	511	4	US-09-925-065A-760089	Sequence 760089,
C 866	11.4	81.4	446	3	US-09-918-995-1383	Sequence 1383, Ap	C 939	11.4	81.4	511	7	US-10-242-535A-16421	Sequence 16421, A
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869	11.4	81.4	446	5	US-10-027-632-266512	Sequence 266512,	C 942	11.4	81.4	512	7	US-10-430-201-709	Sequence 709, App
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C 881	11.4	81.4	458	3	US-09-864-761-14121	Sequence 14121, A	C 954	11.4	81.4	522	7	US-10-027-632-278378	Sequence 278378,
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C 889	11.4	81.4	463	8	US-10-468-488-181	Sequence 181, App	C 962	11.4	81.4	525	9	US-10-997-535-47	Sequence 535, Ap
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C 892	11.4	81.4	465	3	US-09-062-113-12	Sequence 12, Appl	C 965	11.4	81.4	533	4	US-09-925-065A-392824	Sequence 392824,
C 893	11.4	81.4	465	5	US-10-060-036-3715	Sequence 3715, Ap	C 966	11.4	81.4	535	3	US-09-764-875-92	Sequence 92, Appl
C 894	11.4	81.4	465	5	US-10-232-858-12	Sequence 12, Appl	C 967	11.4	81.4	536	3	US-09-764-875-92	Sequence 92, Appl
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C 898	11.4	81.4	465	8	US-10-929-748-12	Sequence 12, Appl	C 971	11.4	81.4	536	7	US-10-158-057-35	Sequence 35, Appl
C 899	11.4	81.4	465	9	US-10-979-303-12	Sequence 12, Appl	C 972	11.4	81.4	537	4	US-09-925-065A-553536	Sequence 553536,

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C 977 11.4 81.4 539 6 US-10-027-632-73292 Sequence 73292, A  
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C 984 11.4 81.4 542 5 US-10-106-698-4281 Sequence 4281, A  
985 11.4 81.4 543 4 US-09-925-065A-42076 Sequence 42076, A  
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C 987 11.4 81.4 546 8 US-10-363-345A-11587 Sequence 31587, A  
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C 989 11.4 81.4 546 9 US-10-363-483A-31588 Sequence 31588, A  
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C 991 11.4 81.4 548 4 US-09-925-065A-12538 Sequence 12538, A  
992 11.4 81.4 548 4 US-09-925-065A-42462 Sequence 42462, A  
C 993 11.4 81.4 550 7 US-10-437-963-566 Sequence 566, A  
C 994 11.4 81.4 551 4 US-09-925-065A-768235 Sequence 768235, A  
995 11.4 81.4 551 4 US-09-925-065A-790929 Sequence 790929, A  
996 11.4 81.4 551 4 US-09-925-065A-790930 Sequence 790930, A  
997 11.4 81.4 552 5 US-10-027-632-266511 Sequence 266511, A  
C 998 11.4 81.4 552 6 US-10-027-632-266511 Sequence 266511, A  
C 999 11.4 81.4 552 7 US-10-424-599-59319 Sequence 59319, A  
1000 11.4 81.4 552 7 US-10-767-701-25051 Sequence 25051, A

## ALIGNMENTS

RESULT 1  
US-10-800-926-2  
Sequence 2, Application US/10800926  
Publication No. US20050032731A1  
GENERAL INFORMATION:  
APPLICANT: MARSHALL, WILLIAM E.  
TITLE OF INVENTION: OLIGORIBONUCLEOTIDES ALERT THE IMMUNE SYSTEM OF ANIMALS  
TITLE OF INVENTION: TO THE IMMUNITY OF MICROBIAL INFECTION  
FILE REFERENCE: P01936US06  
CURRENT APPLICATION NUMBER: US/10/800,926  
PRIOR FILING DATE: 2004-03-15  
PRIOR APPLICATION NUMBER: 09/883,550  
PRIOR FILING DATE: 2001-06-18  
PRIOR APPLICATION NUMBER: 09/193,653  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 08/739,264  
PRIOR FILING DATE: 1996-10-29  
PRIOR APPLICATION NUMBER: 08/517,016  
PRIOR FILING DATE: 1995-08-18  
PRIOR APPLICATION NUMBER: 08/376,175  
PRIOR FILING DATE: 1995-01-20  
PRIOR APPLICATION NUMBER: 08/059,745  
PRIOR FILING DATE: 1993-05-11  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 2  
LENGTH: 14  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-800-926-2

Query Match 100.0%; Score 14; DB 8; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGUACUGCACTCG 14  
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Db 1 CGUACUGCACTCG 14

RESULT 2  
US-09-925-065A-30493/C  
Sequence 30493, Application US/09925065A  
Publication No. US20050228172A9  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 30493  
LENGTH: 542  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-30493

Query Match 100.0%; Score 14; DB 4; Length 542;  
Best Local Similarity 78.6%; Pred. No. 4e+02;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14  
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Db 423 CGTACTGCACTCG 410

RESULT 3  
US-10-369-493-36408  
Sequence 36408, Application US/10369493  
Publication No. US20030233675A1  
GENERAL INFORMATION:  
APPLICANT: Cao, Yongwei  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Goldman, Barry S.  
APPLICANT: Chen, Xianfeng  
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
FILE REFERENCE: 38-10(52052)B  
CURRENT APPLICATION NUMBER: US/10/369,493  
PRIOR FILING DATE: 2003-02-28  
PRIOR APPLICATION NUMBER: US 60/360,039  
PRIOR FILING DATE: 2002-02-21  
NUMBER OF SEQ ID NOS: 47374  
SEQ ID NO 36408  
LENGTH: 1786  
TYPE: DNA  
ORGANISM: Aspergillus nidulans  
US-10-369-493-36408

Query Match 100.0%; Score 14; DB 6; Length 1786;  
Best Local Similarity 78.6%; Pred. No. 4.2e+02;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14  
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Db 128 CGTACTGCACTCG 141



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RESULT 4
US-10-369-493-28056/c
; Sequence 28056, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 28056
; LENGTH: 1981
; TYPE: DNA
; ORGANISM: Burkholderia fungorum
US-10-369-493-28056

Query Match      100.0%; Score 14; DB 6; Length 1981;
Best Local Similarity 78.6%; Pred. No. 4.2e+02;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Cy      1 CGUACUGCAACUCG 14
Db      1510 CGTACTGCAACTCG 1497

RESULT 5
US-10-282-122A-12964/c
; Sequence 12964, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyekind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
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;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 78614
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 12964
;; LENGTH: 1986
;; TYPE: DNA
;; ORGANISM: Burkholderia fungorum
US-10-282-122A-12964

Query Match      100.0%; Score 14; DB 7; Length 1986;
Best Local Similarity 78.6%; Pred. No. 4.2e+02;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Cy      1 CGUACUGCAACUCG 14
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RESULT 6
US-10-369-493-30810/c
; Sequence 30810, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 30810
; LENGTH: 2080
; TYPE: DNA
; ORGANISM: Burkholderia cepacia
US-10-369-493-30810

Query Match      100.0%; Score 14; DB 6; Length 2080;
Best Local Similarity 78.6%; Pred. No. 4.2e+02;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Cy      1 CGUACUGCAACUCG 14
Db      1510 CGTACTGCAACTCG 1497

RESULT 7
US-10-282-122A-33109/c
; Sequence 33109, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyekind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
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/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 33109
/ TYPE: DNA
/ LENGTH: 2460
/ ORGANISM: Pseudomonas syringae
US-10-282-122A-33109
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Query Match      100.0%; Score 14; DB 7; Length 2460;
Best Local Similarity 78.6%; Pred. No. 4.2e+02;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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DB      1408 GCTACTGCAACTCG 1395
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US-10-437-963-61758/C
/ Sequence 61758, Application US/10437963
/ Publication No. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barbazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 61758
/ LENGTH: 6024
/ TYPE: DNA
/ ORGANISM: Oryza sativa
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_6315C.1
US-10-437-963-61758
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Query Match      100.0%; Score 14; DB 7; Length 6024;
Best Local Similarity 78.6%; Pred. No. 4.3e+02;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 CGUACUGCAACTCG 14
      ||:||:|||||:|
DB      3493 GCTACTGCAACTCG 3480
```

```
RESULT 9
US-10-437-963-87284/C
/ Sequence 87284, Application US/10437963
/ Publication No. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barbazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 87284
/ LENGTH: 6808
/ TYPE: DNA
/ ORGANISM: Oryza sativa
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)...(6808)
/ OTHER INFORMATION: unsure at all n locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_86244C.1
US-10-437-963-87284
```

```
Query Match      100.0%; Score 14; DB 7; Length 6808;
Best Local Similarity 78.6%; Pred. No. 4.4e+02;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 CGUACUGCAACTCG 14
      ||:||:|||||:|
DB      3715 GCTACTGCAACTCG 3702
```

```
RESULT 10
US-09-908-975-23753
/ Sequence 23753, Application US/09908975
/ Publication No. US20030165843A1
/ GENERAL INFORMATION:
/ APPLICANT: SHOSHAN, Avi
/ APPLICANT: WASSERMAN, Alon
/ APPLICANT: MINTZ, Eli
/ APPLICANT: MINTZ, Ilan
/ APPLICANT: FAIGLER, Simcha
/ TITLE OF INVENTION: Oligonucleotide Library for Detecting RNA Transcripts and Splice
/ TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
/ FILE REFERENCE: 36688-0005
/ CURRENT APPLICATION NUMBER: US/09/908,975
/ CURRENT FILING DATE: 2001-07-20
/ PRIOR APPLICATION NUMBER: US 60/287,724
/ PRIOR FILING DATE: 2001-05-02
/ PRIOR APPLICATION NUMBER: US 60/221,607
/ PRIOR FILING DATE: 2000-07-28
/ NUMBER OF SEQ ID NOS: 32337
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 23753
/ LENGTH: 65
/ TYPE: DNA
/ ORGANISM: Mus musculus
/ OTHER INFORMATION:
US-09-908-975-23753
```

```
Query Match      92.9%; Score 13; DB 3; Length 65;
Best Local Similarity 76.9%; Pred. No. 1.5e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

Cy	1	CGUACUGCAACUC	13
		:::   ::	
Db	428	CGUACTGCAACTC	416

Query Match           92.9%   Score 13; DB 8; Length 653;  
Best Local Similarity     76.9%  
Pred. No. 1.6e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

## RESULT 15

US-10-437-963-98896  
; Sequence 98896, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Bardazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221) B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; PRIOR FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 98896  
; LENGTH: 838  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_96760C.1  
US-10-437-963-98896

## Query Match

Best Local Similarity 92.9%; Score 13; DB 7; Length 838;  
Pred. No. 1.6e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GUACUGCAACUCG 14  
||:|||||:  
Db 649 GTACTGCAACTCG 661

## RESULT 16

US-10-437-963-84553/c  
; Sequence 84553, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Bardazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221) B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; PRIOR FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 84553  
; LENGTH: 1042  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_83779C.1  
US-10-437-963-84553

## Query Match

Best Local Similarity 92.9%; Score 13; DB 7; Length 1042;  
Pred. No. 1.6e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUC 13  
||:|||||:  
Db 1019 GTACTGCAACTC 1007

## RESULT 17

US-10-156-761-4883  
; Sequence 4883, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; PRIOR FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 4883  
; LENGTH: 1239  
; TYPE: DNA  
; ORGANISM: Streptomyces avermitilis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1239)  
US-10-156-761-4883

## Query Match

Best Local Similarity 92.9%; Score 13; DB 6; Length 1239;  
Pred. No. 1.6e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GUACUGCAACUCG 14  
||:|||||:  
Db 1176 GTACTGCAACTCG 1188

## RESULT 18

US-10-369-493-29486  
; Sequence 29486, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052) B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; PRIOR FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 29486  
; LENGTH: 1306  
; TYPE: DNA  
; ORGANISM: Caenorhabditis elegans  
US-10-369-493-29486

## Query Match

Best Local Similarity 92.9%; Score 13; DB 6; Length 1306;  
Pred. No. 1.6e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUC 13  
||:|||||:  
Db 701 GTACTGCAACTC 713

```
RESULT 19
US-10-450-763-8883
; Sequence 8883, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 8883
; LENGTH: 1359
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (142)..(699)
; OTHER INFORMATION: 72% homologous to Escherichia coli Rhd protein, accession
; OTHER INFORMATION: number X60999, Smith-Waterman Score=684.
US-10-450-763-8883

Query Match          92.9%; Score 13; DB 9; Length 1359;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GUACGCAACUCG 14
       |:|:|:|:|:|:|
DB      1204 GTACTGCAACTCG 1216

RESULT 20
US-10-957-828-11/c
; Sequence 11, Application US/10957828
; Publication No. US20050221453A1
; GENERAL INFORMATION:
; APPLICANT: TAKAGI, HIROSHI
; APPLICANT: NAKAMORI, SHIGERU
; APPLICANT: YAMAGUCHI, AKIHITO
; APPLICANT: NISHINO, KUNIHICO
; TITLE OF INVENTION: L-CYSTEINE PRODUCING MICROORGANISM AND METHOD FOR PRODUCING
; FILE REFERENCE: 259781USO
; CURRENT APPLICATION NUMBER: US/10/957,828
; CURRENT FILING DATE: 2004-10-05
; PRIOR APPLICATION NUMBER: JP 2004-103652
; PRIOR FILING DATE: 2004-03-31
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 1473
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1473)
US-10-957-828-11

Query Match          92.9%; Score 13; DB 9; Length 1473;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GUACGCAACUCG 14
       |:|:|:|:|:|:|
DB      1359 GTACTGCAACTCG 1347
```

```
RESULT 21
US-09-815-242-6126/c
; Sequence 6126, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyckind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6126
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1647)
US-09-815-242-6126

Query Match          92.9%; Score 13; DB 3; Length 1647;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GUACGCAACUCG 14
       |:|:|:|:|:|:|
DB      1533 GTACTGCAACTCG 1521

RESULT 22
US-10-282-122A-20432/c
; Sequence 20432, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyckind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
```

```

; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20432
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-283-122A-20432
```

```

Query Match          92.9%; Score 13; DB 7; Length 1647;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      2 GUACUGCACTCG 14
        ||:||:||:||:
Db      1533 GTACTGCACTCG 1521
```

```

RESULT 23
US-09-801-042-1/c
; Sequence 1, Application US/09801042
; Patent No. US20020127678A1
; GENERAL INFORMATION:
; APPLICANT: RIEPING, MECHTHILD
; APPLICANT: THIERBACH, GEORG
; APPLICANT: VAN DER REST, MICHEL, EDUARD
; APPLICANT: MOLNAR, DOUME
; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE
; FILE REFERENCE: MAS/21123/280410
; CURRENT APPLICATION NUMBER: US/09/801,042
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/229,329
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: DE 100 34 833.5
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: DE 101 03874.7
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1720
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1593)
; OTHER INFORMATION: mqo gene
US-09-801-042-1
```

```

Query Match          92.9%; Score 13; DB 3; Length 1720;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      2 GUACUGCACTCG 14
        ||:||:||:||:
Db      1482 GTACTGCACTCG 1470
```

```

RESULT 24
US-10-450-763-28629/c
; Sequence 28629, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 28629
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (11005)..(343)
; OTHER INFORMATION: 94% homologous to Escherichia coli K12 putative flagellin
; OTHER INFORMATION: structural protein, accession number AB000144, Smith-Waterman Score=
US-10-450-763-28629
```

```

Query Match          92.9%; Score 13; DB 9; Length 1732;
Best Local Similarity 76.9%; Pred. No. 1.6e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      2 GUACUGCACTCG 14
        ||:||:||:||:
Db      1683 GTACTGCACTCG 1671
```

```

RESULT 25
US-10-450-763-25885/c
; Sequence 25885, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 25885
; LENGTH: 1919
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (11005)..(343)
; OTHER INFORMATION: 94% homologous to Escherichia coli K12 putative flagellin
; OTHER INFORMATION: structural protein, accession number AB000144, Smith-Waterman Score=
US-10-450-763-25885
```

US-10-450-763-25885

Query Match 92.9%; Score 13; DB 9; Length 1919;  
Best Local Similarity 76.9%; Pred. No. 1.6e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCACTCG 14  
DB 1683 GACTGCACTCG 1671

## RESULT 26

US-09-864-761-4533  
; Sequence 4533, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wenheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
; FILE REFERENCE: Aecm1ca-X-1  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 4533  
; LENGTH: 1945  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL021808.1  
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.1  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.3  
; OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 2.3  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1  
; OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 1.9  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1  
US-09-864-761-4533

Query Match 92.9%; Score 13; DB 3; Length 1945;  
Best Local Similarity 76.9%; Pred. No. 1.6e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCACTCG 14  
DB 263 GACTGCACTCG 275

## RESULT 27

US-10-450-763-23995/c  
; Sequence 23995, Application US/10450763  
; Publication No. US20050196754A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIP3/US  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 23995  
; LENGTH: 2133  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIMILAR  
; LOCATION: (1)..(774)  
; OTHER INFORMATION: 90% homologous to Escherichia coli ATP-dependent helicase  
; OTHER INFORMATION: HTPA homolog, accession number D90780, Smith-Waterman Score=1183.  
US-10-450-763-23995

Query Match 92.9%; Score 13; DB 9; Length 2133;  
Best Local Similarity 76.9%; Pred. No. 1.7e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCACTCG 14  
DB 2019 GACTGCACTCG 2007

## RESULT 28

US-10-156-761-2636/c  
; Sequence 2636, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, TUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: US/10/156,761  
; PRIOR FILING DATE: 2001-05-30

```
/ PRIOR APPLICATION NUMBER: JP 2001-272697
/ PRIOR FILING DATE: 2001-08-02
/ NUMBER OF SEQ ID NOS: 15109
/ SEQ ID NO 2636
/ LENGTH: 2559
/ TYPE: DNA
/ ORGANISM: Streptomyces avermitilis
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(2559)
US-10-156-761-2636

Query Match          92.9%; Score 13; DB 6; Length 2559;
Best Local Similarity 76.9%; Pred. No. 1.7e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GUACUGCAACUCG 14
DB      669 GTACTGCAACTCG 657

RESULT 29
US-10-450-763-25886/C
/ Sequence 25886, Application US/10450763
/ Publication No. US20050196754A1
/ GENERAL INFORMATION:
/ APPLICANT: HySeq, Inc
/ TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
/ FILE REFERENCE: 790CIP3/US
/ CURRENT APPLICATION NUMBER: US/10/450,763
/ PRIOR FILING DATE: 2003-06-11
/ PRIOR APPLICATION NUMBER: PCT/US01/08631
/ PRIOR FILING DATE: 2001-03-30
/ PRIOR APPLICATION NUMBER: 09/540,217
/ PRIOR FILING DATE: 2000-03-31
/ PRIOR APPLICATION NUMBER: 09/649,167
/ PRIOR FILING DATE: 2000-08-23
/ NUMBER OF SEQ ID NOS: 60736
/ SOFTWARE: Custom
/ SEQ ID NO 25886
/ LENGTH: 3222
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SIMILAR
/ LOCATION: (1)..(774)
/ OTHER INFORMATION: 90% homologous to Escherichia coli ATP-dependent helicase
US-10-450-763-25886

Query Match          92.9%; Score 13; DB 9; Length 3222;
Best Local Similarity 76.9%; Pred. No. 1.7e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GUACUGCAACUCG 14
DB      2019 GTACTGCAACTCG 2007

RESULT 30
US-10-057-475B-10475/C
/ Sequence 10475, Application US/10057475B
/ Publication No. US20040002068A1
/ GENERAL INFORMATION:
/ APPLICANT: Gaiger, Alexander
/ APPLICANT: Algate, Paul A.
/ APPLICANT: Mammon, Jane
/ APPLICANT: Clapper, Jonathan David
/ APPLICANT: Wang, Aijun
/ APPLICANT: Ordonez, Nadia
/ APPLICANT: Carter, Lauren
/ APPLICANT: McNeill, Patricia Dianne
/ APPLICANT: Corixa Corporation
```

```
/ TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
/ FILE REFERENCE: 014058-014402US
/ CURRENT APPLICATION NUMBER: US/10/057,475B
/ CURRENT FILING DATE: 2002-01-22
/ PRIOR APPLICATION NUMBER: US 60/186,126
/ PRIOR FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: US 60/190,479
/ PRIOR FILING DATE: 2000-03-17
/ PRIOR APPLICATION NUMBER: US 60/200,545
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 60/200,303
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,779
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,999
/ PRIOR FILING DATE: 2000-05-01
/ PRIOR APPLICATION NUMBER: US 60/202,084
/ PRIOR FILING DATE: 2000-05-04
/ PRIOR APPLICATION NUMBER: US 60/206,201
/ PRIOR FILING DATE: 2000-05-22
/ PRIOR APPLICATION NUMBER: US 60/218,950
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: US 60/222,903
/ PRIOR FILING DATE: 2000-08-03
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 10979
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 10475
/ LENGTH: 51657
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)..(51657)
/ OTHER INFORMATION: n = G, A, C or T
US-10-057-475B-10475

Query Match          92.9%; Score 13; DB 6; Length 51657;
Best Local Similarity 76.9%; Pred. No. 1.8e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGUACUGCACTC 13
DB      44702 CACTGCAACTC 44690

RESULT 31
US-10-154-884B-10475/C
/ Sequence 10475, Application US/10154884B
/ Publication No. US20040005561A1
/ GENERAL INFORMATION:
/ APPLICANT: Gaiger, Alexander
/ APPLICANT: Algate, Paul A.
/ APPLICANT: Mammon, Jane
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Corixa Corporation
/ TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
/ TITLE OF INVENTION: Hematological Malignancies
/ FILE REFERENCE: 014058-013521US
/ CURRENT APPLICATION NUMBER: US/10/154,884B
/ CURRENT FILING DATE: 2002-05-23
/ PRIOR APPLICATION NUMBER: US 60/186,126
/ PRIOR FILING DATE: 2000-03-01
/ PRIOR APPLICATION NUMBER: US 60/190,479
/ PRIOR FILING DATE: 2000-03-17
/ PRIOR APPLICATION NUMBER: US 60/200,545
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 60/200,303
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,779
/ PRIOR FILING DATE: 2000-04-28
/ PRIOR APPLICATION NUMBER: US 60/200,999
```



PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: US 60/202,084  
PRIOR FILING DATE: 2000-05-04  
PRIOR APPLICATION NUMBER: US 60/206,201  
PRIOR FILING DATE: 2000-05-22  
PRIOR APPLICATION NUMBER: US 60/218,950  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 60/222,903  
PRIOR FILING DATE: 2000-08-03  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 11290  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 10475  
LENGTH: 51657  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(51657)  
OTHER INFORMATION: n = g, a, c or t  
US-10-154-884B-10475

Query Match 92.9%; Score 13; DB 6; Length 51657;  
Best Local Similarity 76.9%; Pred. No. 1.8e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGUACUGCACTC 13  
DB 44702 CGTACTGCACTC 44690

RESULT 32  
US-10-331-053-61/C  
Sequence 61, Application US/10331053  
Publication No. US2004019778A1  
GENERAL INFORMATION:  
APPLICANT: David W. Morris  
TITLE OF INVENTION: Novel Compositions and Methods in Cancer  
FILE REFERENCE: 529452001100  
CURRENT APPLICATION NUMBER: US/10/331,053  
CURRENT FILING DATE: 2002-12-26  
NUMBER OF SEQ ID NOS: 86  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 61  
LENGTH: 83493  
TYPE: DNA  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(83493)  
OTHER INFORMATION: n = A,T,C or G  
US-10-331-053-61

Query Match 92.9%; Score 13; DB 8; Length 83493;  
Best Local Similarity 76.9%; Pred. No. 1.8e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGUACUGCACTC 13  
DB 36317 CGTACTGCACTC 36305

RESULT 33  
US-10-398-221-9/C  
Sequence 9, Application US/10398221  
Publication No. US20040018514A1  
GENERAL INFORMATION:  
APPLICANT: KUNST, Frederick  
APPLICANT: GLASER, Philippe  
TITLE OF INVENTION: Listeria innocua, genome and applications  
FILE REFERENCE: 344 702 - US  
CURRENT APPLICATION NUMBER: US/10/398,221

CURRENT FILING DATE: 2003-03-27  
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061  
PRIOR FILING DATE: 2001-10-04  
PRIOR APPLICATION NUMBER: FR 00/12 697  
PRIOR FILING DATE: 2000-10-04  
NUMBER OF SEQ ID NOS: 4025  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 9  
LENGTH: 684707  
TYPE: DNA  
ORGANISM: Listeria innocua  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(end)  
OTHER INFORMATION: n can be any nucleotide: a, g, c or t/u  
US-10-398-221-9

Query Match 92.9%; Score 13; DB 7; Length 684707;  
Best Local Similarity 76.9%; Pred. No. 1.8e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGUACUGCACTC 13  
DB 646081 CGTACTGCACTC 646069

RESULT 34  
US-10-398-221-2058  
Sequence 2058, Application US/10398221  
Publication No. US20040018514A1  
GENERAL INFORMATION:  
APPLICANT: KUNST, Frederick  
APPLICANT: GLASER, Philippe  
TITLE OF INVENTION: Listeria innocua, genome and applications  
FILE REFERENCE: 344 702 - US  
CURRENT APPLICATION NUMBER: US/10/398,221  
CURRENT FILING DATE: 2003-03-27  
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061  
PRIOR FILING DATE: 2001-10-04  
PRIOR APPLICATION NUMBER: FR 00/12 697  
PRIOR FILING DATE: 2000-10-04  
NUMBER OF SEQ ID NOS: 4025  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2058  
LENGTH: 3011208  
TYPE: DNA  
ORGANISM: Listeria innocua  
US-10-398-221-2058

Query Match 92.9%; Score 13; DB 7; Length 3011208;  
Best Local Similarity 76.9%; Pred. No. 1.8e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGUACUGCACTC 13  
DB 2634732 CGTACTGCACTC 2634744

RESULT 35  
US-10-156-761-1  
Sequence 1, Application US/10156761  
Publication No. US20030119018A1  
GENERAL INFORMATION:  
APPLICANT: OMIURA, SATOSHI  
APPLICANT: IKEDA, HARUO  
APPLICANT: ISHIKAWA, JUN  
APPLICANT: HORIKAWA, HIROSHI  
APPLICANT: SHIBA, TADAYOSHI  
APPLICANT: SAKAKI, YOSHIYUKI  
APPLICANT: HATTORI, MASAHISA  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-262  
CURRENT APPLICATION NUMBER: US/10/156,761

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; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match          92.9%; Score 13; DB 6; Length 9025608;
Best Local Similarity 76.9%; Pred. No. 8.2e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GUACUGCAACUCG 14
DB      3248037 GTAGTCGCACTCG 3248049

RESULT 36
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match          92.9%; Score 13; DB 6; Length 9025608;
Best Local Similarity 76.9%; Pred. No. 8.2e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      2 GUACUGCAACUCG 14
DB      5955055 GTAGTCGCACTCG 5955043

RESULT 37
US-10-843-527-74019
; Sequence 74019, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus

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; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 74019
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-74019

Query Match          88.6%; Score 12.4; DB 9; Length 25;
Best Local Similarity 78.6%; Pred. No. 3.3e+03;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGUACUGCAACUCG 14
DB      6 CGTAGCGCACTCG 19

RESULT 38
US-10-843-527-74993
; Sequence 74993, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 74993
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-74993

Query Match          88.6%; Score 12.4; DB 9; Length 25;
Best Local Similarity 71.4%; Pred. No. 3.3e+03;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGUACUGCAACUCG 14
DB      8 CGTAGCGCACTCG 21

RESULT 39
US-10-843-527-163184/c
; Sequence 163184, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 163184
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-163184

```

```
Query Match      88.6%; Score 12.4; DB 9; Length 25;
Best Local Similarity 71.4%; Pred. No. 3.3e+03;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CGUACUGCAACUCG 14
       ||:||:||:||||
Db      18 CCGACTGCAAACTCG 5

RESULT 40
US-10-843-527-164158/c
; Sequence 164158, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittleman
; APPLICANT: Eric Schnell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT APPLICATION NUMBER: US/10/843,527
; PRIOR FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 164158
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-164158

Query Match      88.6%; Score 12.4; DB 9; Length 25;
Best Local Similarity 78.6%; Pred. No. 3.3e+03;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CGUACUGCAACUCG 14
       ||:||:||:||||
Db      20 CCGTACCGCAACTCG 7

RESULT 41
US-10-767-701-28070/c
; Sequence 28070, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53353)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 28070
; LENGTH: 110
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 7535295
US-10-767-701-28070

Query Match      88.6%; Score 12.4; DB 7; Length 110;
Best Local Similarity 71.4%; Pred. No. 3.4e+03;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CGUACUGCAACUCG 14
       ||:||:||:||||
Db      51 CCGACTGCAACTCG 38

RESULT 42
US-10-425-115-49773/c
; Sequence 49773, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 49773
; LENGTH: 219
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_145392C.1
US-10-425-115-49773

Query Match      88.6%; Score 12.4; DB 8; Length 219;
Best Local Similarity 78.6%; Pred. No. 3.5e+03;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CGUACUGCAACUCG 14
       ||:||:||:||||
Db      18 CCGACTGCAACGCG 5

RESULT 43
US-10-424-599-53399
; Sequence 53399, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 53399
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_19232C.1
US-10-424-599-53399

Query Match      88.6%; Score 12.4; DB 7; Length 229;
Best Local Similarity 71.4%; Pred. No. 3.5e+03;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CGUACUGCAACUCG 14
       ||:||:||:||||
Db      24 CCGACTGCAACTCG 37

RESULT 44
US-10-424-599-133643
; Sequence 133643, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
```

;; CURRENT APPLICATION NUMBER: US/10/424,599  
;; CURRENT FILING DATE: 2003-04-28  
;; NUMBER OF SEQ ID NOS: 285684  
;; SEQ ID NO 133643  
;; LENGTH: 258  
;; TYPE: DNA  
;; ORGANISM: Glycine max  
;; FEATURE:  
;; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_91686C.1  
US-10-424-599-133643

Query Match                    88.6%; Score 12.4; DB 7; Length 258;  
Best Local Similarity        71.4%; Pred. No. 3.5e+03;  
Matches    10; Conservative    3; Mismatches    1; Indels    0; Gaps    0;

QY                    1 CGUACUGCAACUG 14  
                     ||:|:|:|:|:|:|:|  
DB                    18 CGTCTGCACTCG 31

RESULT 45  
US-10-425-115-2980  
; Sequence 2980, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(5322)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 2980  
; LENGTH: 285  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(285)  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_102715C.1  
US-10-425-115-2980

Query Match                    88.6%; Score 12.4; DB 8; Length 285;  
Best Local Similarity        71.4%; Pred. No. 3.5e+03;  
Matches    10; Conservative    3; Mismatches    1; Indels    0; Gaps    0;

QY                    1 CGUACUGCAACUG 14  
                     ||:|:|:|:|:|:|:|  
DB                    101 CGTCTGCACTCG 114

RESULT 46  
US-10-424-599-106360  
; Sequence 106360, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(5322)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 106360  
; LENGTH: 308

;; TYPE: DNA  
;; ORGANISM: Glycine max  
;; FEATURE:  
;; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_6705C.1  
US-10-424-599-106360

Query Match                    88.6%; Score 12.4; DB 7; Length 308;  
Best Local Similarity        71.4%; Pred. No. 3.5e+03;  
Matches    10; Conservative    3; Mismatches    1; Indels    0; Gaps    0;

QY                    1 CGUACUGCAACUG 14  
                     ||:|:|:|:|:|:|:|  
DB                    61 CGTCTGCACTCG 74

RESULT 47  
US-10-425-115-86279  
; Sequence 86279, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(5322)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 86279  
; LENGTH: 312  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_178697C.1  
US-10-425-115-86279

Query Match                    88.6%; Score 12.4; DB 8; Length 312;  
Best Local Similarity        71.4%; Pred. No. 3.5e+03;  
Matches    10; Conservative    3; Mismatches    1; Indels    0; Gaps    0;

QY                    1 CGUACUGCAACUG 14  
                     ||:|:~|:|:|:|:|:|  
DB                    228 CGTACTGGAACCTCG 241

RESULT 48  
US-10-425-115-161997  
; Sequence 161997, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(5322)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 161997  
; LENGTH: 322  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_79318C.1  
US-10-425-115-161997

Query Match                    88.6%; Score 12.4; DB 8; Length 322;  
Best Local Similarity        78.6%; Pred. No. 3.6e+03;  
Matches    11; Conservative    2; Mismatches    1; Indels    0; Gaps    0;

QY 1 CGUACUGCACTCG 14  
 ||:|||||:  
 Db 267 CGTACCGCACTCG 280

## RESULT 49

US-10-424-599-68441/C  
 ; Sequence 68441, Application US/10424599  
 ; Publication No. US20040031072A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa Thomas J  
 ; APPLICANT: Kovalic David K  
 ; APPLICANT: Zhou Yihua  
 ; APPLICANT: Cao Yongwei  
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53223)B  
 ; CURRENT APPLICATION NUMBER: US/10/424,599  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 285684  
 ; SEQ ID NO 68441  
 ; LENGTH: 331  
 ; TYPE: DNA  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_32815C.1  
 US-10-424-599-68441

## Query Match

Best Local Similarity 88.6%; Score 12.4; DB 7; Length 331;  
 Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14  
 ||:|||||:  
 Db 192 CGTCTGCACTCG 179

## RESULT 50

US-10-424-599-139244/C  
 ; Sequence 139244, Application US/10424599  
 ; Publication No. US20040031072A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa Thomas J  
 ; APPLICANT: Kovalic David K  
 ; APPLICANT: Zhou Yihua  
 ; APPLICANT: Cao Yongwei  
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53223)B  
 ; CURRENT APPLICATION NUMBER: US/10/424,599  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 285684  
 ; SEQ ID NO 139244  
 ; LENGTH: 343  
 ; TYPE: DNA  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_96745C.1  
 US-10-424-599-139244

## Query Match

Best Local Similarity 88.6%; Score 12.4; DB 7; Length 343;  
 Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14  
 ||:|||||:  
 Db 241 CGTCTGCACTCG 228

Search completed: March 19, 2006, 07:53:06  
 Job time : 2134.77 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 18:35:23 ; Search time 53.5769 Seconds  
(without alignments)  
464.488 Million cell updates/sec

Title: US-10-800-926-2  
Perfect score: 14  
Sequence: 1 cguacgacacug 14

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues  
Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Issued Patents NA:\*

- 1: /cgn2\_6/ptodaca/1/ina/1 COMB.seq:\*
- 2: /cgn2\_6/ptodaca/1/ina/5 COMB.seq:\*
- 3: /cgn2\_6/ptodaca/1/ina/6A COMB.seq:\*
- 4: /cgn2\_6/ptodaca/1/ina/6B COMB.seq:\*
- 5: /cgn2\_6/ptodaca/1/ina/H COMB.seq:\*
- 6: /cgn2\_6/ptodaca/1/ina/PCPUS COMB.seq:\*
- 7: /cgn2\_6/ptodaca/1/ina/PP COMB.seq:\*
- 8: /cgn2\_6/ptodaca/1/ina/RE COMB.seq:\*
- 9: /cgn2\_6/ptodaca/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13	92.9	601	3	US-09-949-016-147054
C 2	13	92.9	1720	3	US-09-801-042-1
C 3	13	92.9	21372	3	US-09-949-016-16941
C 4	13	92.9	374159	3	US-09-949-016-15868
C 5	12.4	88.6	140	3	US-09-270-767-27123
C 6	12.4	88.6	323	3	US-09-513-999C-2299
C 7	12.4	88.6	349	3	US-08-303-861-15
C 8	12.4	88.6	339	3	US-09-621-976-681
C 9	12.4	88.6	435	3	US-09-252-991A-79
C 10	12.4	88.6	504	3	US-09-252-991A-1326
C 11	12.4	88.6	543	3	US-09-252-991A-233
C 12	12.4	88.6	543	3	US-09-252-991A-7705
C 13	12.4	88.6	597	3	US-09-270-767-5447
C 14	12.4	88.6	597	3	US-09-270-767-50729
C 15	12.4	88.6	669	3	US-09-252-991A-100
C 16	12.4	88.6	726	3	US-09-252-991A-9718
C 17	12.4	88.6	726	3	US-09-252-991A-14097
C 18	12.4	88.6	737	3	US-09-270-767-11527
C 19	12.4	88.6	756	3	US-09-252-991A-94
C 20	12.4	88.6	834	3	US-09-252-991A-6447
C 21	12.4	88.6	867	3	US-09-902-540-5805
C 22	12.4	88.6	930	3	US-09-252-991A-6103
C 23	12.4	88.6	1005	3	US-09-902-540-7341
C 24	12.4	88.6	1007	3	US-09-902-540-70

25	12.4	88.6	1017	3	US-09-107-532A-2165	Sequence 2165, Ap
C 26	12.4	88.6	1065	3	US-09-252-991A-90	Sequence 90, Appl
C 27	12.4	88.6	1104	3	US-09-489-039A-2883	Sequence 2883, Ap
C 28	12.4	88.6	1137	3	US-09-252-991A-6183	Sequence 6183, Ap
C 29	12.4	88.6	1152	3	US-09-252-991A-13050	Sequence 13050, A
C 30	12.4	88.6	1203	3	US-09-252-991A-7557	Sequence 7557, Ap
C 31	12.4	88.6	1203	3	US-09-252-991A-9574	Sequence 9574, Ap
C 32	12.4	88.6	1206	3	US-09-996-008B-1	Sequence 1, Appl
C 33	12.4	88.6	1233	3	US-09-252-991A-13225	Sequence 13225, A
C 34	12.4	88.6	1314	3	US-09-252-991A-7784	Sequence 7784, Ap
C 35	12.4	88.6	1359	3	US-09-489-039A-4444	Sequence 4444, Ap
C 36	12.4	88.6	1563	3	US-09-252-991A-12900	Sequence 12900, A
C 37	12.4	88.6	1629	3	US-09-252-991A-104	Sequence 104, App
C 38	12.4	88.6	1737	3	US-09-252-991A-252	Sequence 252, App
C 39	12.4	88.6	1737	3	US-09-252-991A-279	Sequence 279, App
C 40	12.4	88.6	1776	3	US-09-252-991A-12189	Sequence 12189, A
C 41	12.4	88.6	1800	3	US-09-252-991A-4152	Sequence 4152, Ap
C 42	12.4	88.6	1827	3	US-09-252-991A-1375	Sequence 1375, Ap
C 43	12.4	88.6	2262	3	US-09-252-991A-1416	Sequence 1416, Ap
C 44	12.4	88.6	2298	3	US-09-252-991A-12254	Sequence 12254, A
C 45	12.4	88.6	2346	3	US-09-252-991A-9536	Sequence 9536, Ap
C 46	12.4	88.6	2346	3	US-09-252-991A-13355	Sequence 13355, Ap
C 47	12.4	88.6	2370	3	US-09-489-039A-1363	Sequence 1363, Ap
C 48	12.4	88.6	2391	3	US-09-252-991A-1192	Sequence 1192, Ap
C 49	12.4	88.6	2472	3	US-09-252-991A-4456	Sequence 4456, Ap
C 50	12.4	88.6	2495	3	US-09-620-312D-272	Sequence 272, App
C 51	12.4	88.6	2622	3	US-09-489-039A-4584	Sequence 4584, Ap
C 52	12.4	88.6	2838	3	US-09-252-991A-14128	Sequence 14128, A
C 53	12.4	88.6	2847	2	US-08-087-007-2	Sequence 2, Appl1
C 54	12.4	88.6	2847	3	US-08-483-433-2	Sequence 2, Appl1
C 55	12.4	88.6	2847	3	US-09-566-254A-2	Sequence 2, Appl1
C 56	12.4	88.6	2847	6	PCR-US92-05920-2	Sequence 2, Appl1
C 57	12.4	88.6	2934	3	US-09-252-991A-84	Sequence 84, Appl
C 58	12.4	88.6	3897	3	US-09-252-991A-17008	Sequence 14008, A
C 59	12.4	88.6	6203	3	US-09-902-540-811	Sequence 811, App
C 60	12.4	88.6	22118	3	US-09-815-981A-5	Sequence 5, Appl1
C 61	12.4	88.6	72704	3	US-09-902-540-1273	Sequence 1273, Ap
C 62	12.4	88.6	108440	3	US-09-949-016-12065	Sequence 12065, A
C 63	12.4	88.6	108441	3	US-09-949-016-14990	Sequence 14090, A
C 64	12.4	88.6	440365	3	US-09-103-840A-2	Sequence 2, Appl1
C 65	12.4	88.6	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
C 66	12	85.7	80	2	US-08-353-476-59	Sequence 59, Appl
C 67	12	85.7	423	3	US-09-248-796A-11879	Sequence 11879, A
C 68	12	85.7	552	3	US-09-802-540-5146	Sequence 5146, Ap
C 69	12	85.7	601	3	US-09-949-016-51279	Sequence 51279, A
C 70	12	85.7	601	3	US-09-949-016-89184	Sequence 89184, A
C 71	12	85.7	601	3	US-09-949-016-121311	Sequence 121311, A
C 72	12	85.7	601	3	US-09-949-016-121312	Sequence 121312, A
C 73	12	85.7	601	3	US-09-949-016-121313	Sequence 121313, A
C 74	12	85.7	601	3	US-09-949-016-121314	Sequence 121314, A
C 75	12	85.7	601	3	US-09-949-016-142961	Sequence 142961, A
C 76	12	85.7	601	3	US-09-949-016-142962	Sequence 142962, A
C 77	12	85.7	701	3	US-09-949-016-142963	Sequence 142963, A
C 78	12	85.7	701	3	US-09-533-559-6348	Sequence 6348, Ap
C 79	12	85.7	714	3	US-09-056-105-28	Sequence 28, Appl
C 80	12	85.7	812	3	US-09-270-767-4491	Sequence 4491, Ap
C 81	12	85.7	812	3	US-09-270-767-19773	Sequence 19773, A
C 82	12	85.7	819	3	US-09-248-796A-1668	Sequence 1668, Ap
C 83	12	85.7	864	3	US-09-328-352-1652	Sequence 1652, Ap
C 84	12	85.7	882	3	US-09-937-8628-59	Sequence 59, Appl
C 85	12	85.7	1047	3	US-09-937-8628-59	Sequence 59, Appl
C 86	12	85.7	1338	3	US-09-134-001C-1234	Sequence 1234, Ap
C 87	12	85.7	1338	3	US-09-134-001C-1624	Sequence 1624, Ap
C 88	12	85.7	1368	3	US-09-453-702B-199	Sequence 199, App
C 89	12	85.7	1368	3	US-10-114-170-199	Sequence 199, App
C 90	12	85.7	1434	3	US-09-328-352-3639	Sequence 3639, Ap
C 91	12	85.7	1457	3	US-09-256-000-22	Sequence 22, Appl
C 92	12	85.7	1457	3	US-10-034-015A-22	Sequence 22, Appl
C 93	12	85.7	1457	3	US-10-083-620A-22	Sequence 22, Appl
C 94	12	85.7	1458	3	US-09-248-796A-6365	Sequence 6365, Ap
C 95	12	85.7	1537	3	US-09-620-312D-561	Sequence 561, App
C 96	12	85.7	1677	3	US-09-902-540-7773	Sequence 7773, Ap
C 97	12	85.7	1887	3	US-09-256-000-18	Sequence 18, Appl



98	12	85.7	1887	3	US-10-034-015A-18	Sequence 18, Appl	C 171	11.4	81.4	25	3	US-09-396-196G-109932	Sequence 109932,
99	12	85.7	1887	3	US-10-083-620A-18	Sequence 18, Appl	C 172	11.4	81.4	25	3	US-09-396-196G-109933	Sequence 109933,
100	12	85.7	1967	3	US-09-256-000-20	Sequence 20, Appl	C 173	11.4	81.4	25	3	US-09-396-196G-109934	Sequence 109934,
101	12	85.7	1967	3	US-10-034-015A-20	Sequence 20, Appl	C 174	11.4	81.4	30	2	US-07-661-378A-4	Sequence 4, Appl1
102	12	85.7	1967	3	US-10-083-620A-20	Sequence 20, Appl	C 175	11.4	81.4	33	6	PCT-US94-09653A-6	Sequence 6, Appl1
103	12	85.7	1989	3	US-09-949-016-5214	Sequence 5214, Ap	C 176	11.4	81.4	35	2	US-07-818-318-3	Sequence 3, Appl1
104	12	85.7	1997	2	US-08-967-466-2	Sequence 2, Appl1	C 177	11.4	81.4	134	3	US-09-270-767-169	Sequence 169, Ap
105	12	85.7	1997	2	US-09-240-359-2	Sequence 2, Appl1	C 178	11.4	81.4	134	3	US-09-270-767-16931	Sequence 16931, A
106	12	85.7	1997	3	US-09-802-741-2	Sequence 2, Appl1	C 179	11.4	81.4	160	3	US-09-270-767-25360	Sequence 25360, A
107	12	85.7	2207	3	US-09-254-504-6	Sequence 6, Appl1	C 180	11.4	81.4	168	6	PCT-US94-09653A-26	Sequence 26, Appl
108	12	85.7	2818	3	US-09-710-279-4012	Sequence 4012, Ap	C 181	11.4	81.4	171	6	PCT-US94-09653A-31	Sequence 31, Appl
109	12	85.7	3030	3	US-09-710-279-4001	Sequence 4001, Ap	C 182	11.4	81.4	177	3	US-09-270-767-27203	Sequence 27203, A
110	12	85.7	3108	3	US-09-937-521-11	Sequence 11, Appl	C 183	11.4	81.4	183	6	PCT-US94-09653A-30	Sequence 30, Appl
111	12	85.7	3150	3	US-09-710-279-3893	Sequence 3893, Ap	C 184	11.4	81.4	195	3	US-09-134-000C-371	Sequence 3251, Ap
112	12	85.7	3348	3	US-09-759-451-302	Sequence 456, App	C 185	11.4	81.4	243	3	US-09-540-236-371	Sequence 371, App
113	12	85.7	3511	3	US-09-799-451-456	Sequence 456, App	C 186	11.4	81.4	291	3	US-09-702-705-832	Sequence 832, App
114	12	85.7	4121	3	US-09-604-978-4	Sequence 4, Appl1	C 187	11.4	81.4	291	3	US-09-736-457-832	Sequence 832, App
115	12	85.7	4121	3	US-09-604-978-4	Sequence 4, Appl1	C 188	11.4	81.4	291	3	US-09-614-1248-832	Sequence 832, App
116	12	85.7	4835	3	US-10-325-878-4	Sequence 16, Appl	C 189	11.4	81.4	291	3	US-09-614-1248-832	Sequence 832, App
117	12	85.7	4835	3	US-09-937-521-16	Sequence 16, Appl	C 190	11.4	81.4	291	3	US-09-614-1248-832	Sequence 832, App
118	12	85.7	6250	3	US-09-902-540-773	Sequence 773, App	C 191	11.4	81.4	291	3	US-09-614-1248-832	Sequence 832, App
119	12	85.7	14449	3	US-09-949-016-12108	Sequence 12108, A	C 192	11.4	81.4	291	3	US-09-614-1248-832	Sequence 832, App
120	12	85.7	18448	3	US-09-949-016-15345	Sequence 15345, A	C 193	11.4	81.4	292	3	US-09-614-1248-832	Sequence 832, App
121	12	85.7	22683	3	US-09-949-016-14054	Sequence 14054, A	C 194	11.4	81.4	308	3	US-09-313-294X-3894	Sequence 3894, Ap
122	12	85.7	22683	3	US-09-949-016-14054	Sequence 14054, A	C 195	11.4	81.4	321	3	US-09-313-294X-3894	Sequence 3894, Ap
123	12	85.7	22728	3	US-09-949-016-13774	Sequence 13774, A	C 196	11.4	81.4	321	3	US-09-313-294X-3894	Sequence 3894, Ap
124	12	85.7	29559	3	US-09-902-540-1254	Sequence 1254, Ap	C 197	11.4	81.4	321	3	US-09-313-294X-3894	Sequence 3894, Ap
125	12	85.7	31769	3	US-09-949-002-734	Sequence 734, App	C 198	11.4	81.4	405	3	US-09-711-164-224	Sequence 224, App
126	12	85.7	42894	3	US-09-949-016-12301	Sequence 12301, A	C 199	11.4	81.4	407	3	US-09-370-767-27503	Sequence 27503, A
127	12	85.7	42898	3	US-09-949-016-15904	Sequence 15904, A	C 200	11.4	81.4	432	3	US-10-332-858-98	Sequence 98, Appl
128	12	85.7	76321	3	US-09-949-002-578	Sequence 578, App	C 201	11.4	81.4	432	3	US-09-338-063A-98	Sequence 98, Appl
129	12	85.7	76321	3	US-09-949-002-578	Sequence 578, App	C 202	11.4	81.4	438	3	US-09-270-767-1211	Sequence 1211, Ap
130	12	85.7	91232	3	US-09-949-002-803	Sequence 803, App	C 203	11.4	81.4	438	3	US-09-270-767-16493	Sequence 16493, A
131	12	85.7	105733	3	US-09-949-016-13080	Sequence 13080, A	C 204	11.4	81.4	438	3	US-10-332-858-114	Sequence 114, Appl
132	12	85.7	121427	3	US-09-949-016-11950	Sequence 11950, A	C 205	11.4	81.4	438	3	US-09-338-063A-14	Sequence 14, Appl
133	12	85.7	121433	3	US-09-949-016-13230	Sequence 13230, A	C 206	11.4	81.4	438	3	US-09-338-063A-14	Sequence 14, Appl
134	12	85.7	125672	3	US-09-949-016-16956	Sequence 16956, A	C 207	11.4	81.4	438	3	US-10-357-886-25	Sequence 25, Appl
135	12	85.7	141454	3	US-09-949-016-12055	Sequence 12055, A	C 208	11.4	81.4	445	3	US-10-332-858-112	Sequence 12, Appl
136	12	85.7	141455	3	US-09-949-016-17100	Sequence 17100, A	C 209	11.4	81.4	455	3	US-09-338-063A-12	Sequence 12, Appl
137	12	85.7	142783	3	US-09-949-016-15127	Sequence 15127, A	C 210	11.4	81.4	477	3	US-09-270-767-11854	Sequence 11854, A
138	12	85.7	237510	3	US-09-949-016-15779	Sequence 15779, A	C 211	11.4	81.4	480	3	US-09-352-991A-13670	Sequence 13670, A
139	12	85.7	265038	3	US-09-949-016-15779	Sequence 15779, A	C 212	11.4	81.4	487	3	US-09-621-976-16601	Sequence 16601, A
140	12	85.7	421118	3	US-09-949-016-16297	Sequence 16297, A	C 213	11.4	81.4	513	3	US-09-533-559-3845	Sequence 3845, Ap
141	11.4	81.4	81.4	20	US-08-754-490-7	Sequence 7, Appl1	C 214	11.4	81.4	515	3	US-09-270-767-31092	Sequence 31092, A
142	11.4	81.4	81.4	20	US-08-754-490-7	Sequence 7, Appl1	C 215	11.4	81.4	515	3	US-09-270-767-31092	Sequence 31092, A
143	11.4	81.4	81.4	20	US-08-923-505A-7	Sequence 7, Appl1	C 216	11.4	81.4	515	3	US-09-489-039A-2781	Sequence 2781, Ap
144	11.4	81.4	81.4	20	US-08-923-505A-7	Sequence 7, Appl1	C 217	11.4	81.4	535	3	US-08-997-918-47	Sequence 47, Appl
145	11.4	81.4	81.4	20	US-09-260-952A-18	Sequence 18, Appl	C 218	11.4	81.4	535	3	US-09-270-767-11598	Sequence 11598, A
146	11.4	81.4	81.4	20	US-09-260-952A-18	Sequence 18, Appl	C 219	11.4	81.4	543	3	US-09-252-991A-16197	Sequence 16197, A
147	11.4	81.4	81.4	20	US-09-253-341-7	Sequence 7, Appl1	C 220	11.4	81.4	543	3	US-10-332-858-102	Sequence 102, App
148	11.4	81.4	81.4	20	US-09-253-341-7	Sequence 7, Appl1	C 221	11.4	81.4	543	3	US-09-338-063A-102	Sequence 102, App
149	11.4	81.4	81.4	20	US-09-253-341A-7	Sequence 7, Appl1	C 222	11.4	81.4	543	3	US-09-533-559-900	Sequence 900, App
150	11.4	81.4	81.4	20	US-09-253-341A-7	Sequence 7, Appl1	C 223	11.4	81.4	543	3	US-10-332-858-97	Sequence 97, Appl
151	11.4	81.4	81.4	20	US-09-261-040-7	Sequence 7, Appl1	C 224	11.4	81.4	543	3	US-09-338-063A-97	Sequence 97, Appl
152	11.4	81.4	81.4	20	US-09-261-040-7	Sequence 7, Appl1	C 225	11.4	81.4	543	3	US-08-721-925A-2	Sequence 2, Appl
153	11.4	81.4	81.4	20	US-09-916-956A-7	Sequence 7, Appl1	C 226	11.4	81.4	601	3	US-09-949-016-50542	Sequence 50542, A
154	11.4	81.4	81.4	20	US-09-916-956A-7	Sequence 7, Appl1	C 227	11.4	81.4	601	3	US-09-949-016-50543	Sequence 50543, A
155	11.4	81.4	81.4	20	US-09-873-873-7	Sequence 7, Appl1	C 228	11.4	81.4	601	3	US-09-949-016-70903	Sequence 70903, A
156	11.4	81.4	81.4	20	US-09-873-873-7	Sequence 7, Appl1	C 229	11.4	81.4	601	3	US-09-949-016-71129	Sequence 71129, A
157	11.4	81.4	81.4	20	US-09-997-914-7	Sequence 7, Appl1	C 230	11.4	81.4	601	3	US-09-949-016-133708	Sequence 133708, A
158	11.4	81.4	81.4	20	US-09-997-914-7	Sequence 7, Appl1	C 231	11.4	81.4	601	3	US-09-949-016-133709	Sequence 133709, A
159	11.4	81.4	81.4	20	US-09-636-746B-7	Sequence 7, Appl1	C 232	11.4	81.4	601	3	US-09-949-016-133710	Sequence 133710, A
160	11.4	81.4	81.4	20	US-09-636-746B-7	Sequence 7, Appl1	C 233	11.4	81.4	601	3	US-09-949-016-133710	Sequence 133710, A
161	11.4	81.4	81.4	20	US-10-365-645-7	Sequence 7, Appl1	C 234	11.4	81.4	601	3	US-09-949-016-156986	Sequence 156986, A
162	11.4	81.4	81.4	20	US-10-365-645-7	Sequence 7, Appl1	C 235	11.4	81.4	601	3	US-09-949-016-157032	Sequence 157032, A
163	11.4	81.4	81.4	20	US-10-817-182-7	Sequence 7, Appl1	C 236	11.4	81.4	601	3	US-09-949-016-170061	Sequence 170061, A
164	11.4	81.4	81.4	20	US-10-817-182-7	Sequence 7, Appl1	C 237	11.4	81.4	601	3	US-09-949-016-170062	Sequence 170062, A
165	11.4	81.4	81.4	20	US-10-672-163-7	Sequence 7, Appl1	C 238	11.4	81.4	601	3	US-09-949-016-170063	Sequence 170063, A
166	11.4	81.4	81.4	20	US-10-672-163-7	Sequence 7, Appl1	C 239	11.4	81.4	601	3	US-09-949-016-170175	Sequence 170175, A
167	11.4	81.4	81.4	25	US-08-737-607-3	Sequence 3, Appl1	C 240	11.4	81.4	603	3	US-09-949-016-185753	Sequence 185753, A
168	11.4	81.4	81.4	25	US-09-396-196G-6531	Sequence 6531, Ap	C 241	11.4	81.4	603	3	US-09-270-767-3161	Sequence 3161, Ap
169	11.4	81.4	81.4	25	US-09-396-196G-87490	Sequence 87490, A	C 242	11.4	81.4	603	3	US-09-270-767-18443	Sequence 18443, A
170	11.4	81.4	81.4	25	US-09-396-196G-87491	Sequence 87491, A	C 243	11.4	81.4	628	3	US-09-949-016-3207	Sequence 3207, Ap

C 244	11.4	81.4	633	3	US-09-322-409-77	Sequence 77, Appl	C 317	11.4	81.4	1105	3	US-10-023-888-15	Sequence 15, Appl
C 245	11.4	81.4	633	3	US-09-322-409-77	Sequence 79, Appl	C 318	11.4	81.4	1107	3	US-09-614-221A-398	Sequence 398, Appl
C 246	11.4	81.4	633	3	US-09-451-527-77	Sequence 77, Appl	C 319	11.4	81.4	1113	3	US-09-252-991A-1342	Sequence 342, Appl
C 247	11.4	81.4	633	3	US-09-451-527-77	Sequence 79, Appl	C 320	11.4	81.4	1122	3	US-09-902-540-9255	Sequence 9255, Appl
C 248	11.4	81.4	671	3	US-09-533-559-6036	Sequence 6036, Ap	C 321	11.4	81.4	1128	3	US-09-710-279-2171	Sequence 2171, Ap
C 249	11.4	81.4	709	3	US-09-270-767-10032	Sequence 10032, A	C 322	11.4	81.4	1150	3	US-09-931-407B-1	Sequence 1, Appl
C 250	11.4	81.4	717	3	US-09-252-991A-352	Sequence 352, Ap	C 323	11.4	81.4	1159	3	US-09-891-735-1	Sequence 1, Appl
C 251	11.4	81.4	726	3	US-09-328-352-3033	Sequence 3033, Ap	C 324	11.4	81.4	1169	3	US-09-270-767-14840	Sequence 14840, A
C 252	11.4	81.4	735	3	US-09-270-767-13913	Sequence 13913, A	C 325	11.4	81.4	1170	3	US-08-988-111-1	Sequence 1, Appl
C 253	11.4	81.4	762	3	US-09-543-681A-1624	Sequence 1624, Ap	C 326	11.4	81.4	1177	3	US-09-387-922-1	Sequence 1, Appl
C 254	11.4	81.4	766	3	US-09-270-767-1140	Sequence 1140, Ap	C 327	11.4	81.4	1170	3	US-09-949-016-1681	Sequence 1681, Ap
C 255	11.4	81.4	766	3	US-09-270-767-16422	Sequence 16422, A	C 328	11.4	81.4	1182	3	US-10-232-858-100	Sequence 100, Appl
C 256	11.4	81.4	777	3	US-09-252-991A-313	Sequence 313, Ap	C 329	11.4	81.4	1182	3	US-09-338-063A-100	Sequence 100, Appl
C 257	11.4	81.4	780	3	US-09-322-409-75	Sequence 75, Appl	C 330	11.4	81.4	1195	3	US-09-549-831-9	Sequence 9, Appl
C 258	11.4	81.4	780	3	US-09-322-409-76	Sequence 76, Appl	C 331	11.4	81.4	1200	3	US-10-232-858-94	Sequence 94, Appl
C 259	11.4	81.4	780	3	US-09-451-527-75	Sequence 75, Appl	C 332	11.4	81.4	1200	3	US-09-338-063A-94	Sequence 94, Appl
C 260	11.4	81.4	780	3	US-09-451-527-75	Sequence 76, Appl	C 333	11.4	81.4	1206	3	US-10-232-858-6	Sequence 6, Appl
C 261	11.4	81.4	788	3	US-09-142-623-10	Sequence 10, Appl	C 334	11.4	81.4	1206	3	US-10-232-858-83	Sequence 83, Appl
C 262	11.4	81.4	819	3	US-10-232-858-96	Sequence 96, Appl	C 335	11.4	81.4	1206	3	US-10-232-858-84	Sequence 84, Appl
C 263	11.4	81.4	819	3	US-09-338-063A-96	Sequence 96, Appl	C 336	11.4	81.4	1206	3	US-10-232-858-85	Sequence 85, Appl
C 264	11.4	81.4	849	3	US-09-252-991A-1357	Sequence 1357, Ap	C 337	11.4	81.4	1206	3	US-10-232-858-86	Sequence 86, Appl
C 265	11.4	81.4	861	3	US-09-489-039A-474	Sequence 474, Ap	C 338	11.4	81.4	1206	3	US-10-232-858-87	Sequence 87, Appl
C 266	11.4	81.4	867	3	US-09-902-540-3225	Sequence 3225, Ap	C 339	11.4	81.4	1206	3	US-09-338-063A-87	Sequence 87, Appl
C 267	11.4	81.4	879	2	US-08-158-682A-1	Sequence 1, Appl	C 340	11.4	81.4	1206	3	US-09-338-063A-83	Sequence 83, Appl
C 268	11.4	81.4	879	2	US-08-015-203-1	Sequence 1, Appl	C 341	11.4	81.4	1206	3	US-09-338-063A-84	Sequence 84, Appl
C 269	11.4	81.4	879	2	US-09-252-991A-13591	Sequence 13591, A	C 342	11.4	81.4	1206	3	US-09-338-063A-85	Sequence 85, Appl
C 270	11.4	81.4	885	3	US-09-322-409-72	Sequence 72, Appl	C 343	11.4	81.4	1206	3	US-09-338-063A-86	Sequence 86, Appl
C 271	11.4	81.4	885	3	US-09-322-409-74	Sequence 74, Appl	C 344	11.4	81.4	1206	3	US-09-338-063A-87	Sequence 87, Appl
C 272	11.4	81.4	885	3	US-09-451-527-72	Sequence 72, Appl	C 345	11.4	81.4	1221	3	US-09-134-001C-1078	Sequence 1078, Ap
C 273	11.4	81.4	885	3	US-09-451-527-74	Sequence 74, Appl	C 346	11.4	81.4	1224	3	US-09-489-039A-753	Sequence 753, Appl
C 274	11.4	81.4	886	3	US-08-134-231C-31	Sequence 31, Appl	C 347	11.4	81.4	1251	3	US-09-107-532A-1897	Sequence 1897, Ap
C 275	11.4	81.4	886	3	US-08-728-160-31	Sequence 31, Appl	C 348	11.4	81.4	1275	3	US-09-489-039A-566	Sequence 566, Appl
C 276	11.4	81.4	933	3	US-09-252-991A-326	Sequence 326, Appl	C 349	11.4	81.4	1307	3	US-09-270-767-1261	Sequence 1261, A
C 277	11.4	81.4	940	2	US-09-533-559-1571	Sequence 1571, Ap	C 350	11.4	81.4	1341	2	US-07-627-535G-6	Sequence 6, Appl
C 278	11.4	81.4	954	2	US-08-343-443B-106	Sequence 106, Ap	C 351	11.4	81.4	1355	3	US-08-974-022-5	Sequence 5, Appl
C 279	11.4	81.4	966	3	US-10-232-858-101	Sequence 101, Appl	C 352	11.4	81.4	1355	3	US-08-795-447A-5	Sequence 5, Appl
C 280	11.4	81.4	966	3	US-09-338-063A-101	Sequence 101, Appl	C 353	11.4	81.4	1355	3	US-08-795-447A-5	Sequence 5, Appl
C 281	11.4	81.4	981	3	US-10-232-858-92	Sequence 92, Appl	C 354	11.4	81.4	1355	3	US-08-974-166-5	Sequence 5, Appl
C 282	11.4	81.4	981	3	US-09-338-063A-92	Sequence 92, Appl	C 355	11.4	81.4	1355	3	US-08-795-447A-5	Sequence 5, Appl
C 283	11.4	81.4	984	3	US-10-232-858-93	Sequence 93, Appl	C 356	11.4	81.4	1355	3	US-08-706-945D-127	Sequence 127, Appl
C 284	11.4	81.4	984	3	US-09-338-063A-93	Sequence 93, Appl	C 357	11.4	81.4	1355	3	US-08-577-788C-5	Sequence 5, Appl
C 285	11.4	81.4	987	3	US-09-489-039A-6045	Sequence 6045, Ap	C 358	11.4	81.4	1355	3	US-09-064-823-1	Sequence 1, Appl
C 286	11.4	81.4	996	3	US-09-919-039-114	Sequence 114, Ap	C 359	11.4	81.4	1359	3	US-09-489-039A-529	Sequence 529, Appl
C 287	11.4	81.4	1014	3	US-09-248-796A-3864	Sequence 3864, Ap	C 360	11.4	81.4	1362	3	US-09-533-555-5689	Sequence 5689, Ap
C 288	11.4	81.4	1017	3	US-09-489-039A-3501	Sequence 3501, Ap	C 361	11.4	81.4	1377	3	US-09-252-991A-4240	Sequence 4240, Ap
C 289	11.4	81.4	1023	3	US-09-543-681A-796	Sequence 796, Ap	C 362	11.4	81.4	1392	3	US-09-247-155-144	Sequence 144, Appl
C 290	11.4	81.4	1024	3	US-09-949-016-5707	Sequence 5707, Ap	C 363	11.4	81.4	1399	3	US-09-902-540-8223	Sequence 8223, Ap
C 291	11.4	81.4	1042	3	US-09-949-016-4802	Sequence 4802, Ap	C 364	11.4	81.4	1407	3	US-09-903-190-144	Sequence 144, Appl
C 292	11.4	81.4	1050	3	US-09-230-132-3	Sequence 3, Appl	C 365	11.4	81.4	1407	3	US-09-248-796A-3205	Sequence 3205, Ap
C 293	11.4	81.4	1054	3	US-08-956-171E-556	Sequence 556, Appl	C 366	11.4	81.4	1416	3	US-09-949-016-1961	Sequence 1961, Ap
C 294	11.4	81.4	1054	3	US-08-781-986A-556	Sequence 556, Appl	C 367	11.4	81.4	1422	3	US-09-252-991A-333	Sequence 333, Appl
C 295	11.4	81.4	1056	3	US-10-232-858-95	Sequence 95, Appl	C 368	11.4	81.4	1443	2	US-08-673-312-1	Sequence 1, Appl
C 296	11.4	81.4	1056	3	US-09-338-063A-95	Sequence 95, Appl	C 369	11.4	81.4	1443	3	US-08-902-937A-2	Sequence 2, Appl
C 297	11.4	81.4	1071	3	US-09-270-767-1061	Sequence 1061, Ap	C 370	11.4	81.4	1446	3	US-08-787-091-1	Sequence 1, Appl
C 298	11.4	81.4	1071	3	US-09-270-767-16343	Sequence 16343, A	C 371	11.4	81.4	1454	2	US-08-657-392-1	Sequence 1, Appl
C 299	11.4	81.4	1080	3	US-10-232-858-91	Sequence 91, Appl	C 372	11.4	81.4	1454	2	PCR-US94-02539-1	Sequence 1, Appl
C 300	11.4	81.4	1080	3	US-09-338-063A-91	Sequence 91, Appl	C 373	11.4	81.4	1455	2	US-08-657-392-26	Sequence 26, Appl
C 301	11.4	81.4	1083	3	US-09-549-831-12	Sequence 12, Appl	C 374	11.4	81.4	1455	6	PCR-US94-02539-26	Sequence 26, Appl
C 302	11.4	81.4	1083	3	US-09-902-540-8475	Sequence 8475, Ap	C 375	11.4	81.4	1476	3	US-09-902-540-6246	Sequence 6246, Ap
C 303	11.4	81.4	1083	3	US-10-232-858-88	Sequence 88, Appl	C 376	11.4	81.4	1480	3	US-09-902-540-342	Sequence 342, Appl
C 304	11.4	81.4	1083	3	US-09-338-063A-88	Sequence 88, Appl	C 377	11.4	81.4	1480	3	US-09-578-194-6	Sequence 6, Appl
C 305	11.4	81.4	1089	3	US-10-232-858-10	Sequence 10, Appl	C 378	11.4	81.4	1480	3	US-09-235-153-4	Sequence 4, Appl
C 306	11.4	81.4	1089	3	US-09-338-063A-10	Sequence 10, Appl	C 379	11.4	81.4	1480	3	US-09-270-767-7175	Sequence 7175, Ap
C 307	11.4	81.4	1092	3	US-10-232-858-90	Sequence 90, Appl	C 380	11.4	81.4	1480	3	US-09-270-767-22457	Sequence 22457, A
C 308	11.4	81.4	1092	3	US-09-338-063A-90	Sequence 90, Appl	C 381	11.4	81.4	1480	3	US-08-968-563-1	Sequence 1, Appl
C 309	11.4	81.4	1092	3	US-09-635-872A-17	Sequence 17, Appl	C 382	11.4	81.4	1480	3	US-08-968-563A-1	Sequence 1, Appl
C 310	11.4	81.4	1105	3	US-09-636-077A-17	Sequence 17, Appl	C 383	11.4	81.4	1480	3	US-09-307-973A-6	Sequence 6, Appl
C 311	11.4	81.4	1105	3	US-09-636-060C-17	Sequence 17, Appl	C 384	11.4	81.4	1480	3	US-09-308-207-1	Sequence 1, Appl
C 312	11.4	81.4	1105	3	US-09-986-552-17	Sequence 17, Appl	C 385	11.4	81.4	1480	3	US-09-489-039A-2187	Sequence 2187, Ap
C 313	11.4	81.4	1105	3	US-09-636-596C-17	Sequence 17, Appl	C 386	11.4	81.4	1480	3	US-09-489-039A-2187	Sequence 2187, Ap
C 314	11.4	81.4	1105	3	US-10-023-894-15	Sequence 15, Appl	C 387	11.4	81.4	1480	3	US-08-472-429A-3	Sequence 3, Appl
C 315	11.4	81.4	1105	3	US-10-306-686-17	Sequence 17, Appl	C 388	11.4	81.4	1480	3	PCR-US96-05330A-541	Sequence 541, Appl
C 316	11.4	81.4	1105	3	US-09-895-072-17	Sequence 17, Appl	C 389	11.4	81.4	1718	2	US-08-675-153-3	Sequence 3, Appl

C 390	11.4	81.4	1718	2	US-08-841-252-3	Sequence 3, Appl1	463	11.4	81.4	3090	3	US-09-653-730-14	Sequence 14, Appl1
C 391	11.4	81.4	1718	2	US-08-881-571-3	Sequence 3, Appl1	464	11.4	81.4	3102	3	US-09-252-991A-4040	Sequence 4040, Ap
C 392	11.4	81.4	1718	3	US-09-282-054-3	Sequence 3, Appl1	C 465	11.4	81.4	3105	3	US-08-542-635-1	Sequence 1, Appl1
C 393	11.4	81.4	1718	3	US-09-665-638-3	Sequence 3, Appl1	C 466	11.4	81.4	3108	3	US-09-710-279-3427	Sequence 3427, Ap
C 394	11.4	81.4	1737	3	US-09-252-991A-1205	Sequence 105, Ap	C 467	11.4	81.4	3273	3	US-09-902-540-6446	Sequence 6446, Ap
C 395	11.4	81.4	1740	3	US-10-328-226A-16	Sequence 16, Appl	C 468	11.4	81.4	3275	3	US-09-902-540-436	Sequence 436, App
C 396	11.4	81.4	1794	3	US-09-012-515A-13	Sequence 13, Appl	C 469	11.4	81.4	3334	3	US-09-991-181-288	Sequence 288, App
C 397	11.4	81.4	1794	3	US-08-360-144A-13	Sequence 13, Appl	C 470	11.4	81.4	3334	3	US-09-990-444-288	Sequence 288, App
C 398	11.4	81.4	1794	3	US-09-012-504A-13	Sequence 13, Appl	C 471	11.4	81.4	3334	3	US-09-997-333-288	Sequence 288, App
C 399	11.4	81.4	1794	3	US-09-012-399A-13	Sequence 13, Appl	C 472	11.4	81.4	3334	3	US-09-992-598-288	Sequence 288, App
C 400	11.4	81.4	1794	6	PCT-US95-06722-13	Sequence 13, Appl	C 473	11.4	81.4	3395	3	US-10-104-047-842	Sequence 842, App
C 401	11.4	81.4	1815	2	US-08-606-288-6	Sequence 6, Appl1	C 474	11.4	81.4	3411	3	US-09-002-285-77	Sequence 77, Appl
C 402	11.4	81.4	1815	2	US-09-347-483-6	Sequence 6, Appl1	C 475	11.4	81.4	3411	3	US-09-589-477-77	Sequence 77, Appl
C 403	11.4	81.4	1821	3	US-09-248-796A-173	Sequence 173, App	C 476	11.4	81.4	3411	3	US-10-099-285A-77	Sequence 2556, Ap
C 404	11.4	81.4	1825	3	US-09-919-039-115	Sequence 115, App	C 477	11.4	81.4	3445	3	US-09-949-016-2556	Sequence 9, Appl1
C 405	11.4	81.4	1867	2	US-08-675-153-6	Sequence 6, Appl1	C 478	11.4	81.4	3468	3	US-09-668-650-9	Sequence 9, Appl1
C 406	11.4	81.4	1867	2	US-08-841-252-6	Sequence 6, Appl1	C 479	11.4	81.4	3471	3	US-09-002-285-71	Sequence 71, Appl
C 407	11.4	81.4	1867	2	US-08-881-571-6	Sequence 6, Appl1	C 480	11.4	81.4	3471	3	US-09-589-477-71	Sequence 71, Appl
C 408	11.4	81.4	1867	3	US-09-282-054-6	Sequence 6, Appl1	C 481	11.4	81.4	3471	3	US-10-099-285A-71	Sequence 71, Appl
C 409	11.4	81.4	1867	3	US-09-665-638-6	Sequence 6, Appl1	C 482	11.4	81.4	3471	3	US-07-828-788A-15	Sequence 15, Appl
C 410	11.4	81.4	1872	3	US-09-252-991A-4634	Sequence 4634, Ap	C 483	11.4	81.4	3567	2	US-08-356-034-5	Sequence 5, Appl1
C 411	11.4	81.4	1896	3	US-09-732-615-7	Sequence 7, Appl1	C 484	11.4	81.4	3567	2	US-08-602-737-1	Sequence 1, Appl1
C 412	11.4	81.4	1896	3	US-10-273-051-7	Sequence 7, Appl1	C 485	11.4	81.4	3567	2	US-08-980-071-1	Sequence 1, Appl1
C 413	11.4	81.4	1905	3	US-09-142-623-2	Sequence 2, Appl1	C 486	11.4	81.4	3567	2	US-08-980-071-3	Sequence 3, Appl1
C 414	11.4	81.4	1907	3	US-08-771-986A-1	Sequence 1, Appl1	C 487	11.4	81.4	3567	2	US-08-980-071-5	Sequence 5, Appl1
C 415	11.4	81.4	1907	3	US-08-769-802A-1	Sequence 1, Appl1	C 488	11.4	81.4	3567	2	US-08-980-071-7	Sequence 7, Appl1
C 416	11.4	81.4	1907	3	US-07-627-539G-1	Sequence 1, Appl1	C 489	11.4	81.4	3567	2	US-08-980-071-9	Sequence 9, Appl1
C 417	11.4	81.4	1993	2	US-07-627-539G-1	Sequence 1, Appl1	C 490	11.4	81.4	3567	2	US-08-980-071-11	Sequence 11, Appl
C 418	11.4	81.4	2001	3	US-09-487-558B-35	Sequence 35, Appl	C 491	11.4	81.4	3567	2	US-08-980-071-58	Sequence 58, Appl
C 419	11.4	81.4	2017	3	US-09-270-767-12350	Sequence 12350, A	C 492	11.4	81.4	3567	2	US-08-980-071-60	Sequence 60, Appl
C 420	11.4	81.4	2076	3	US-09-489-039A-2842	Sequence 2842, Ap	C 493	11.4	81.4	3567	2	US-08-980-071-60	Sequence 60, Appl
C 421	11.4	81.4	2094	3	US-09-252-991A-4535	Sequence 4535, Ap	C 494	11.4	81.4	3567	2	US-08-757-536-3	Sequence 3, Appl1
C 422	11.4	81.4	2106	3	US-09-774-528-667	Sequence 267, App	C 495	11.4	81.4	3567	2	US-08-757-536-5	Sequence 5, Appl1
C 423	11.4	81.4	2106	3	US-10-120-988-667	Sequence 267, App	C 496	11.4	81.4	3567	2	US-08-757-536-7	Sequence 7, Appl1
C 424	11.4	81.4	2118	3	US-09-328-352-2553	Sequence 2553, App	C 497	11.4	81.4	3567	2	US-08-757-536-9	Sequence 9, Appl1
C 425	11.4	81.4	2136	3	US-09-252-991A-13089	Sequence 13089, A	C 498	11.4	81.4	3567	2	US-08-757-536-11	Sequence 11, Appl
C 426	11.4	81.4	2140	3	US-10-104-047-883	Sequence 283, App	C 499	11.4	81.4	3567	2	US-09-314-093-1	Sequence 1, Appl1
C 427	11.4	81.4	2207	9	5221620-3	Patent No. 5221620	C 500	11.4	81.4	3567	3	US-09-314-093-3	Sequence 3, Appl1
C 428	11.4	81.4	2226	3	US-09-252-991A-13762	Sequence 13762, A	C 501	11.4	81.4	3567	3	US-09-314-093-5	Sequence 5, Appl1
C 429	11.4	81.4	2265	3	US-09-270-767-4284	Sequence 14284, A	C 502	11.4	81.4	3567	3	US-09-314-093-7	Sequence 7, Appl1
C 430	11.4	81.4	2274	3	US-09-772-647-3	Sequence 3, Appl1	C 503	11.4	81.4	3567	3	US-09-314-093-9	Sequence 9, Appl1
C 431	11.4	81.4	2274	3	US-10-228-931-3	Sequence 3, Appl1	C 504	11.4	81.4	3567	3	US-09-314-093-11	Sequence 11, Appl
C 432	11.4	81.4	2340	3	US-09-252-991A-13580	Sequence 13580, A	C 505	11.4	81.4	3567	3	US-09-314-093-11	Sequence 11, Appl
C 433	11.4	81.4	2348	3	US-09-270-767-13975	Sequence 13975, A	C 506	11.4	81.4	3567	3	US-09-314-093-58	Sequence 58, Appl
C 434	11.4	81.4	2366	3	US-09-949-016-4483	Sequence 5483, Ap	C 507	11.4	81.4	3567	3	US-09-314-093-60	Sequence 60, Appl
C 435	11.4	81.4	2406	3	US-09-252-991A-12703	Sequence 12703, A	C 508	11.4	81.4	3567	3	US-08-933-891-5	Sequence 5, Appl1
C 436	11.4	81.4	2499	3	US-09-276-531-133	Sequence 133, App	C 509	11.4	81.4	3567	3	US-09-250-848-1	Sequence 1, Appl1
C 437	11.4	81.4	2526	3	US-09-252-991A-13864	Sequence 13864, A	C 510	11.4	81.4	3567	3	US-09-250-848-3	Sequence 3, Appl1
C 438	11.4	81.4	2569	9	5221620-1	Patent No. 5221620	C 511	11.4	81.4	3567	3	US-09-250-848-5	Sequence 5, Appl1
C 439	11.4	81.4	2616	3	US-09-252-991A-12851	Sequence 12851, A	C 512	11.4	81.4	3567	3	US-09-250-848-7	Sequence 7, Appl1
C 440	11.4	81.4	2652	3	US-09-489-039A-4078	Sequence 4078, Ap	C 513	11.4	81.4	3567	3	US-09-250-848-9	Sequence 9, Appl1
C 441	11.4	81.4	2653	2	US-08-295-670-5	Sequence 5, Appl1	C 514	11.4	81.4	3567	3	US-09-251-885-11	Sequence 11, Appl
C 442	11.4	81.4	2653	2	US-08-633-485-5	Sequence 5, Appl1	C 515	11.4	81.4	3567	3	US-09-251-885-3	Sequence 3, Appl1
C 443	11.4	81.4	2693	2	US-08-295-670-7	Sequence 7, Appl1	C 516	11.4	81.4	3567	3	US-09-251-885-5	Sequence 5, Appl1
C 444	11.4	81.4	2693	2	US-08-633-485-7	Sequence 7, Appl1	C 517	11.4	81.4	3567	3	US-09-251-885-7	Sequence 7, Appl1
C 445	11.4	81.4	2711	2	US-08-461-551-1	Sequence 1, Appl1	C 518	11.4	81.4	3567	3	US-09-251-885-9	Sequence 9, Appl1
C 446	11.4	81.4	2711	3	US-09-037-621A-1	Sequence 1, Appl1	C 519	11.4	81.4	3567	3	US-09-251-885-11	Sequence 11, Appl
C 447	11.4	81.4	2711	3	US-09-583-717-1	Sequence 1, Appl1	C 520	11.4	81.4	3567	3	US-09-001-982-1	Sequence 1, Appl1
C 448	11.4	81.4	2711	3	US-09-918-485-1	Sequence 1, Appl1	C 521	11.4	81.4	3567	3	US-09-337-635-11	Sequence 11, Appl
C 449	11.4	81.4	2716	2	US-08-647-484-1	Sequence 1, Appl1	C 522	11.4	81.4	3567	3	US-09-337-635-3	Sequence 3, Appl1
C 450	11.4	81.4	2716	2	US-08-647-484-3	Sequence 3, Appl1	C 523	11.4	81.4	3567	3	US-09-337-635-5	Sequence 5, Appl1
C 451	11.4	81.4	2716	2	US-08-647-481-1	Sequence 1, Appl1	C 524	11.4	81.4	3567	3	US-09-337-635-7	Sequence 7, Appl1
C 452	11.4	81.4	2716	2	US-08-647-481-3	Sequence 3, Appl1	C 525	11.4	81.4	3567	3	US-09-337-635-9	Sequence 9, Appl1
C 453	11.4	81.4	2716	2	US-08-430-033A-1	Sequence 1, Appl1	C 526	11.4	81.4	3567	3	US-09-337-635-11	Sequence 11, Appl
C 454	11.4	81.4	2716	2	US-08-430-033A-3	Sequence 3, Appl1	C 527	11.4	81.4	3567	3	US-09-337-635-13	Sequence 13, Appl
C 455	11.4	81.4	2716	6	PCT-US96-05792-1	Sequence 1, Appl1	C 528	11.4	81.4	3567	3	US-09-337-635-15	Sequence 15, Appl
C 456	11.4	81.4	2716	6	PCT-US96-05792-3	Sequence 3, Appl1	C 529	11.4	81.4	3567	3	US-09-337-635-17	Sequence 17, Appl
C 457	11.4	81.4	2716	6	US-09-248-796A-2230	Sequence 2230, Ap	C 530	11.4	81.4	3567	3	US-09-337-635-19	Sequence 19, Appl
C 458	11.4	81.4	2886	3	US-09-248-796A-5312	Sequence 5312, Ap	C 531	11.4	81.4	3567	3	US-09-337-280-5	Sequence 5, Appl1
C 459	11.4	81.4	2967	3	US-09-903-540-4397	Sequence 4397, Ap	C 532	11.4	81.4	3567	3	US-09-337-280-7	Sequence 7, Appl1
C 460	11.4	81.4	3002	3	US-09-368-364A-1	Sequence 1, Appl1	C 533	11.4	81.4	3567	3	US-09-337-280-9	Sequence 9, Appl1
C 461	11.4	81.4	3027	2	US-08-680-326-23	Sequence 23, Appl	C 534	11.4	81.4	3567	3	US-09-337-280-11	Sequence 11, Appl
C 462	11.4	81.4	3044	3	US-09-710-279-4290	Sequence 4290, Ap	C 535	11.4	81.4	3567	3	US-09-337-280-13	Sequence 13, Appl

536	11.4	81.4	3567	3	US-09-337-280-58	Sequence 58, Appl	609	11.4	81.4	5763	3	US-08-956-171E-505	Sequence 505, App
537	11.4	81.4	3567	3	US-09-337-280-60	Sequence 60, Appl	610	11.4	81.4	5763	3	US-08-781-986A-505	Sequence 505, App
538	11.4	81.4	3567	3	US-09-521-344-5	Sequence 5, Appl1	611	11.4	81.4	6091	3	US-09-221-017B-803	Sequence 803, App
539	11.4	81.4	3567	3	US-09-837-861A-5	Sequence 5, Appl1	612	11.4	81.4	6394	3	US-09-949-016-14380	Sequence 14380, A
540	11.4	81.4	3567	3	US-09-668-650-1	Sequence 1, Appl1	613	11.4	81.4	6776	3	US-09-252-991A-5283	Sequence 5283, Ap
541	11.4	81.4	3567	3	US-09-972-175-1	Sequence 1, Appl1	614	11.4	81.4	9453	3	US-09-902-540-892	Sequence 892, App
542	11.4	81.4	3567	3	US-09-972-175-3	Sequence 3, Appl1	615	11.4	81.4	9035	3	US-09-902-540-1084	Sequence 1084, Ap
543	11.4	81.4	3567	3	US-09-972-175-5	Sequence 5, Appl1	616	11.4	81.4	9454	3	US-09-949-016-12398	Sequence 12398, A
544	11.4	81.4	3567	3	US-09-972-175-7	Sequence 7, Appl1	617	11.4	81.4	9455	3	US-09-949-016-14650	Sequence 14650, A
545	11.4	81.4	3567	3	US-09-972-175-9	Sequence 9, Appl1	618	11.4	81.4	10190	3	US-10-232-885-105	Sequence 105, App
546	11.4	81.4	3567	3	US-09-972-175-11	Sequence 11, Appl1	619	11.4	81.4	10190	3	US-09-338-063A-105	Sequence 105, App
547	11.4	81.4	3567	3	US-09-972-175-58	Sequence 58, Appl1	620	11.4	81.4	10322	3	US-09-902-540-989	Sequence 989, App
548	11.4	81.4	3567	3	US-09-972-175-60	Sequence 60, Appl1	621	11.4	81.4	10480	3	US-09-732-615-13	Sequence 13, Appl
549	11.4	81.4	3567	3	US-10-200-522-1	Sequence 1, Appl1	622	11.4	81.4	10480	3	US-10-273-051-13	Sequence 13, Appl
550	11.4	81.4	3567	3	US-10-200-522-3	Sequence 3, Appl1	623	11.4	81.4	11268	3	US-09-434-840-5	Sequence 5, Appl1
551	11.4	81.4	3567	3	US-10-200-522-5	Sequence 5, Appl1	624	11.4	81.4	11271	3	US-08-956-171E-11	Sequence 11, Appl1
552	11.4	81.4	3567	3	US-10-200-522-7	Sequence 7, Appl1	625	11.4	81.4	11271	3	US-08-781-986A-11	Sequence 11, Appl1
553	11.4	81.4	3567	3	US-10-200-522-9	Sequence 9, Appl1	626	11.4	81.4	12145	3	US-08-968-563-19	Sequence 19, Appl1
554	11.4	81.4	3567	3	US-10-200-522-11	Sequence 11, Appl1	627	11.4	81.4	12145	3	US-08-969-689A-19	Sequence 19, Appl1
555	11.4	81.4	3567	3	US-10-200-522-58	Sequence 58, Appl1	628	11.4	81.4	12145	3	US-09-369-796-1	Sequence 1, Appl1
556	11.4	81.4	3567	3	US-10-200-522-60	Sequence 60, Appl1	629	11.4	81.4	12145	3	US-09-307-972A-10	Sequence 10, Appl1
557	11.4	81.4	3567	6	US-10-200-522-60	Sequence 15, Appl1	630	11.4	81.4	12145	3	US-09-641-652-1	Sequence 1, Appl1
558	11.4	81.4	3567	6	PCT-US92-11337-15	Sequence 15, Appl1	631	11.4	81.4	12145	3	US-09-949-016-16775	Sequence 137, App
559	11.4	81.4	3567	2	US-10-328-226A-17	Sequence 17, Appl1	632	11.4	81.4	12656	3	US-08-961-527-137	Sequence 16775, A
560	11.4	81.4	3579	2	US-08-602-737-7	Sequence 7, Appl1	633	11.4	81.4	12656	3	US-10-127-862-1	Sequence 1, Appl1
561	11.4	81.4	3579	3	US-08-754-490-29	Sequence 29, Appl1	634	11.4	81.4	13543	3	US-09-949-016-14949	Sequence 14949, A
562	11.4	81.4	3579	3	US-08-922-505A-29	Sequence 29, Appl1	635	11.4	81.4	14330	3	US-09-902-540-1121	Sequence 1121, Ap
563	11.4	81.4	3579	3	US-09-001-982-7	Sequence 7, Appl1	636	11.4	81.4	15338	3	US-09-902-540-1067	Sequence 1067, Ap
564	11.4	81.4	3579	3	US-09-260-952A-29	Sequence 29, Appl1	637	11.4	81.4	15482	3	US-09-949-016-17225	Sequence 17225, A
565	11.4	81.4	3579	3	US-09-253-441-29	Sequence 29, Appl1	638	11.4	81.4	15543	3	US-09-902-540-1129	Sequence 1129, Ap
566	11.4	81.4	3579	3	US-09-253-331A-29	Sequence 29, Appl1	639	11.4	81.4	15689	3	US-09-902-540-1161	Sequence 1161, Ap
567	11.4	81.4	3579	3	US-09-251-040-29	Sequence 29, Appl1	640	11.4	81.4	17554	3	US-09-902-540-118	Sequence 118, Ap
568	11.4	81.4	3579	3	US-09-916-956A-29	Sequence 29, Appl1	641	11.4	81.4	17726	3	US-09-949-016-14300	Sequence 14300, A
569	11.4	81.4	3579	3	US-09-873-873-29	Sequence 29, Appl1	642	11.4	81.4	19637	3	US-09-949-016-16544	Sequence 16544, A
570	11.4	81.4	3579	3	US-09-977-914-29	Sequence 29, Appl1	643	11.4	81.4	19637	3	US-09-949-016-15479	Sequence 15479, A
571	11.4	81.4	3579	3	US-09-636-746B-29	Sequence 29, Appl1	644	11.4	81.4	21177	3	US-09-949-016-17427	Sequence 17427, A
572	11.4	81.4	3579	3	US-10-365-645-29	Sequence 29, Appl1	645	11.4	81.4	21180	3	US-09-949-016-12395	Sequence 12395, A
573	11.4	81.4	3579	3	US-09-668-650-7	Sequence 7, Appl1	646	11.4	81.4	23250	3	US-09-949-016-14800	Sequence 14800, A
574	11.4	81.4	3579	3	US-10-817-182-29	Sequence 29, Appl1	647	11.4	81.4	23250	3	US-09-949-016-14300	Sequence 14300, A
575	11.4	81.4	3579	3	US-10-672-163-29	Sequence 29, Appl1	648	11.4	81.4	24459	3	US-09-902-540-5004	Sequence 5004, Ap
576	11.4	81.4	3588	3	US-09-566-921-23	Sequence 23, Appl1	649	11.4	81.4	26050	3	US-09-949-016-17449	Sequence 17449, A
577	11.4	81.4	3722	3	US-09-221-017B-784	Sequence 784, App	650	11.4	81.4	29272	3	US-09-902-540-1217	Sequence 1217, Ap
578	11.4	81.4	3808	3	US-10-104-047-367	Sequence 367, App	651	11.4	81.4	30062	3	US-09-949-016-15866	Sequence 15866, A
579	11.4	81.4	3810	3	US-09-902-540-8379	Sequence 8379, App	652	11.4	81.4	31063	3	US-09-596-002-20	Sequence 20, Appl1
580	11.4	81.4	3813	3	US-09-902-540-1085	Sequence 7085, App	653	11.4	81.4	32241	3	US-09-902-540-1247	Sequence 1247, Ap
581	11.4	81.4	3923	2	US-09-902-540-634	Sequence 634, App	654	11.4	81.4	33529	3	US-09-949-016-12865	Sequence 12865, A
582	11.4	81.4	3923	2	US-08-465-609-4	Sequence 4, Appl1	655	11.4	81.4	33529	3	US-09-949-016-17364	Sequence 17364, A
583	11.4	81.4	3923	3	US-09-176-320-7	Sequence 7, Appl1	656	11.4	81.4	35081	2	US-08-752-760A-1	Sequence 1, Appl1
584	11.4	81.4	3923	3	US-09-661-016-7	Sequence 7, Appl1	657	11.4	81.4	35100	3	US-09-782-378A-26	Sequence 26, Appl1
585	11.4	81.4	4170	2	US-08-619-198-4	Sequence 4, Appl1	658	11.4	81.4	35524	3	US-08-923-137-1	Sequence 1, Appl1
586	11.4	81.4	4200	3	US-09-949-016-1124	Sequence 4124, Ap	659	11.4	81.4	36851	3	US-09-949-016-14674	Sequence 14674, A
587	11.4	81.4	4259	3	US-09-155-183-12	Sequence 12, Appl1	660	11.4	81.4	43804	3	US-09-949-016-12651	Sequence 12651, A
588	11.4	81.4	4259	3	US-09-733-383-12	Sequence 12, Appl1	661	11.4	81.4	43804	3	US-09-171-461-1	Sequence 1, Appl1
589	11.4	81.4	4269	3	US-09-540-236-1101	Sequence 1101, Ap	662	11.4	81.4	45432	3	US-09-970-711-1	Sequence 719, App
590	11.4	81.4	4284	2	US-09-252-991A-4006	Sequence 4006, Ap	663	11.4	81.4	45432	3	US-09-949-016-1739	Sequence 16539, A
591	11.4	81.4	4338	2	US-08-015-986A-1	Sequence 1, Appl1	664	11.4	81.4	45436	3	US-09-949-016-16518	Sequence 16518, A
592	11.4	81.4	4338	2	US-08-446-363-1	Sequence 1, Appl1	665	11.4	81.4	52496	3	US-09-949-016-16139	Sequence 16139, A
593	11.4	81.4	4354	3	US-09-802-937A-1	Sequence 1037, App	666	11.4	81.4	52496	3	US-09-949-016-14298	Sequence 14298, A
594	11.4	81.4	4359	3	US-09-328-352-1037	Sequence 3906, Ap	667	11.4	81.4	53260	3	US-09-949-016-14946	Sequence 14946, A
595	11.4	81.4	4704	3	US-09-252-991A-3906	Sequence 3906, Ap	668	11.4	81.4	55216	3	US-09-949-016-17420	Sequence 17420, A
596	11.4	81.4	4780	3	US-09-584-586-7	Sequence 7, Appl1	669	11.4	81.4	59140	3	US-09-596-002-37	Sequence 37, Appl1
597	11.4	81.4	4810	3	US-09-536-824-5	Sequence 5, Appl1	670	11.4	81.4	63760	3	US-09-949-016-11880	Sequence 11880, A
598	11.4	81.4	4810	3	US-09-885-329-5	Sequence 5, Appl1	671	11.4	81.4	63760	3	US-09-949-016-14088	Sequence 14088, A
599	11.4	81.4	5192	2	US-09-252-991A-5192	Sequence 5192, App	672	11.4	81.4	63760	3	US-09-949-016-13576	Sequence 13576, A
600	11.4	81.4	5192	2	US-08-619-198-8	Sequence 8, Appl1	673	11.4	81.4	67755	3	US-09-949-016-13703	Sequence 13703, A
601	11.4	81.4	5198	2	US-08-619-198-1	Sequence 1, Appl1	674	11.4	81.4	68173	3	US-09-949-016-14046	Sequence 14046, A
602	11.4	81.4	5268	3	US-09-830-751-9	Sequence 9, Appl1	675	11.4	81.4	84571	3	US-09-949-016-117820	Sequence 117820, A
603	11.4	81.4	5280	3	US-09-902-540-770	Sequence 770, App	676	11.4	81.4	99639	3	US-09-949-016-11880	Sequence 11880, A
604	11.4	81.4	5391	3	US-08-811-519-2	Sequence 2, Appl1	677	11.4	81.4	125188	3	US-09-949-016-16564	Sequence 16564, A
605	11.4	81.4	5519	3	US-09-902-540-849	Sequence 849, App	678	11.4	81.4	133368	3	US-09-949-016-12651	Sequence 12651, A
606	11.4	81.4	5519	3	US-08-737-607-1	Sequence 1, Appl1	679	11.4	81.4	133368	3	US-09-949-016-13841	Sequence 13841, A
607	11.4	81.4	5610	3	US-09-262-537-57	Sequence 57, Appl1	680	11.4	81.4	134008	3	US-09-949-016-12886	Sequence 12886, A
608	11.4	81.4	5693	3	US-09-262-537-19	Sequence 19, Appl1	681	11.4	81.4	152582	3	US-09-949-016-12886	Sequence 12886, A

C 682	11.4	81.4	152583	3	US-09-949-016-17300	Sequence 17390, A	C 755	11	78.6	301	3	US-09-685-1664-281	Sequence 281, App
C 683	11.4	81.4	152583	3	US-09-949-016-17301	Sequence 17391, A	C 756	11	78.6	301	3	US-09-688-489-281	Sequence 281, App
C 684	11.4	81.4	174493	3	US-09-804-471A-3	Sequence 3, Appl1	C 757	11	78.6	301	3	US-09-679-426-281	Sequence 281, App
C 685	11.4	81.4	174493	3	US-10-238-709-3	Sequence 3, Appl1	C 758	11	78.6	301	3	US-09-759-143-281	Sequence 281, App
C 686	11.4	81.4	174493	3	US-10-724-594-3	Sequence 3, Appl1	C 759	11	78.6	301	3	US-09-651-236-281	Sequence 281, App
C 687	11.4	81.4	175236	3	US-09-949-016-14353	Sequence 14353, A	C 760	11	78.6	301	3	US-09-657-279-281	Sequence 281, App
C 688	11.4	81.4	187580	3	US-09-949-016-13266	Sequence 13266, A	C 761	11	78.6	301	3	US-10-012-896-281	Sequence 281, App
C 689	11.4	81.4	194714	3	US-09-949-016-11869	Sequence 11869, A	C 762	11	78.6	302	3	US-09-303-1208-1	Sequence 1, Appl1
C 690	11.4	81.4	196714	3	US-09-949-016-15474	Sequence 15474, A	C 763	11	78.6	302	3	US-09-820-576-1	Sequence 1, Appl1
C 691	11.4	81.4	198942	3	US-09-949-016-13209	Sequence 13209, A	C 764	11	78.6	302	3	US-09-966-608-1	Sequence 1, Appl1
C 692	11.4	81.4	200663	3	US-09-949-016-12559	Sequence 12559, A	C 765	11	78.6	306	3	US-09-252-991A-7727	Sequence 7727, App
C 693	11.4	81.4	203093	3	US-09-949-016-14445	Sequence 14445, A	C 766	11	78.6	319	3	US-09-513-999C-1442	Sequence 1442, App
C 694	11.4	81.4	227730	3	US-09-949-016-17175	Sequence 17175, A	C 767	11	78.6	324	3	US-09-489-039A-3825	Sequence 5825, App
C 695	11.4	81.4	245286	3	US-09-949-016-15447	Sequence 15497, A	C 768	11	78.6	326	3	US-09-270-767-7262	Sequence 7264, App
C 696	11.4	81.4	246240	2	US-08-724-394A-20	Sequence 20, Appl1	C 769	11	78.6	336	3	US-09-470-767-22544	Sequence 22544, App
C 697	11.4	81.4	246240	2	US-08-724-394A-21	Sequence 21, Appl1	C 770	11	78.6	348	3	US-09-513-999C-1770	Sequence 1770, App
C 698	11.4	81.4	246240	2	US-08-724-394A-22	Sequence 22, Appl1	C 771	11	78.6	370	3	US-09-640-211A-1783	Sequence 1783, App
C 699	11.4	81.4	255679	3	US-09-949-016-17189	Sequence 17189, A	C 772	11	78.6	389	3	US-08-956-1718-4442	Sequence 4442, App
C 700	11.4	81.4	276687	3	US-09-949-016-13840	Sequence 13840, A	C 773	11	78.6	389	3	US-08-781-986A-4442	Sequence 4442, App
C 701	11.4	81.4	312474	3	US-09-949-016-17434	Sequence 17434, A	C 774	11	78.6	396	3	US-09-328-352-680	Sequence 680, App
C 702	11.4	81.4	312957	3	US-09-949-001-31	Sequence 31, Appl1	C 775	11	78.6	399	3	US-09-107-532A-936	Sequence 936, App
C 703	11.4	81.4	312957	3	US-09-949-001-34	Sequence 34, Appl1	C 776	11	78.6	404	3	US-09-370-767-30960	Sequence 30960, A
C 704	11.4	81.4	331814	3	US-09-949-016-12008	Sequence 12008, A	C 777	11	78.6	420	2	US-08-528-057-4	Sequence 4, Appl1
C 705	11.4	81.4	331814	3	US-09-214-808-1	Sequence 17056, A	C 778	11	78.6	435	3	US-08-956-1718-3792	Sequence 3792, App
C 706	11.4	81.4	336165	3	US-09-214-808-1	Sequence 1, Appl1	C 779	11	78.6	435	3	US-08-781-986A-3792	Sequence 3792, App
C 707	11.4	81.4	636591	3	US-09-949-016-11808	Sequence 11808, A	C 780	11	78.6	452	3	US-09-513-999C-87	Sequence 87, Appl1
C 708	11.4	81.4	636591	3	US-09-949-016-13388	Sequence 13388, A	C 781	11	78.6	463	3	US-08-956-1718-3850	Sequence 3850, App
C 709	11.4	81.4	640681	3	US-09-790-988-1	Sequence 1, Appl1	C 782	11	78.6	463	3	US-08-781-986A-3850	Sequence 3850, App
C 710	11.4	81.4	1230025	3	US-09-198-452A-1	Sequence 1, Appl1	C 783	11	78.6	468	3	US-09-712-363-9	Sequence 9, Appl1
C 711	11.4	81.4	1230230	3	US-09-438-185A-1	Sequence 1, Appl1	C 784	11	78.6	473	3	US-09-621-976-2359	Sequence 2359, App
C 712	11.4	81.4	1830121	3	US-09-557-884-1	Sequence 1, Appl1	C 785	11	78.6	474	3	US-09-452-991A-11794	Sequence 11794, App
C 713	11.4	81.4	1830121	3	US-09-557-884-1	Sequence 1, Appl1	C 786	11	78.6	501	3	US-09-270-767-9764	Sequence 9764, App
C 714	11.4	81.4	1830121	3	US-09-643-990A-1	Sequence 1, Appl1	C 787	11	78.6	501	3	US-09-270-767-25046	Sequence 25046, A
C 715	11.4	81.4	1830121	3	US-09-643-990A-1	Sequence 1, Appl1	C 788	11	78.6	510	3	US-09-252-991A-8655	Sequence 8655, App
C 716	11.4	81.4	1830121	3	US-10-158-865-1	Sequence 1, Appl1	C 789	11	78.6	513	3	US-09-270-767-9282	Sequence 9282, App
C 717	11.4	81.4	1830121	3	US-10-158-865-1	Sequence 1, Appl1	C 790	11	78.6	513	3	US-09-270-767-24564	Sequence 24564, A
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C 719	11.4	81.4	4411529	3	US-09-103-840A-1	Sequence 1, Appl1	C 792	11	78.6	517	3	US-09-621-976-2773	Sequence 2773, App
C 720	11.2	80.0	402	3	US-09-471-276-95	Sequence 95, Appl1	C 793	11	78.6	528	3	US-09-270-767-18276	Sequence 18276, A
C 721	11	78.6	25	3	US-09-396-196G-87492	Sequence 87492, A	C 794	11	78.6	541	3	US-09-949-016-2185	Sequence 2185, App
C 722	11	78.6	47	3	US-09-671-317-674	Sequence 674, App	C 795	11	78.6	541	3	US-09-949-016-17619	Sequence 17619, A
C 723	11	78.6	65	2	US-08-528-057-23	Sequence 23, Appl1	C 796	11	78.6	548	3	US-09-270-767-13936	Sequence 13936, A
C 724	11	78.6	110	3	US-08-513-999C-13785	Sequence 13785, A	C 797	11	78.6	574	3	US-09-854-133-456	Sequence 456, App
C 725	11	78.6	178	2	US-08-485-657A-9	Sequence 9, Appl1	C 798	11	78.6	585	3	US-09-328-352-770	Sequence 770, App
C 726	11	78.6	178	3	US-09-366-380-9	Sequence 9, Appl1	C 799	11	78.6	591	3	US-09-248-796A-2459	Sequence 2459, App
C 727	11	78.6	180	6	PCT-US95-02303-9	Sequence 9, Appl1	C 800	11	78.6	600	3	US-09-489-039A-6037	Sequence 6037, App
C 728	11	78.6	189	2	US-08-358-160-145	Sequence 145, App	C 801	11	78.6	601	3	US-09-949-016-17619	Sequence 17619, A
C 729	11	78.6	204	3	US-09-489-039A-6085	Sequence 6085, App	C 802	11	78.6	601	3	US-09-949-016-17619	Sequence 17619, A
C 730	11	78.6	217	3	US-09-134-000C-1075	Sequence 1075, App	C 803	11	78.6	601	3	US-09-949-016-22323	Sequence 22323, A
C 731	11	78.6	221	3	US-09-533-559-7860	Sequence 7860, App	C 804	11	78.6	601	3	US-09-949-016-24529	Sequence 24529, A
C 732	11	78.6	222	3	US-09-016-434-383	Sequence 383, App	C 805	11	78.6	601	3	US-09-949-016-30628	Sequence 30628, A
C 733	11	78.6	222	3	US-09-471-276-178	Sequence 178, App	C 806	11	78.6	601	3	US-09-949-016-54463	Sequence 54463, A
C 734	11	78.6	225	3	US-09-313-294A-4003	Sequence 4003, App	C 807	11	78.6	601	3	US-09-949-016-54327	Sequence 54327, A
C 735	11	78.6	242	2	US-09-513-999C-19172	Sequence 19172, A	C 808	11	78.6	601	3	US-09-949-016-54377	Sequence 54377, A
C 736	11	78.6	261	2	US-08-482-148-11	Sequence 11, Appl1	C 809	11	78.6	601	3	US-09-949-016-54378	Sequence 54378, A
C 737	11	78.6	261	6	PCT-US95-02944-11	Sequence 11, Appl1	C 810	11	78.6	601	3	US-09-949-016-54379	Sequence 54379, A
C 738	11	78.6	273	3	US-09-107-532A-2898	Sequence 2898, App	C 811	11	78.6	601	3	US-09-949-016-57487	Sequence 57487, A
C 739	11	78.6	276	3	US-08-938-085A-42	Sequence 42, Appl1	C 812	11	78.6	601	3	US-09-949-016-57702	Sequence 57702, A
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C 741	11	78.6	276	3	US-10-072-844-42	Sequence 42, Appl1	C 814	11	78.6	601	3	US-09-949-016-60520	Sequence 60520, A
C 742	11	78.6	276	3	US-10-072-844-44	Sequence 44, Appl1	C 815	11	78.6	601	3	US-09-949-016-61371	Sequence 61371, A
C 743	11	78.6	276	3	US-10-072-841A-42	Sequence 42, Appl1	C 816	11	78.6	601	3	US-09-949-016-63378	Sequence 63378, A
C 744	11	78.6	276	3	US-10-072-841A-44	Sequence 44, Appl1	C 817	11	78.6	601	3	US-09-949-016-63379	Sequence 63379, A
C 745	11	78.6	276	3	US-10-219-631A-42	Sequence 42, Appl1	C 818	11	78.6	601	3	US-09-949-016-63379	Sequence 63379, A
C 746	11	78.6	276	3	US-10-219-631A-44	Sequence 44, Appl1	C 819	11	78.6	601	3	US-09-949-016-67018	Sequence 67018, A
C 747	11	78.6	280	3	US-09-270-767-30008	Sequence 30008, A	C 820	11	78.6	601	3	US-09-949-016-67019	Sequence 67019, A
C 748	11	78.6	281	3	US-09-513-999C-9571	Sequence 9571, App	C 821	11	78.6	601	3	US-09-949-016-72867	Sequence 72867, A
C 749	11	78.6	289	3	US-09-313-294A-4907	Sequence 4907, App	C 822	11	78.6	601	3	US-09-949-016-73131	Sequence 73131, A
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C 751	11	78.6	301	3	US-09-353-616A-281	Sequence 281, App	C 824	11	78.6	601	3	US-09-949-016-85432	Sequence 85432, A
C 752	11	78.6	301	3	US-09-237-149A-281	Sequence 281, App	C 825	11	78.6	601	3	US-09-949-016-85817	Sequence 85817, A
C 753	11	78.6	301	3	US-09-159-812-281	Sequence 281, App	C 826	11	78.6	601	3	US-09-949-016-121883	Sequence 121883, A
C 754	11	78.6	301	3	US-09-636-215-281	Sequence 281, App	C 827	11	78.6	601	3	US-09-949-016-121922	Sequence 121922, A



C 828	11	78.6	601	3	US-09-949-016-122004	Sequence 122004,	C 901	11	78.6	1247	2	US-08-528-057-41	Sequence 41, Appl
C 829	11	78.6	601	3	US-09-949-016-122486	Sequence 122486,	C 902	11	78.6	1248	3	US-09-949-016-346	Sequence 346, Appl
C 830	11	78.6	601	3	US-09-949-016-126218	Sequence 126218,	C 903	11	78.6	1249	2	US-08-523-376-1	Sequence 1, Appl
C 831	11	78.6	601	3	US-09-949-016-126488	Sequence 126488,	C 904	11	78.6	1250	3	US-09-949-016-126488	Sequence 126488,
C 832	11	78.6	601	3	US-09-949-016-127110	Sequence 127110,	C 905	11	78.6	1251	3	US-09-949-016-127110	Sequence 127110,
C 833	11	78.6	601	3	US-09-949-016-128781	Sequence 128781,	C 906	11	78.6	1252	3	US-09-949-016-128781	Sequence 128781,
C 834	11	78.6	601	3	US-09-949-016-128782	Sequence 128782,	C 907	11	78.6	1253	3	US-09-949-016-128782	Sequence 128782,
C 835	11	78.6	601	3	US-09-949-016-128937	Sequence 128937,	C 908	11	78.6	1254	3	US-09-949-016-128937	Sequence 128937,
C 836	11	78.6	601	3	US-09-949-016-130697	Sequence 130697,	C 909	11	78.6	1255	3	US-09-949-016-130697	Sequence 130697,
C 837	11	78.6	601	3	US-09-949-016-131699	Sequence 131699,	C 910	11	78.6	1256	3	US-09-949-016-131699	Sequence 131699,
C 838	11	78.6	601	3	US-09-949-016-132824	Sequence 132824,	C 911	11	78.6	1257	3	US-09-949-016-132824	Sequence 132824,
C 839	11	78.6	601	3	US-09-949-016-133482	Sequence 133482,	C 912	11	78.6	1258	3	US-09-949-016-133482	Sequence 133482,
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C 841	11	78.6	601	3	US-09-949-016-153758	Sequence 153758,	C 914	11	78.6	1260	3	US-09-949-016-153758	Sequence 153758,
C 842	11	78.6	601	3	US-09-949-016-153759	Sequence 153759,	C 915	11	78.6	1261	3	US-09-949-016-153759	Sequence 153759,
C 843	11	78.6	601	3	US-09-949-016-163937	Sequence 163937,	C 916	11	78.6	1262	3	US-09-949-016-163937	Sequence 163937,
C 844	11	78.6	601	3	US-09-949-016-163938	Sequence 163938,	C 917	11	78.6	1263	3	US-09-949-016-163938	Sequence 163938,
C 845	11	78.6	601	3	US-09-949-016-163939	Sequence 163939,	C 918	11	78.6	1264	3	US-09-949-016-163939	Sequence 163939,
C 846	11	78.6	601	3	US-09-949-016-1725	Sequence 1725, App	C 919	11	78.6	1265	3	US-09-949-016-1725	Sequence 1725, App
C 847	11	78.6	601	3	US-09-949-016-7004	Sequence 7004, Ap	C 920	11	78.6	1266	3	US-09-949-016-7004	Sequence 7004, Ap
C 848	11	78.6	612	3	US-09-248-796A-3118	Sequence 3118, Ap	C 921	11	78.6	1267	3	US-09-248-796A-3118	Sequence 3118, Ap
C 849	11	78.6	612	3	US-09-966-316-15	Sequence 15, Appl	C 922	11	78.6	1268	3	US-09-966-316-15	Sequence 15, Appl
C 850	11	78.6	631	2	US-09-949-016-127	Sequence 727, App	C 923	11	78.6	1269	3	US-09-949-016-127	Sequence 727, App
C 851	11	78.6	631	3	US-09-949-016-3580	Sequence 3580, Ap	C 924	11	78.6	1270	3	US-09-949-016-3580	Sequence 3580, Ap
C 852	11	78.6	631	3	US-09-252-991A-4256	Sequence 4256, Ap	C 925	11	78.6	1271	3	US-09-252-991A-4256	Sequence 4256, Ap
C 853	11	78.6	678	3	US-08-998-416-128	Sequence 128, App	C 926	11	78.6	1272	3	US-08-998-416-128	Sequence 128, App
C 854	11	78.6	689	3	US-09-533-559-6293	Sequence 6293, App	C 927	11	78.6	1273	3	US-09-533-559-6293	Sequence 6293, App
C 855	11	78.6	690	3	US-09-976-594-394	Sequence 394, App	C 928	11	78.6	1274	3	US-09-976-594-394	Sequence 394, App
C 856	11	78.6	714	3	US-09-328-352-3454	Sequence 3454, Ap	C 929	11	78.6	1275	3	US-09-328-352-3454	Sequence 3454, Ap
C 857	11	78.6	732	3	US-09-270-767-14491	Sequence 14491, A	C 930	11	78.6	1276	3	US-09-270-767-14491	Sequence 14491, A
C 858	11	78.6	749	3	US-08-998-416-669	Sequence 769, App	C 931	11	78.6	1277	3	US-08-998-416-669	Sequence 769, App
C 859	11	78.6	821	3	US-09-247-155-52	Sequence 52, Appl	C 932	11	78.6	1278	3	US-09-247-155-52	Sequence 52, Appl
C 860	11	78.6	821	3	US-09-903-130-52	Sequence 52, Appl	C 933	11	78.6	1279	3	US-09-903-130-52	Sequence 52, Appl
C 861	11	78.6	822	3	US-09-252-991A-11668	Sequence 11668, A	C 934	11	78.6	1280	3	US-09-252-991A-11668	Sequence 11668, A
C 862	11	78.6	840	3	US-09-134-000C-1074	Sequence 1074, Ap	C 935	11	78.6	1281	3	US-09-134-000C-1074	Sequence 1074, Ap
C 863	11	78.6	872	3	US-09-566-921-64	Sequence 64, Appl	C 936	11	78.6	1282	3	US-09-566-921-64	Sequence 64, Appl
C 864	11	78.6	899	3	US-09-270-767-12418	Sequence 12418, A	C 937	11	78.6	1283	3	US-09-270-767-12418	Sequence 12418, A
C 865	11	78.6	909	3	US-09-023-655-1101	Sequence 1101, Ap	C 938	11	78.6	1284	3	US-09-023-655-1101	Sequence 1101, Ap
C 866	11	78.6	909	3	US-09-546-013-79	Sequence 79, Appl	C 939	11	78.6	1285	3	US-09-546-013-79	Sequence 79, Appl
C 867	11	78.6	939	3	US-09-248-796A-2887	Sequence 2887, Ap	C 940	11	78.6	1286	3	US-09-248-796A-2887	Sequence 2887, Ap
C 868	11	78.6	945	3	US-08-793-418-5	Sequence 5, Appl1	C 941	11	78.6	1287	3	US-08-793-418-5	Sequence 5, Appl1
C 869	11	78.6	960	3	US-09-489-039A-2094	Sequence 2094, Ap	C 942	11	78.6	1288	3	US-09-489-039A-2094	Sequence 2094, Ap
C 870	11	78.6	963	3	US-09-991-181-423	Sequence 423, App	C 943	11	78.6	1289	3	US-09-991-181-423	Sequence 423, App
C 871	11	78.6	963	3	US-09-990-444-423	Sequence 423, App	C 944	11	78.6	1290	3	US-09-990-444-423	Sequence 423, App
C 872	11	78.6	963	3	US-09-997-333-423	Sequence 423, App	C 945	11	78.6	1291	3	US-09-997-333-423	Sequence 423, App
C 873	11	78.6	963	3	US-09-992-598-423	Sequence 423, App	C 946	11	78.6	1292	3	US-09-992-598-423	Sequence 423, App
C 874	11	78.6	986	3	US-09-270-767-11348	Sequence 11348, A	C 947	11	78.6	1293	3	US-09-270-767-11348	Sequence 11348, A
C 875	11	78.6	1001	3	US-09-671-317-181	Sequence 181, App	C 948	11	78.6	1294	3	US-09-671-317-181	Sequence 181, App
C 876	11	78.6	1050	3	US-08-126-505A-18	Sequence 18, Appl	C 949	11	78.6	1295	3	US-08-126-505A-18	Sequence 18, Appl
C 877	11	78.6	1056	3	US-09-902-540-8983	Sequence 8983, Ap	C 950	11	78.6	1296	3	US-09-902-540-8983	Sequence 8983, Ap
C 878	11	78.6	1074	3	US-09-636-215-824	Sequence 824, App	C 951	11	78.6	1297	3	US-09-636-215-824	Sequence 824, App
C 879	11	78.6	1074	3	US-09-685-166A-824	Sequence 824, App	C 952	11	78.6	1298	3	US-09-685-166A-824	Sequence 824, App
C 880	11	78.6	1074	3	US-09-679-426-824	Sequence 824, App	C 953	11	78.6	1299	3	US-09-679-426-824	Sequence 824, App
C 881	11	78.6	1074	3	US-09-759-143-824	Sequence 824, App	C 954	11	78.6	1300	3	US-09-759-143-824	Sequence 824, App
C 882	11	78.6	1074	3	US-09-651-236-824	Sequence 824, App	C 955	11	78.6	1301	3	US-09-651-236-824	Sequence 824, App
C 883	11	78.6	1074	3	US-09-657-279-824	Sequence 824, App	C 956	11	78.6	1302	3	US-09-657-279-824	Sequence 824, App
C 884	11	78.6	1074	3	US-10-012-896-824	Sequence 824, App	C 957	11	78.6	1303	3	US-10-012-896-824	Sequence 824, App
C 885	11	78.6	1086	3	US-09-252-991A-13444	Sequence 13444, A	C 958	11	78.6	1304	3	US-09-252-991A-13444	Sequence 13444, A
C 886	11	78.6	1092	3	US-09-252-991A-13444	Sequence 13444, A	C 959	11	78.6	1305	3	US-09-252-991A-13444	Sequence 13444, A
C 887	11	78.6	1125	3	US-09-248-796A-1905	Sequence 1905, App	C 960	11	78.6	1306	3	US-09-248-796A-1905	Sequence 1905, App
C 888	11	78.6	1134	3	US-08-793-418-1	Sequence 1, Appl1	C 961	11	78.6	1307	3	US-08-793-418-1	Sequence 1, Appl1
C 889	11	78.6	1134	3	US-08-793-418-2	Sequence 2, Appl1	C 962	11	78.6	1308	3	US-08-793-418-2	Sequence 2, Appl1
C 890	11	78.6	1134	3	US-08-793-418-3	Sequence 3, Appl1	C 963	11	78.6	1309	3	US-08-793-418-3	Sequence 3, Appl1
C 891	11	78.6	1134	3	US-08-793-418-4	Sequence 4, Appl1	C 964	11	78.6	1310	3	US-08-793-418-4	Sequence 4, Appl1
C 892	11	78.6	1161	3	US-09-252-991A-11607	Sequence 11607, A	C 965	11	78.6	1311	3	US-09-252-991A-11607	Sequence 11607, A
C 893	11	78.6	1161	3	US-09-252-991A-11607	Sequence 11607, A	C 966	11	78.6	1312	3	US-09-252-991A-11607	Sequence 11607, A
C 894	11	78.6	1197	3	US-09-252-991A-2917	Sequence 2917, App	C 967	11	78.6	1313	3	US-09-252-991A-2917	Sequence 2917, App
C 895	11	78.6	1209	3	US-09-252-991A-9958	Sequence 9958, App	C 968	11	78.6	1314	3	US-09-252-991A-9958	Sequence 9958, App
C 896	11	78.6	1222	3	US-08-861-774E-83	Sequence 83, Appl	C 969	11	78.6	1315	3	US-08-861-774E-83	Sequence 83, Appl
C 897	11	78.6	1233	3	US-09-710-279-4293	Sequence 4293, App	C 970	11	78.6	1316	3	US-09-710-279-4293	Sequence 4293, App
C 898	11	78.6	1237	3	US-09-270-767-877	Sequence 877, App	C 971	11	78.6	1317	3	US-09-270-767-877	Sequence 877, App
C 899	11	78.6	1237	3	US-09-270-767-16159	Sequence 16159, A	C 972	11	78.6	1318	3	US-09-270-767-16159	Sequence 16159, A
C 900	11	78.6	1245	3	US-09-248-796A-129	Sequence 129, App	C 973	11	78.6	1319	3	US-09-248-796A-129	Sequence 129, App

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974 11 78.6 2089 3 US-09-369-247-19 Sequence 19, Appl
975 11 78.6 2089 3 US-10-062-548-19 Sequence 15, Appl
976 11 78.6 2094 3 US-09-252-91A-7575 Sequence 7575, Ap
c 977 11 78.6 2124 2 US-08-087-007-1 Sequence 1, Appl
c 978 11 78.6 2124 2 US-08-483-433-1 Sequence 1, Appl
c 979 11 78.6 2124 3 US-09-566-254A-1 Sequence 1, Appl
c 980 11 78.6 2124 6 PCT-US92-05920-1 Sequence 1, Appl
c 981 11 78.6 2136 3 US-09-252-91A-3111 Sequence 3111, Ap
c 982 11 78.6 2138 3 US-09-949-016-3454 Sequence 3454, Ap
c 983 11 78.6 2231 3 US-09-949-016-3418 Sequence 3418, Ap
c 984 11 78.6 2235 3 US-09-252-991A-7032 Sequence 7032, Ap
c 985 11 78.6 2255 3 US-09-252-991A-6199 Sequence 6199, Ap
c 986 11 78.6 2337 3 US-09-583-110-1269 Sequence 1269, Ap
c 987 11 78.6 2341 3 US-08-714-918-102 Sequence 102, Ap
c 988 11 78.6 2341 3 US-09-265-315-102 Sequence 102, Ap
c 989 11 78.6 2341 3 US-09-265-315-102 Sequence 102, Ap
c 990 11 78.6 2341 3 US-09-266-417-102 Sequence 102, Ap
c 991 11 78.6 2341 3 US-09-528-709-102 Sequence 102, Ap
c 992 11 78.6 2341 3 US-09-527-745-102 Sequence 102, Ap
c 993 11 78.6 2361 3 US-09-107-433-1290 Sequence 1290, Ap
c 994 11 78.6 2401 3 US-09-949-016-4875 Sequence 4875, Ap
c 995 11 78.6 2403 3 US-09-248-796A-5998 Sequence 5998, Ap
c 996 11 78.6 2469 3 US-09-252-991A-6352 Sequence 6352, Ap
c 997 11 78.6 2469 3 US-09-087-727-1 Sequence 1, Appl
c 998 11 78.6 2469 3 US-09-853-053-1 Sequence 1, Appl
c 999 11 78.6 2469 3 US-09-949-016-155 Sequence 155, Ap
c1000 11 78.6 2471 2 US-08-920-812-14 Sequence 14, Appl
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## ALIGNMENTS

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RESULT 1
US-09-949-016-147054/c
; Sequence 147054, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 147054
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-147054
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Query Match 92.9%; Score 13; DB 3; Length 601;
Best Local Similarity 76.9%; Pred. No. 3.7e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GGUACUGCAACUC 13
Db 393 GCTACTGCACTC 381
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RESULT 2
US-09-801-042-1/c
; Sequence 1, Application US/09801042
; Patent No. 6630332
; GENERAL INFORMATION:
; APPLICANT: RIEPING, MECHTHILD
; APPLICANT: THIERBACH, GEORG
```

```
; APPLICANT: VAN DER REST, MICHEL EDUARD
; APPLICANT: MOLENAAR, DOUWE
; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE
; FILE REFERENCE: MAS/21133/80410
; CURRENT APPLICATION NUMBER: US/09/801,042
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/229,329
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: DE 100 34 833.5
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: DE 101 03874.7
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1720
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1593)
; OTHER INFORMATION: mqo gene
US-09-801-042-1
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Query Match 92.9%; Score 13; DB 3; Length 1720;
Best Local Similarity 76.9%; Pred. No. 4.3e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 GUACUGCACTCG 14
Db 1482 GCTACTGCACTCG 1470
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RESULT 3
US-09-949-016-16941/c
; Sequence 16941, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16941
; LENGTH: 21372
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16941
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Query Match 92.9%; Score 13; DB 3; Length 21372;
Best Local Similarity 76.9%; Pred. No. 5.9e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 GUACUGCAACUC 14
Db 14063 GCTACTGCACTCG 14051
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RESULT 4
US-09-949-016-15868
; Sequence 15868, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CU001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO: 15868  
; LENGTH: 374159  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-15868

Query Match 92.9%; Score 13; DB 3; Length 374159;  
Best Local Similarity 76.9%; Pred. No. 7.7e+02;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13  
||:|||||:  
Db 237891 CGTACTGCACTC 237903

RESULT 5  
US-09-270-767-27123  
; Sequence 27123, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/770,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 27123  
; LENGTH: 140  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-27123

Query Match 88.6%; Score 12.4; DB 3; Length 140;  
Best Local Similarity 71.4%; Pred. No. 7.1e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 14  
||:|||||:  
Db 19 CGTACTGCACTAG 32

RESULT 6  
US-09-513-999C-2299/c  
; Sequence 2299, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Mline Edwards, J.B.  
; APPLICANT: Ductert, A.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59, US2, REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; PRIOR APPLICATION NUMBER: US/09/513,999C  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO: 2299

LENGTH: 323  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 23..322  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 9  
; OTHER INFORMATION: m=a or c  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 246  
; OTHER INFORMATION: r=a or g  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 247  
; OTHER INFORMATION: r=a or g  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 75  
; OTHER INFORMATION: Xaa=Glu or Gly  
US-09-513-999C-2299

Query Match 88.6%; Score 12.4; DB 3; Length 323;  
Best Local Similarity 71.4%; Pred. No. 7.9e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 14  
||:|||||:  
Db 44 CGTACTGCACTCG 31

RESULT 7  
US-08-303-861-15  
; Sequence 15, Application US/08303861  
; Patent No. 6086902  
; GENERAL INFORMATION:  
; APPLICANT: ZAMB, TIMOTHY  
; APPLICANT: LIANG, XIAOPING  
; APPLICANT: BABIUK, LORNE A.  
; TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE I  
; TITLE OF INVENTION: VACCINES  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: MORRISON & FORSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/303,861  
; FILING DATE: 09-SEP-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PARK, FREDIE K.  
; REGISTRATION NUMBER: 35,636  
; REFERENCE/DOCKET NUMBER: 29310-20020.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 349 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single

TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 157..348  
US-08-303-861-15

Query Match 88.6%; Score 12.4; DB 3; Length 349;  
Best Local Similarity 78.6%; Pred. No. 8e+02;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUCG 14  
Db 332 CGTACTGCACACG 345

RESULT 8  
US-09-621-976-681/C  
Sequence 681, Application US/09621976  
Patent No. 6639063  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Jobert, S.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
FILE REFERENCE: GENSET.054PR2  
CURRENT FILING DATE: US/09/621,976  
NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO 681  
LENGTH: 399  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 13..399  
US-09-621-976-681

Query Match 88.6%; Score 12.4; DB 3; Length 399;  
Best Local Similarity 71.4%; Pred. No. 8.1e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUCG 14  
Db 34 CGTACTCCACTCG 21

RESULT 9  
US-09-252-991A-79/C  
Sequence 79, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT FILING DATE: US/09/252,991A  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 79  
LENGTH: 435  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-79

Query Match 88.6%; Score 12.4; DB 3; Length 435;  
Best Local Similarity 78.6%; Pred. No. 8.2e+02;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUCG 14  
Db 378 CGAATCGCACTCG 365

RESULT 10  
US-09-252-991A-1326/C  
Sequence 1326, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT FILING DATE: US/09/252,991A  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 1326  
LENGTH: 504  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-1326

Query Match 88.6%; Score 12.4; DB 3; Length 504;  
Best Local Similarity 71.4%; Pred. No. 8.4e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUCG 14  
Db 213 CGTACTGCACCTCG 200

RESULT 11  
US-09-252-991A-233/C  
Sequence 233, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT FILING DATE: US/09/252,991A  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 233  
LENGTH: 543  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-233

Query Match 88.6%; Score 12.4; DB 3; Length 543;  
Best Local Similarity 71.4%; Pred. No. 8.5e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUCG 14  
Db 180 CGTACTGCATTCG 167

RESULT 12  
US-09-252-991A-7705  
Sequence 7705, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 7705  
LENGTH: 543  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-7705

Query Match 88.6%; Score 12.4; DB 3; Length 543;  
Best Local Similarity 71.4%; Pred. No. 8.5e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14  
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Db 151 CGTCTGCACTCG 164

RESULT 13  
US-09-270-767-5447/c  
Sequence 5447, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-084  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5447  
LENGTH: 597  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
US-09-270-767-5447

Query Match 88.6%; Score 12.4; DB 3; Length 597;  
Best Local Similarity 71.4%; Pred. No. 8.6e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14  
||:|||||:  
Db 357 CGTCTGCACTCG 344

RESULT 14  
US-09-270-767-20729/c  
Sequence 20729, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 20729  
LENGTH: 597  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
US-09-270-767-20729

Query Match 88.6%; Score 12.4; DB 3; Length 597;  
Best Local Similarity 71.4%; Pred. No. 8.6e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14  
||:|||||:  
Db 357 CGTCTGCACTCG 344

RESULT 15  
US-09-252-991A-100  
Sequence 100, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 100  
LENGTH: 669  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-100

Query Match 88.6%; Score 12.4; DB 3; Length 669;  
Best Local Similarity 78.6%; Pred. No. 8.7e+02;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14  
||:|||||:  
Db 285 CGAATGCACTCG 298

RESULT 16  
US-09-252-991A-9718/c  
Sequence 9718, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 9718  
LENGTH: 696  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-9718

Query Match 88.6%; Score 12.4; DB 3; Length 696;  
Best Local Similarity 78.6%; Pred. No. 8.7e+02;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14  
||:|||||:  
Db 682 CGAATGCACTCG 669

RESULT 17  
US-09-252-991A-14097/c  
Sequence 14097, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 14097  
LENGTH: 726  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-14097

Query Match 88.6%; Score 12.4; DB 3; Length 726;  
Best Local Similarity 71.4%; Pred. No. 8.8e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGUACUGCACTCG 14  
||:|||||:  
Db 524 CGTACTGCACCTCG 511

RESULT 18  
US-09-270-767-11527  
Sequence 11527, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 11527  
LENGTH: 737  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
US-09-270-767-11527

Query Match 88.6%; Score 12.4; DB 3; Length 737;  
Best Local Similarity 71.4%; Pred. No. 8.8e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGUACUGCACTCG 14  
||:|||||:  
Db 616 CGTACTGCACCTAG 629

RESULT 19  
US-09-252-991A-94  
Sequence 94, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 94  
LENGTH: 756  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-94

Query Match 88.6%; Score 12.4; DB 3; Length 756;  
Best Local Similarity 78.6%; Pred. No. 8.8e+02;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGUACUGCACTCG 14  
||:|||||:  
Db 199 CGAATCGCACTCG 212

RESULT 20  
US-09-252-991A-6447/c  
Sequence 6447, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 6447  
LENGTH: 834  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-6447

Query Match 88.6%; Score 12.4; DB 3; Length 834;  
Best Local Similarity 78.6%; Pred. No. 8.9e+02;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGUACUGCACTCG 14  
||:|||||:  
Db 307 CGTACTGCACCCG 294

RESULT 21  
US-09-902-540-5805  
Sequence 5805, Application US/09902540  
Patent No. 6833447  
GENERAL INFORMATION:  
APPLICANT: Goldman, Barry S.  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Wiegand, Roger C.  
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
FILE REFERENCE: 38-10(15849)B  
CURRENT APPLICATION NUMBER: US/09/902,540  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 2001-07-10  
PRIOR FILING DATE: 2000-07-10  
NUMBER OF SEQ ID NOS: 16825  
SEQ ID NO 5805  
LENGTH: 867  
TYPE: DNA  
ORGANISM: Myxococcus xanthus  
US-09-902-540-5805

Query Match 88.6%; Score 12.4; DB 3; Length 867;  
Best Local Similarity 78.6%; Pred. No. 9e+02;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGUACUGCACTCG 14  
||:|||||:  
Db 702 CGTACGCACTCG 715

RESULT 22  
US-09-252-991A-6103  
; Sequence 6103, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 6103  
; LENGTH: 930  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-6103

Query Match 88.6%; Score 12.4; DB 3; Length 930;  
Best Local Similarity 78.6%; Pred. No. 9.1e+02;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGUACUGCAACUG 14  
||:|||||:  
Db 417 CGTACTGCACACCG 430

RESULT 23  
US-09-902-540-7341  
; Sequence 7341, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: MYXOCOCCUS XANTHUS Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(115849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 7341  
; LENGTH: 1005  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-7341

Query Match 88.6%; Score 12.4; DB 3; Length 1005;  
Best Local Similarity 71.4%; Pred. No. 9.1e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGUACUGCAACUG 14  
||:|||||:  
Db 612 CGTCTGCAACTCG 625

RESULT 24  
US-09-902-540-70  
; Sequence 70, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: MYXOCOCCUS XANTHUS Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(115849)B

CURRENT APPLICATION NUMBER: US/09/902,540  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 60/217,883  
PRIOR FILING DATE: 2000-07-10  
NUMBER OF SEQ ID NOS: 16825  
SEQ ID NO 70  
LENGTH: 1007  
TYPE: DNA  
ORGANISM: Myxococcus xanthus  
US-09-902-540-70

Query Match 88.6%; Score 12.4; DB 3; Length 1007;  
Best Local Similarity 71.4%; Pred. No. 9.1e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGUACUGCAACUG 14  
||:|||||:  
Db 614 CGTCTGCAACTCG 627

RESULT 25  
US-09-107-532A-2165  
; Sequence 2165, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arinello, Pamela Denke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781) 893-5007  
; TELEFAX: (781) 893-8277  
; INFORMATION FOR SEQ ID NO: 2165:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1017 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULAR TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (B) LOCATION 1...1017  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2165:  
US-09-107-532A-2165

Query Match 88.6%; Score 12.4; DB 3; Length 1017;  
Best Local Similarity 71.4%; Pred. No. 9.2e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGUACUGCACTCG 14  
DB 924 CGTACTGCACTCG 937

RESULT 26  
US-09-252-991A-90/C  
Sequence 90; Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 90  
LENGTH: 1065  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-90

Query Match 88.6%; Score 12.4; DB 3; Length 1065;  
Best Local Similarity 78.6%; Pred. No. 9.2e+02;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGUACUGCACTCG 14  
DB 253 CGAAGTCACTCG 240

RESULT 27  
US-09-489-039A-2883  
Sequence 2883; Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 2883  
LENGTH: 1104  
TYPE: DNA  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-2883

Query Match 88.6%; Score 12.4; DB 3; Length 1104;  
Best Local Similarity 78.6%; Pred. No. 9.2e+02;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGUACUGCACTCG 14  
DB 509 CGTACGCACTCG 522

RESULT 28  
US-09-252-991A-6183  
Sequence 6183; Application US/09252991A  
Patent No. 6551795

GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 6183  
LENGTH: 1137  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-6183

Query Match 88.6%; Score 12.4; DB 3; Length 1137;  
Best Local Similarity 78.6%; Pred. No. 9.3e+02;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGUACUGCACTCG 14  
DB 14 CGTACTGCACTCG 27

RESULT 29  
US-09-252-991A-13050  
Sequence 13050; Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 13050  
LENGTH: 1152  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-13050

Query Match 88.6%; Score 12.4; DB 3; Length 1152;  
Best Local Similarity 71.4%; Pred. No. 9.3e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGUACUGCACTCG 14  
DB 422 CGTCTGCACTCG 435

RESULT 30  
US-09-252-991A-7557  
Sequence 7557; Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 7557  
LENGTH: 1203  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-7557

Query Match 88.6%; Score 12.4; DB 3; Length 1203;  
Best Local Similarity 71.4%; Pred. No. 9.3e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14  
||:|||||:  
DB 189 CGTCTGCACTCG 202

RESULT 31  
US-09-252-991A-9574  
Sequence 9574, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 9574  
LENGTH: 1203  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-9574

Query Match 88.6%; Score 12.4; DB 3; Length 1203;  
Best Local Similarity 78.6%; Pred. No. 9.3e+02;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14  
||:|||||:  
DB 492 CGAAGTCACTCG 505

RESULT 32  
US-09-996-008B-1  
Sequence 1, Application US/09996008B  
Patent No. 6830907  
GENERAL INFORMATION:  
APPLICANT: Mitsuhashi, Kazuya  
APPLICANT: Yamamoto, Hiroaki  
APPLICANT: Kimoto, No. 68309071hiro  
TITLE OF INVENTION: MUTANTS OF MYCOBACTERIUM VACCAR- DERIVED  
FILE REFERENCE: 14879-093001  
CURRENT APPLICATION NUMBER: US/09/996,008B  
CURRENT FILING DATE: 2001-11-28  
PRIOR APPLICATION NUMBER: 2000-11-28  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: JP 2001-254631  
PRIOR FILING DATE: 2001-08-24  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 1206  
TYPE: DNA  
ORGANISM: Mycobacterium vaccae  
US-09-996-008B-1

Query Match 88.6%; Score 12.4; DB 3; Length 1206;

Best Local Similarity 71.4%; Pred. No. 9.4e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14  
||:|||||:  
DB 431 CCTCTGCACTCG 444

RESULT 33  
US-09-252-991A-13225  
Sequence 13225, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 13225  
LENGTH: 1233  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-13225

Query Match 88.6%; Score 12.4; DB 3; Length 1233;  
Best Local Similarity 71.4%; Pred. No. 9.4e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14  
||:|||||:  
DB 1177 CGTCTGCACTCG 1190

RESULT 34  
US-09-252-991A-7784/c  
Sequence 7784, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 7784  
LENGTH: 1314  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-7784

Query Match 88.6%; Score 12.4; DB 3; Length 1314;  
Best Local Similarity 71.4%; Pred. No. 9.5e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14  
||:|||||:  
DB 1024 CGTCTGCACTCG 1011

RESULT 35  
US-09-489-039A-4444  
Sequence 4444, Application US/09489039A



Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; PRIOR FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 4444  
; LENGTH: 1359  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-4444

Query Match 88.6%; Score 12.4; DB 3; Length 1359;  
Best Local Similarity 71.4%; Pred. No. 9.5e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CGUACUGCAATCG 14  
||:|||||:|  
Db 975 CGTACTGCACTCG 988

RESULT 36  
US-09-252-991A-12900  
; Sequence 12900, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 12900  
; LENGTH: 1563  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-12900

Query Match 88.6%; Score 12.4; DB 3; Length 1563;  
Best Local Similarity 71.4%; Pred. No. 9.7e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CGUACUGCAATCG 14  
||:|||||:|  
Db 1530 CGTCTGCACTCG 1543

RESULT 37  
US-09-252-991A-104  
; Sequence 104, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 104  
; LENGTH: 1629  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-104

Query Match 88.6%; Score 12.4; DB 3; Length 1629;  
Best Local Similarity 78.6%; Pred. No. 9.7e+02;  
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CGUACUGCAATCG 14  
||:|||||:|  
Db 50 CGAATGCACTCG 63

RESULT 38  
US-09-252-991A-252/C  
; Sequence 252, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 252  
; LENGTH: 1737  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-252

Query Match 88.6%; Score 12.4; DB 3; Length 1737;  
Best Local Similarity 71.4%; Pred. No. 9.8e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CGUACUGCAATCG 14  
||:|||||:|  
Db 463 CGTACTGCAATCG 450

RESULT 39  
US-09-252-991A-279  
; Sequence 279, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 279  
; LENGTH: 1737  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-279

Query Match 88.6%; Score 12.4; DB 3; Length 1737;  
Best Local Similarity 71.4%; Pred. No. 9.8e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CGUACUGCAATCG 14

Db 1452 CGTACTGCAATCG 1465

RESULT 40  
US-09-252-991A-12189/c  
Sequence 12189, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 12189  
LENGTH: 1776  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-12189

Query Match 88.6%; Score 12.4; DB 3; Length 1776;  
Best Local Similarity 71.4%; Pred. No. 9.8e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCACTCG 14  
1637 CGTCTGCACTCG 1624

RESULT 41  
US-09-252-991A-4152  
Sequence 4152, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 4152  
LENGTH: 1800  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-4152

Query Match 88.6%; Score 12.4; DB 3; Length 1800;  
Best Local Similarity 71.4%; Pred. No. 9.8e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCACTCG 14  
1143 CGTACTGCAATTCG 1156

RESULT 42  
US-09-252-991A-1375/c  
Sequence 1375, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 1375  
LENGTH: 1827  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-1375

Query Match 88.6%; Score 12.4; DB 3; Length 1827;  
Best Local Similarity 71.4%; Pred. No. 9.9e+02;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCACTCG 14  
1754 CGTACTGCACTCG 1741

RESULT 43  
US-09-252-991A-1416/c  
Sequence 1416, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 1416  
LENGTH: 2262  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-1416

Query Match 88.6%; Score 12.4; DB 3; Length 2262;  
Best Local Similarity 71.4%; Pred. No. 1e+03;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGUACUGCACTCG 14  
1708 CGTACTGCACTCG 1695

RESULT 44  
US-09-252-991A-12254/c  
Sequence 12254, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 12254  
LENGTH: 2298

TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-12254

Query Match 88.6%; Score 12.4; DB 3; Length 2298;  
Best Local Similarity 71.4%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;  
Matches 10; Conservative 3; Mismatches 1;

Oy 1 CGUACUGCAACUCG 14  
||:|||||:  
Db 2185 CGTCTCGCACTCG 2172

RESULT 45  
US-09-252-991A-9636/c  
Sequence 9636, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 9636  
LENGTH: 2346  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-9636

Query Match 88.6%; Score 12.4; DB 3; Length 2346;  
Best Local Similarity 78.6%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;  
Matches 11; Conservative 2; Mismatches 1;

Oy 1 CGUACUGCAACUCG 14  
||:|||||:  
Db 438 CGAAGTGCACCTCG 425

RESULT 46  
US-09-252-991A-12355  
Sequence 12355, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 12355  
LENGTH: 2346  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-12355

Query Match 88.6%; Score 12.4; DB 3; Length 2346;  
Best Local Similarity 71.4%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;  
Matches 10; Conservative 3; Mismatches 1;

Oy 1 CGUACUGCAACUCG 14  
||:|||||:  
Db 297 CGTCTCGCACTCG 310

RESULT 47  
US-09-489-039A-1363  
Sequence 1363, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 1363  
LENGTH: 2370  
TYPE: DNA  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-1363

Query Match 88.6%; Score 12.4; DB 3; Length 2370;  
Best Local Similarity 71.4%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;  
Matches 10; Conservative 3; Mismatches 1;

Oy 1 CGUACUGCAACUCG 14  
||:|||||:  
Db 684 CGTCTCGCACTCG 697

RESULT 48  
US-09-252-991A-1192  
Sequence 1192, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 1192  
LENGTH: 2391  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-1192

Query Match 88.6%; Score 12.4; DB 3; Length 2391;  
Best Local Similarity 71.4%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;  
Matches 10; Conservative 3; Mismatches 1;

Oy 1 CGUACUGCAACUCG 14  
||:|||||:  
Db 1098 CGTCTCGCACTCG 1111

RESULT 49  
US-09-252-991A-4456/c  
Sequence 4456, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788  
 PRIOR FILING DATE: 1998-02-18  
 PRIOR APPLICATION NUMBER: US 60/094,190  
 PRIOR FILING DATE: 1998-07-27  
 NUMBER OF SEQ ID NOS: 33142  
 SEQ ID NO 4456  
 LENGTH: 2472  
 TYPE: DNA  
 ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-4456

Query Match 88.6%; Score 12.4; DB 3; Length 2472;  
 Best Local Similarity 71.4%; Pred. No. 1e+03;  
 Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUG 14  
 ||:|||||:||  
 Db 715 CGTACTGCATTCG 702

RESULT 50

US-09-620-312D-272/c  
 Sequence 272, Application US/09620312D  
 Patent No. 6569662

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom  
 APPLICANT: Liu, Chenghua  
 APPLICANT: Asundi, Vinod  
 APPLICANT: Zhang, Jie  
 APPLICANT: Ren, Feiyun  
 APPLICANT: Chen, Rui-hong  
 APPLICANT: Zhao, Qing A.  
 APPLICANT: Weinman, Tom  
 APPLICANT: Xue, Aйдong J.  
 APPLICANT: Yang, Yonghong  
 APPLICANT: Wang, Jian-Rui  
 APPLICANT: Zhou, Ping  
 APPLICANT: Ma, Yundong  
 APPLICANT: Wang, Dunrui  
 APPLICANT: Wang, Zhiwei  
 APPLICANT: John Tillinghast  
 APPLICANT: Drmanac, Radoje T.  
 TITLE OF INVENTION: No. 6569662el Nucleic Acids and  
 TITLE OF INVENTION: Polypeptides  
 FILE REFERENCE: 784CIP2B  
 CURRENT APPLICATION NUMBER: US/09/620,312D  
 CURRENT FILING DATE: 2000-07-19  
 PRIOR APPLICATION NUMBER: 09/552,317  
 PRIOR FILING DATE: 2000-04-25  
 PRIOR APPLICATION NUMBER: 09/488,725  
 PRIOR FILING DATE: 2000-01-21  
 NUMBER OF SEQ ID NOS: 1105  
 SOFTWARE: PL\_FL\_genes Version 1.0  
 SEQ ID NO 272  
 LENGTH: 2495

TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (411)..(812)  
 US-09-620-312D-272

Query Match 88.6%; Score 12.4; DB 3; Length 2495;  
 Best Local Similarity 71.4%; Pred. No. 1e+03;  
 Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUG 14  
 ||:|||||:||  
 Db 88 CGTACTGCATTCG 75

Search completed: March 18, 2006, 18:39:44  
 Job time : 77.5769 secs

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OM nucleic - nucleic search, using bw model

Run on: March 18, 2006, 18:35:23 ; Search time 1318.15 Seconds  
(without alignments)  
496.922 Million cell updates/sec

Title: US-10-800-926-2

Perfect score: 14

Sequence: 1 cguacugcaucug 14

Scoring table: IDENTITY\_NTC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	100.0	353	2	BF764590 CM3-CS004
2	14	100.0	419	7	CF849219 PMA009XM
3	14	100.0	525	3	BI602980 603249479
4	14	100.0	547	3	BI873693 963110B09
5	14	100.0	564	2	BE568772 601342118
6	14	100.0	564	10	CZ662415 OM_Ba021
7	14	100.0	587	5	BQ456457 Kc39a08.Y
8	14	100.0	614	2	BP422187 Fw1.12.G1
9	14	100.0	640	9	CZ660542 OM_Ba021
10	14	100.0	670	9	BZ563771 BZ563771
11	14	100.0	711	9	BH565722 BCGP49TR
12	14	100.0	730	7	CF849609 PMA011XC
13	14	100.0	751	10	CM525116 OM_Ba004
14	14	100.0	759	9	BH435200 BCG2M10TR
15	14	100.0	776	10	CM528167 OM_Ba002
16	14	100.0	851	10	CM780591 OM_Ba008
17	14	100.0	855	10	CM519957 OM_Ba002
18	14	100.0	859	2	BF031922 601559533
19	14	100.0	884	2	BF207946 601862463
20	14	100.0	916	10	CM776517 SP_0106.A
21	14	100.0	943	9	AZ209474 SP_0106.A
22	14	100.0	1195	8	DN693741 CGX90-B12

23	14	100.0	1200	8	DN663186
24	14	100.0	1211	8	DN738151
25	14	100.0	1289	8	DN660653
26	13	92.9	157	9	AO661032
27	13	92.9	205	7	CR555866
28	13	92.9	255	5	BU640724
29	13	92.9	285	6	CA374069
30	13	92.9	290	10	CM452335
31	13	92.9	292	10	CM772355
32	13	92.9	344	1	AJ578024
33	13	92.9	345	5	BY111672
34	13	92.9	364	8	DR073074
35	13	92.9	366	7	CV724006
36	13	92.9	367	7	CK749390
37	13	92.9	368	11	FR0030316
38	13	92.9	369	6	CD733604
39	13	92.9	376	2	BI120564
40	13	92.9	379	1	AI059369
41	13	92.9	399	1	AM425513
42	13	92.9	402	3	BM032972
43	13	92.9	403	9	AQ123512
44	13	92.9	408	5	BM915405
45	13	92.9	409	5	BQ852614
46	13	92.9	410	3	BJ646387
47	13	92.9	413	10	CL555282
48	13	92.9	426	1	AJ679628
49	13	92.9	437	1	AM929623
50	13	92.9	459	7	CV723505
51	13	92.9	460	2	BF398311
52	13	92.9	463	2	BF398981
53	13	92.9	463	3	AQ431011
54	13	92.9	465	3	BJ658245
55	13	92.9	466	7	CO520101
56	13	92.9	469	6	CF509531
57	13	92.9	470	10	CM449589
58	13	92.9	474	5	BU426615
59	13	92.9	475	5	AZ212523
60	13	92.9	477	7	CV723433
61	13	92.9	479	7	CV724150
62	13	92.9	480	6	CB536466
63	13	92.9	497	1	AM061392
64	13	92.9	500	3	BP185556
65	13	92.9	500	3	BP186086
66	13	92.9	500	3	BP187269
67	13	92.9	500	3	BP187391
68	13	92.9	500	3	BP188449
69	13	92.9	503	2	BC659795
70	13	92.9	503	2	BH785265
71	13	92.9	506	6	CA371538
72	13	92.9	507	1	AM004087
73	13	92.9	512	1	BR031816
74	13	92.9	517	3	BM033583
75	13	92.9	521	9	AQ289494
76	13	92.9	521	9	BH765203
77	13	92.9	521	10	AC915387
78	13	92.9	523	6	CF066281
79	13	92.9	524	3	BO088045
80	13	92.9	527	7	CM477104
81	13	92.9	528	8	CR955809
82	13	92.9	528	8	CC909426
83	13	92.9	529	7	CB719309
84	13	92.9	529	7	CK737648
85	13	92.9	532	6	CO083741
86	13	92.9	535	6	CA758576
87	13	92.9	537	1	AL865005
88	13	92.9	537	1	AL875997
89	13	92.9	537	1	BP184473
90	13	92.9	538	1	AY604121
91	13	92.9	538	6	CB934921
92	13	92.9	539	10	CM031907
93	13	92.9	540	10	CM629939
94	13	92.9	542	9	AO509742
95	13	92.9			

96	13	548	7	CN467225	CN467225 CB 01 VR	169	13	688	5	BW942458	BW942458
97	13	549	1	AMC54043	AMC54043 103261 MA	170	13	689	2	BE228384	BE228384
98	13	550	7	CN466725	CN466725 CB 01 VR	171	13	689	10	CM177588	CM177588
99	13	550	1	AM654044	AM654044 103262 MA	172	13	690	3	BJ803349	BJ803349
100	13	551	2	BE557270	BE557270 EK97H04.Y	173	13	691	3	BH995300	BH995300
101	13	552	2	BE557250	BE557250 EK97E03.Y	174	13	694	7	CV637847	CV637847
102	13	553	1	AM018127	AM018127 614067C06	175	13	694	7	CV647112	CV647112
103	13	553	11	TA780C10	TA780C10 T. brucei	176	13	694	8	DR791359	DR791359
104	13	561	3	BJ101572	BJ101572 BJ101572	177	13	697	4	AY432168	AY432168
105	13	561	3	BH583561	BH583561 BQGRP407F	178	13	697	4	BH880885	BH880885
106	13	566	9	AQ711536	AQ711536 HS_5358_B	179	13	698	8	DR817431	DR817431
107	13	569	6	CF190100	CF190100 K7G04J2.X	180	13	703	7	CN232315	CN232315
108	13	569	6	AQ887057	AQ887057 HS_5548_B	181	13	704	8	CM439019	CM439019
109	13	573	8	CX717002	CX717002 1333467.N	182	13	705	8	CV824083	CV824083
110	13	574	8	BZ589812	BZ589812 3590.1.72	183	13	706	9	BH382037	BH382037
111	13	576	8	CX418757	CX418757 JGI_XZG65	184	13	706	9	BH436861	BH436861
112	13	577	8	BH191034	BH191034 TC3-40K14	185	13	707	10	CM418230	CM418230
113	13	578	3	BJ658058	BJ658058 BJ658058	186	13	707	10	CM418230	CM418230
114	13	582	10	CZ664573	CZ664573 OM_Ba021	187	13	711	10	CM21001	CM21001
115	13	584	10	CM150544	CM150544 104_551.1	188	13	711	10	CZ750914	CZ750914
116	13	587	9	AQ688502	AQ688502 nbxb0077F	189	13	711	10	CL792860	CL792860
117	13	589	7	CO528867	CO528867 3530.1.19	190	13	713	10	CM418229	CM418229
118	13	595	3	BJ042040	BJ042040 BJ042040	191	13	723	6	CD803412	CD803412
119	13	596	1	AM741393	AM741393 ur54d01.x	192	13	723	7	CO529627	CO529627
120	13	596	8	CX418758	CX418758 JGI_XZG65	193	13	725	9	BZ337062	BZ337062
121	13	600	8	BZ892284	BZ892284 Hm2_0179.	194	13	726	9	CL708094	CL708094
122	13	601	5	BU400278	BU400278 64139591	195	13	730	5	BW784120	BW784120
123	13	602	1	AI133308	AI133308 HAI1910.Hu	196	13	730	9	BH385439	BH385439
124	13	602	11	DR512121	DR512121 Danilo Ter	197	13	730	10	CM015366	CM015366
125	13	606	3	BI393321	BI393321 PGPIn.pko	198	13	734	10	AG183248	AG183248
126	13	609	1	AL679884	AL679884 AL679884	199	13	736	9	AQ290167	AQ290167
127	13	609	10	CM483909	CM483909 fdbb001f2	200	13	739	8	DR813790	DR813790
128	13	610	10	CG525263	CG525263 CGXCN41TV	201	13	740	7	CN727123	CN727123
129	13	611	9	AQ543601	AQ543601 RPCI-11-3	202	13	740	8	CM454978	CM454978
130	13	614	10	CM201410	CM201410 104_627.1	203	13	740	10	CZ781676	CZ781676
131	13	616	10	CZ630710	CZ630710 OM_Ba017	204	13	742	9	BZ085699	BZ085699
132	13	616	10	CZ708893	CZ708893 OM_Ba002	205	13	742	10	CZ846109	CZ846109
133	13	616	10	CL464626	CL464626 OR_CBA006	206	13	744	8	DR970990	DR970990
134	13	617	3	BI347827	BI347827 de48f09.x	207	13	744	10	BZ362590	BZ362590
135	13	619	9	CC141398	CC141398 NDU.14021	208	13	745	10	CL770586	CL770586
136	13	620	7	CO524641	CO524641 3530.1.16	209	13	745	11	BZ003839	BZ003839
137	13	620	10	CL162015	CL162015 104_354.1	210	13	745	11	CM830386	CM830386
138	13	627	7	CO975415	CO975415 B6G0N16B	211	13	747	7	CO527731	CO527731
139	13	631	1	AI774062	AI774062 BSR255162	212	13	749	8	DR798727	DR798727
140	13	631	1	AM476684	AM476684 uc81c03.y	213	13	753	5	CZ764403	CZ764403
141	13	632	3	BM605111	BM605111 170006870	214	13	753	5	BU296068	BU296068
142	13	636	9	CC059056	CC059056 1118f09.b	215	13	755	9	BH055256	BH055256
143	13	637	10	CM309193	CM309193 104_797.1	216	13	758	8	BH519128	BH519128
144	13	640	7	CA199614	CA199614 SCRFEL103	217	13	759	8	DR956314	DR956314
145	13	640	7	CK144466	CK144466 3530.1.11	218	13	769	10	CL865497	CL865497
146	13	642	2	BG292260	BG292260 602366707	219	13	770	7	CO518704	CO518704
147	13	642	9	CC335534	CC335534 OGUCAS0TH	220	13	770	7	CO511663	CO511663
148	13	646	10	AG975145	AG975145 Drosophila	221	13	774	9	CC906501	CC906501
149	13	651	3	BJ123372	BJ123372 BJ123372	222	13	777	10	CM832821	CM832821
150	13	651	10	CL834896	CL834896 OR_CBA005	223	13	778	7	CN324854	CN324854
151	13	652	10	CZ2440024	CZ2440024 AIAA-aag3	224	13	780	7	CK603293	CK603293
152	13	657	7	CV611970	CV611970 L_Ai-aa0	225	13	780	7	CO521217	CO521217
153	13	659	8	CX233841	CX233841 MEM14919	226	13	781	7	CO521217	CO521217
154	13	659	8	CX930272	CX930272 JGI_CAA07	227	13	781	10	CG439299	CG439299
155	13	660	3	BM064027	BM064027 KS01062C0	228	13	785	8	DR792703	DR792703
156	13	661	9	BH681509	BH681509 BQGRP407F	229	13	785	8	DR958676	DR958676
157	13	662	10	CL190555	CL190555 104_408.1	230	13	789	9	BH54570	BH54570
158	13	664	3	BJ769134	BJ769134 BJ769134	231	13	792	11	CR216292	CR216292
159	13	667	9	AQ159092	AQ159092 nbxb0012P	232	13	792	11	CR216292	CR216292
160	13	669	6	CB554423	CB554423 MMSPP0024	233	13	793	7	CO524137	CO524137
161	13	670	6	CA067268	CA067268 SCFAD0101	234	13	794	11	CM033039	CM033039
162	13	675	10	CM657296	CM657296 rt47906.y	235	13	797	10	CR200005	CR200005
163	13	676	10	CM229382	CM229382 104_670.1	236	13	799	8	DR955033	DR955033
164	13	682	10	CL830859	CL830859 OR_CBA005	237	13	804	8	DR804046	DR804046
165	13	683	3	BI650943	BI650943 603297273	238	13	806	10	CZ871318	CZ871318
166	13	686	3	BJ661351	BJ661351 BJ661351	239	13	810	8	DR802647	DR802647
167	13	687	10	AG329549	AG329549 MMS mubcu	240	13	811	8	CM839154	CM839154
168	13	687	10	AG329549	AG329549 MMS mubcu	241	13	811	8	CM839154	CM839154



C 242	13	92.9	811	8	DR968237	ZM	BRP008	DR968237	ZM	BRP008	315	12.4	88.6	188	1	AA218591
C 243	13	92.9	813	6	CF676734	CCAD766TR		CF676734	CCAD766TR		316	12.4	88.6	191	3	BM288010
C 244	13	92.9	813	6	CF924665	JG1 CAANI		CF924665	JG1 CAANI		317	12.4	88.6	195	6	CB337879
C 245	13	92.9	816	8	CK020327	BST938646		CK020327	BST938646		318	12.4	88.6	197	8	DN845077
C 246	13	92.9	817	8	DR965755	ZM	BRP008	DR965755	ZM	BRP008	319	12.4	88.6	202	7	DN845077
C 247	13	92.9	818	9	BH529662	BOGR487P		BH529662	BOGR487P		320	12.4	88.6	205	8	DN898745
C 248	13	92.9	819	5	BU251499	603402852		BU251499	603402852		321	12.4	88.6	205	10	CG018573
C 249	13	92.9	819	6	CF681181	CCAD555TR		CF681181	CCAD555TR		322	12.4	88.6	208	7	CG185737
C 250	13	92.9	819	7	CO521506	3530.1.14		CO521506	3530.1.14		323	12.4	88.6	209	4	AX181678
C 251	13	92.9	821	8	DR815170	ZM	BRP004	DR815170	ZM	BRP004	324	12.4	88.6	213	9	BZ263398
C 252	13	92.9	824	9	AQ362718	ndxb0050D		AQ362718	ndxb0050D		325	12.4	88.6	215	7	CV368695
C 253	13	92.9	827	10	CL696141	PR1018D	B	CL696141	PR1018D	B	326	12.4	88.6	223	3	BI470080
C 254	13	92.9	832	8	BI465005	603206401		BI465005	603206401		327	12.4	88.6	228	1	AJ685525
C 255	13	92.9	835	10	CG326915	JG1 CAANI		CG326915	JG1 CAANI		328	12.4	88.6	229	3	BM085146
C 256	13	92.9	835	10	CG315519	AAIA-aac7		CG315519	AAIA-aac7		329	12.4	88.6	231	6	CF650225
C 257	13	92.9	835	10	CG315519	AAIA-aac7		CG315519	AAIA-aac7		330	12.4	88.6	235	2	BB539355
C 258	13	92.9	837	11	CG315519	AAIA-aac7		CG315519	AAIA-aac7		331	12.4	88.6	238	2	BB584088
C 259	13	92.9	837	11	CG315519	AAIA-aac7		CG315519	AAIA-aac7		332	12.4	88.6	240	7	CR766177
C 260	13	92.9	839	7	CO521859	3530.1.14		CO521859	3530.1.14		333	12.4	88.6	241	10	CL221923
C 261	13	92.9	841	8	DR972051	ZM	BRP009	DR972051	ZM	BRP009	334	12.4	88.6	245	7	CK740234
C 262	13	92.9	842	8	DR970169	ZM	BRP009	DR970169	ZM	BRP009	335	12.4	88.6	248	6	CA966779
C 263	13	92.9	846	8	DR801499	ZM	BRP002	DR801499	ZM	BRP002	336	12.4	88.6	250	10	CL534767
C 264	13	92.9	847	8	DR785242	ZM	BRP000	DR785242	ZM	BRP000	337	12.4	88.6	254	7	CK103504
C 265	13	92.9	848	7	CO389091	AGENCOURT		CO389091	AGENCOURT		338	12.4	88.6	255	7	CK051332
C 266	13	92.9	857	8	CK668188	UCRCPOL.0		CK668188	UCRCPOL.0		339	12.4	88.6	256	6	CB369744
C 267	13	92.9	859	7	CM167308	AGENCOURT		CM167308	AGENCOURT		340	12.4	88.6	257	8	CK535926
C 268	13	92.9	860	5	BU177009	AGENCOURT		BU177009	AGENCOURT		341	12.4	88.6	257	11	CR161926
C 269	13	92.9	867	8	DR806905	ZM	BRP003	DR806905	ZM	BRP003	342	12.4	88.6	258	8	NB1469
C 270	13	92.9	868	8	DR821233	ZM	BRP006	DR821233	ZM	BRP006	343	12.4	88.6	259	1	AM126779
C 271	13	92.9	871	8	DR802784	ZM	BRP002	DR802784	ZM	BRP002	344	12.4	88.6	261	8	CK535972
C 272	13	92.9	874	10	AG154151	Pan trogl		AG154151	Pan trogl		345	12.4	88.6	261	5	CK535972
C 273	13	92.9	876	8	DR970603	ZM	BRP006	DR970603	ZM	BRP006	346	12.4	88.6	265	5	BM585631
C 274	13	92.9	879	8	DR824819	ZM	BRP006	DR824819	ZM	BRP006	347	12.4	88.6	269	10	CG807449
C 275	13	92.9	879	8	DR824819	ZM	BRP006	DR824819	ZM	BRP006	348	12.4	88.6	270	7	CO060744
C 276	13	92.9	893	9	BZ083437	ZM	BRP006	BZ083437	ZM	BRP006	349	12.4	88.6	270	7	CO060744
C 277	13	92.9	895	6	CA792343	AGENCOURT		CA792343	AGENCOURT		350	12.4	88.6	272	8	CK535880
C 278	13	92.9	898	8	DR803425	ZM	BRP002	DR803425	ZM	BRP002	351	12.4	88.6	274	2	BE980274
C 279	13	92.9	905	10	CG376614	QGC181TV		CG376614	QGC181TV		352	12.4	88.6	278	3	BJ971944
C 280	13	92.9	910	8	DR811586	ZM	BRP003	DR811586	ZM	BRP003	353	12.4	88.6	281	3	BM276570
C 281	13	92.9	912	10	CL969851	OBIFCC019		CL969851	OBIFCC019		354	12.4	88.6	283	10	CL167906
C 282	13	92.9	935	5	BY717171	BY717171		BY717171	BY717171		355	12.4	88.6	286	2	BI122262
C 283	13	92.9	940	5	CC636808	OGCAD66TV		CC636808	OGCAD66TV		356	12.4	88.6	286	5	BM559123
C 284	13	92.9	945	10	CGN018CA	AL145547	Anopheles	AL145547	Anopheles		357	12.4	88.6	290	5	BK612537
C 285	13	92.9	963	8	DR746441	AL1	ABCAL	DR746441	AL1	ABCAL	358	12.4	88.6	292	4	CGN09390
C 286	13	92.9	984	5	BU555403	603475821		BU555403	603475821		359	12.4	88.6	292	9	CC466433
C 287	13	92.9	987	5	CC656779	OGCAD66TV		CC656779	OGCAD66TV		360	12.4	88.6	296	9	BZ522723
C 288	13	92.9	989	1	AL539502	AL539502		AL539502	AL539502		361	12.4	88.6	299	4	AK218365
C 289	13	92.9	989	8	DN789023	90943487		DN789023	90943487		362	12.4	88.6	300	8	DN220438
C 290	13	92.9	1004	8	DR747906	H07	ABECS	DR747906	H07	ABECS	363	12.4	88.6	302	3	BI307181
C 291	13	92.9	1024	10	CGN018CA	AL148728	Anopheles	AL148728	Anopheles		364	12.4	88.6	304	5	BM522436
C 292	13	92.9	1029	9	AF300877	AF300877		AF300877	AF300877		365	12.4	88.6	306	2	BR847076
C 293	13	92.9	1053	2	BF208273	601871387		BF208273	601871387		366	12.4	88.6	306	2	BB556479
C 294	13	92.9	1097	7	CR754129	CR754129		CR754129	CR754129		367	12.4	88.6	306	6	CF425710
C 295	13	92.9	1169	2	BG719984	602691342		BG719984	602691342		368	12.4	88.6	307	1	AJ976791
C 296	13	92.9	1236	10	AJ857805	AAIA-aac7		AJ857805	AAIA-aac7		369	12.4	88.6	307	8	D22632
C 297	13	92.9	1280	1	AW730293	GA	BA001	AW730293	GA	BA001	370	12.4	88.6	310	10	CM463769
C 298	13	92.9	1686	10	AG076369	Pan trogl		AG076369	Pan trogl		371	12.4	88.6	311	7	CV220788
C 299	13	92.9	2238	7	AW729508	AW729508		AW729508	AW729508		372	12.4	88.6	313	7	CK720865
C 300	13	92.9	2557	7	CK402923	ALF ifinc		CK402923	ALF ifinc		373	12.4	88.6	317	4	CGN09445
C 301	12.4	88.6	105	6	CF643293	D65	A09 F	CF643293	D65	A09 F	374	12.4	88.6	317	7	CGN566426
C 302	12.4	88.6	110	1	AM671409	I61	343 B	AM671409	I61	343 B	375	12.4	88.6	317	8	CK535810
C 303	12.4	88.6	137	10	CZ757399	PMO-OT001		CZ757399	PMO-OT001		376	12.4	88.6	320	5	CK535863
C 304	12.4	88.6	142	7	CV362370	PMO-OT001		CV362370	PMO-OT001		377	12.4	88.6	325	8	BM548841
C 305	12.4	88.6	150	6	CB091797	he96f05.9		CB091797	he96f05.9		378	12.4	88.6	328	8	CV784671
C 306	12.4	88.6	153	3	DN840183	KECB21-37		DN840183	KECB21-37		379	12.4	88.6	329	7	CC002282
C 307	12.4	88.6	158	3	BO335911	PM3-MT020		BO335911	PM3-MT020		380	12.4	88.6	329	7	CC002282
C 308	12.4	88.6	160	1	AA954856	0020B01.8		AA954856	0020B01.8		381	12.4	88.6	329	10	CM117036
C 309	12.4	88.6	166	10	CG816903	SOVETH2TH		CG816903	SOVETH2TH		382	12.4	88.6	332	7	BM567926
C 310	12.4	88.6	168	8	DN158682	CGW04E01		DN158682	CGW04E01		383	12.4	88.6	334	5	BM567926
C 311	12.4	88.6	170	8	DR041915	NLE000001		DR041915	NLE000001		384	12.4	88.6	335	7	CGN566084
C 312	12.4	88.6	172	1	AW308559	SMOV3MCM		AW308559	SMOV3MCM		385	12.4	88.6	336	3	BM189211
C 313	12.4	88.6	173	2	BF918218	SMOV3MCM		BF918218	SMOV3MCM		386	12.4	88.6	336	3	BM189211
C 314	12.4	88.6	187	2	BF048594	db74D07.y		BF048594	db74D07.y		387	12.4	88.6	336	7	CO286728

388	12.4	88.6	337	7	CO304991	CO304991	EXK46852.	C 461	12.4	88.6	394	6	CH257259	CH257259
389	12.4	88.6	338	7	CN550823	CN550823	radslh10.	C 462	12.4	88.6	397	5	BY095195	BY095195
C 390	12.4	88.6	338	8	CX535866	CX535866	TUASLWMSU	C 463	12.4	88.6	398	4	CNS09978	CNS09978
391	12.4	88.6	338	8	Z21204	Z21204	HSAAADSWX.T	C 464	12.4	88.6	399	3	BT779784	BT779784
C 392	12.4	88.6	341	2	BG464315	BG464315	EMI_72.CO	C 465	12.4	88.6	400	1	ALJ64555	ALJ64555
393	12.4	88.6	341	2	CN200310	CN200310	D26 O. ma	C 466	12.4	88.6	400	1	AW790558	AW790558
394	12.4	88.6	343	8	N82523	N82523	TGSESTZY5540	C 467	12.4	88.6	400	3	BM604064	BM604064
C 395	12.4	88.6	344	3	BM648661	BM648661	170006873	C 468	12.4	88.6	401	3	BO169735	BO169735
C 396	12.4	88.6	345	3	CR546336	CR546336	DKEPZ459M	C 469	12.4	88.6	401	6	CD225492	CD225492
C 397	12.4	88.6	345	8	CX535940	CX535940	TUASLWMSU	C 470	12.4	88.6	402	1	CC063995	CC063995
C 398	12.4	88.6	347	10	CL536257	CL536257	trldp16x1	C 471	12.4	88.6	403	1	AJ7844102	AJ7844102
C 399	12.4	88.6	348	1	AM256101	AM256101	687062B08	C 472	12.4	88.6	403	2	BG464116	BG464116
C 400	12.4	88.6	348	8	CX535885	CX535885	TUASLWMSU	C 473	12.4	88.6	405	8	CX535823	CX535823
C 401	12.4	88.6	349	7	CN966821	CN966821	16318.123	C 474	12.4	88.6	405	8	DN479285	DN479285
C 402	12.4	88.6	351	8	CX535867	CX535867	TUASLWMSU	C 475	12.4	88.6	406	9	AZ213929	AZ213929
C 403	12.4	88.6	353	5	BY024392	BY024392	AL64392	C 476	12.4	88.6	407	8	DN929781	DN929781
C 404	12.4	88.6	354	11	TA119H09P	TA119H09P	AL64392	C 477	12.4	88.6	407	10	CN808876	CN808876
C 405	12.4	88.6	355	2	BF463462	BF463462	UI-M-CGDP	C 478	12.4	88.6	408	1	AL161133	AL161133
C 406	12.4	88.6	355	7	CO190626	CO190626	EXK048859.	C 479	12.4	88.6	408	9	BH528248	BH528248
C 407	12.4	88.6	356	8	DR828194	DR828194	ZM.BPB007	C 480	12.4	88.6	409	7	CN776388	CN776388
C 408	12.4	88.6	357	10	CN809639	CN809639	pine_4303	C 481	12.4	88.6	410	1	AM509808	AM509808
C 409	12.4	88.6	358	8	CX535982	CX535982	TUASLWMSU	C 482	12.4	88.6	412	1	AI975177	AI975177
C 410	12.4	88.6	359	2	BE245283	BE245283	TCBAP1E24	C 483	12.4	88.6	415	7	CN569386	CN569386
C 411	12.4	88.6	361	1	AV706346	AV706346	AV706346	C 484	12.4	88.6	416	5	BX466497	BX466497
C 412	12.4	88.6	361	4	CNS08028	CNS08028	single.re	C 485	12.4	88.6	417	9	CC679563	CC679563
C 413	12.4	88.6	362	1	AI975815	AI975815	EST270409	C 486	12.4	88.6	418	5	AM261294	AM261294
C 414	12.4	88.6	362	6	CA235406	CA235406	SCCFL409	C 487	12.4	88.6	418	5	BY275905	BY275905
C 415	12.4	88.6	364	7	CN922920	CN922920	pJfmgc_01	C 488	12.4	88.6	418	8	DR706064	DR706064
C 416	12.4	88.6	365	7	CN569197	CN569197	rad46609.	C 489	12.4	88.6	420	3	BM040290	BM040290
C 417	12.4	88.6	367	7	CV220789	CV220789	EST804699	C 490	12.4	88.6	421	3	BM697934	BM697934
C 418	12.4	88.6	368	7	CO962577	CO962577	BEI120N30	C 491	12.4	88.6	421	6	CD685508	CD685508
C 419	12.4	88.6	368	8	U38007	U38007	OSU8007.FD	C 492	12.4	88.6	421	9	CN941969	CN941969
C 420	12.4	88.6	369	2	BE187748	BE187748	CRC03-R	C 493	12.4	88.6	421	7	AZ409243	AZ409243
C 421	12.4	88.6	370	6	CA194482	CA194482	SCRFBI02	C 494	12.4	88.6	421	9	BP393397	BP393397
C 422	12.4	88.6	371	7	CO289065	CO289065	EKO70022.	C 495	12.4	88.6	423	2	AO640950	AO640950
C 423	12.4	88.6	372	6	CA940071	CA940071	ru77c12.Y	C 496	12.4	88.6	424	1	AI850762	AI850762
C 424	12.4	88.6	373	5	BY071167	BY071167	BY071167	C 497	12.4	88.6	425	1	DR440172	DR440172
C 425	12.4	88.6	373	7	CV468199	CV468199	eat_1.yan	C 498	12.4	88.6	425	8	CZ489167	CZ489167
C 426	12.4	88.6	374	10	CG177987	CG177987	PUID044TB	C 499	12.4	88.6	425	10	BM368934	BM368934
C 427	12.4	88.6	374	9	AZ404909	AZ404909	IM0173M16	C 500	12.4	88.6	426	3	U92742	U92742
C 428	12.4	88.6	375	5	BM583165	BM583165	BM583165	C 501	12.4	88.6	426	7	CN550735	CN550735
C 429	12.4	88.6	375	7	CO756306	CO756306	MDfrc1047	C 502	12.4	88.6	427	8	CV266051	CV266051
C 430	12.4	88.6	378	10	CL975272	CL975272	OIFPC037	C 503	12.4	88.6	427	7	CV266051	CV266051
C 431	12.4	88.6	379	9	BZ235623	BZ235623	CH230-518	C 504	12.4	88.6	427	8	CX535962	CX535962
C 432	12.4	88.6	380	5	BY278800	BY278800	BI278800	C 505	12.4	88.6	428	1	AM041704	AM041704
C 433	12.4	88.6	380	7	CN922432	CN922432	000410AEL	C 506	12.4	88.6	428	7	AM184453	AM184453
C 434	12.4	88.6	381	9	BH880873	BH880873	hv21f11.b	C 507	12.4	88.6	428	9	AZ852820	AZ852820
C 435	12.4	88.6	382	8	BM030426	BM030426	9494796.MA	C 508	12.4	88.6	430	1	AM312991	AM312991
C 436	12.4	88.6	382	8	DR432127	DR432127	max52d02.	C 509	12.4	88.6	432	1	CC529992	CC529992
C 437	12.4	88.6	385	5	BM578149	BM578149	BM578149	C 510	12.4	88.6	432	9	CX535929	CX535929
C 438	12.4	88.6	386	7	CN896612	CN896612	010629MAZ	C 511	12.4	88.6	433	8	BM498281	BM498281
C 439	12.4	88.6	386	7	CV468467	CV468467	eat_1.yan	C 512	12.4	88.6	435	3	BJ322083	BJ322083
C 440	12.4	88.6	386	9	AZ488442	AZ488442	IM0318A14	C 513	12.4	88.6	436	6	CA713705	CA713705
C 441	12.4	88.6	388	3	BM133039	BM133039	TGSESTYB1	C 514	12.4	88.6	437	1	AM124654	AM124654
C 442	12.4	88.6	388	3	BM133039	BM133039	TGSESTYB1	C 515	12.4	88.6	437	7	CR628549	CR628549
C 443	12.4	88.6	388	3	CB779386	CB779386	AGMSTNC.N	C 516	12.4	88.6	437	7	CR628549	CR628549
C 444	12.4	88.6	389	3	BP822136	BP822136	BP822136	C 517	12.4	88.6	437	10	AG318763	AG318763
C 445	12.4	88.6	390	1	AV801914	AV801914	AV801914	C 518	12.4	88.6	437	10	AG318763	AG318763
C 446	12.4	88.6	390	6	CA287929	CA287929	SCSFS206	C 519	12.4	88.6	440	5	BM573435	BM573435
C 447	12.4	88.6	390	6	CV939194	CV939194	PMrPcC.06	C 520	12.4	88.6	440	5	BM573435	BM573435
C 448	12.4	88.6	391	3	BP942219	BP942219	BP942219	C 521	12.4	88.6	441	8	DR064446	DR064446
C 449	12.4	88.6	391	9	CC872892	CC872892	NDL.101A8	C 522	12.4	88.6	442	3	BM149024	BM149024
C 450	12.4	88.6	392	6	CA278343	CA278343	SCSFS203	C 523	12.4	88.6	442	6	CB001278	CB001278
C 451	12.4	88.6	392	6	CA278343	CA278343	SCSFS203	C 524	12.4	88.6	442	6	CR644661	CR644661
C 452	12.4	88.6	392	10	CL184392	CL184392	CL184392	C 525	12.4	88.6	443	8	CN961370	CN961370
C 453	12.4	88.6	393	3	BI487648	BI487648	gC68C09.Y	C 526	12.4	88.6	443	8	CX535889	CX535889
C 454	12.4	88.6	393	5	CA24870	CA24870	R1C6	C 527	12.4	88.6	443	8	CX535922	CX535922
C 455	12.4	88.6	393	6	CB192267	CB192267	py27b01.Y	C 528	12.4	88.6	443	8	CX535970	CX535970
C 456	12.4	88.6	393	6	CB777267	CB777267	AMGNTNC:N	C 529	12.4	88.6	445	2	BF728957	BF728957
C 457	12.4	88.6	393	7	CD479790	CD479790	eca01-22m	C 530	12.4	88.6	445	2	BF728957	BF728957
C 458	12.4	88.6	393	6	CN241339	CN241339	EST007205	C 531	12.4	88.6	450	1	AA152278	AA152278
C 459	12.4	88.6	393	8	CX535967	CX535967	TUASLWMSU	C 532	12.4	88.6	450	1	AL910478	AL910478
C 460	12.4	88.6	394	4	CNS08KM3	CNS08KM3	single.re	C 533	12.4	88.6	450	1	AM097551	AM097551

CB257259 37-B01166  
BY095195 BY095195  
BX056748 single.re  
BT779784 BEM05.SQ  
ALJ64555 ALJ64555  
AM790558 D000377R  
BM604064 170006870  
BO169735 WHE0965.G  
CD225492 CCG1.3.CO  
CC063995 fCma003d0  
AJ7844102 AJ3B-AAT-  
BG464116 EMI\_69.HO  
CX535823 TUASLWMSU  
DN479285 altx014xk  
AZ213929 sheared.D  
DN929781 4155467.B  
CN808876 pinea.324  
AL161133 ea73e03.Y  
BH528248 BOHOA497F  
CN776388 cae80e05.  
AM509808 ga5H04.Y  
AI975177 EST269771  
CN569386 rad43h03.  
BX466497 EA466497  
CC679563 OGA2767V  
AM261294 687076F03  
BY275905 BY275905  
CV982135 UMC-Bmix  
DR706064 Aen.06391  
BO040290 gd13h06.Y  
BM697934 BEm07.gO  
CD685508 BST2029.h  
CN941969 010917AVB  
AZ409243 IM0180A21  
BF393397 UI-R-CAO-  
AO640950 927P1-3A8  
AI850762 UI-M-BG1-  
DR440172 BST149.13  
CZ489167 f06461-3P  
BM368934 BEm07.SQ  
U92742 BST.116.Bco  
CN550735 rad49e06.  
CV266051 WS02028.B  
CX535962 TUASLWMSU  
AM041704 104.275-1  
AV424703 AY424703  
CN618453 TGESTYm1  
AZ852820 2M015SK05  
AM312991 BMOV3MCAM  
CC529992 CH240\_406  
CX535929 TUASLWMSU  
BZ498281 BONEB22TR  
BJ322083 BJ322083  
CA713705 Wdk3C.pK0  
AM124654 UI-M-BH2.  
CR628549 DKEPZ4591  
AG318763 f8bd001fO  
AG914085 Drooboph11  
BM573435 BM573435  
AJ827215 Drooboph11  
DR064446 1P72B05.9  
BM149024 TCAPAE61  
CB001278 VVB005C04  
CR644661 K24.B09.F  
CN961370 887D\_1002  
CX535889 TUASLWMSU  
CX535922 TUASLWMSU  
CX535970 TUASLWMSU  
CF646747 3530.1.32  
BF728957 1000065G1  
AA152278 mp74C07.f  
AL910478 AL910478  
AM097551 tr46b08.Y

534	12.4	88.6	451	1	AM678429	WS1_15_B0	607	12.4	88.6	489	6	CB620092	CB620092	OSIIRA05A
535	12.4	88.6	451	3	BP953093	BP953093	608	12.4	88.6	489	6	CD812768	CD812768	BN10_023P
536	12.4	88.6	452	1	AM180544	AM180544	609	12.4	88.6	489	8	DR063883	DR063883	1p71d05.g
537	12.4	88.6	452	2	BR452931	BR452931	610	12.4	88.6	489	9	AZ952539	AZ952539	2M0217121
538	12.4	88.6	452	2	BG278241	BG278241	611	12.4	88.6	489	11	TA2440H2Q	TA2440H2Q	bruce1
539	12.4	88.6	454	2	CNS096K8	EX044580 Single re	612	12.4	88.6	490	7	CO723413	CO723413	Mdbb5002j
540	12.4	88.6	454	6	CA683287	CA683287	613	12.4	88.6	490	5	AC0902188	AC0902188	LMARJVL_1
541	12.4	88.6	454	6	CB191541	CB191541	614	12.4	88.6	491	5	CNS09984	CNS09984	BM309984
542	12.4	88.6	455	1	AUI13853	AUI13853	615	12.4	88.6	491	7	CNS60887	CNS60887	taf83c04.
543	12.4	88.6	455	7	CO313690	CO313690	616	12.4	88.6	492	3	BE768197	BE768197	BM168197
544	12.4	88.6	455	7	CR546380	CR546380	617	12.4	88.6	493	2	BE768197	BE768197	MY-19-E-0
545	12.4	88.6	455	11	CR498212	CR498212	618	12.4	88.6	494	1	AJ6680262	AJ6680262	BM033047
546	12.4	88.6	456	1	AJ683384	AJ683384	619	12.4	88.6	494	3	BM033047	BM033047	h62d033.y
547	12.4	88.6	456	1	AM620580	AM620580	620	12.4	88.6	495	2	BM032611	BM032611	AC962221
548	12.4	88.6	456	5	BU332428	BU332428	621	12.4	88.6	495	2	BM369191	BM369191	LERGB08TF
549	12.4	88.6	456	9	AZ916672	AZ916672	622	12.4	88.6	495	7	CO520798	CO520798	BM26355
550	12.4	88.6	457	1	AL910479	AL910479	623	12.4	88.6	496	5	BU339231	BU339231	604145103
551	12.4	88.6	457	6	CD229653	CD229653	624	12.4	88.6	496	5	AC962221	AC962221	BI583362
552	12.4	88.6	457	7	CN241794	CN241794	625	12.4	88.6	497	3	BI583362	BI583362	RH21959.5
553	12.4	88.6	457	10	CZ151873	CZ151873	626	12.4	88.6	498	9	AZ803232	AZ803232	2M0633G04
554	12.4	88.6	458	1	AI944441	AI944441	627	12.4	88.6	498	9	BM26355	BM26355	1006313P1
555	12.4	88.6	458	1	AM678428	AM678428	628	12.4	88.6	499	2	BG465821	BG465821	RH122_45
556	12.4	88.6	458	6	CA704082	CA704082	629	12.4	88.6	499	2	BE498706	BE498706	WHE0965_G
557	12.4	88.6	459	1	AV391824	AV391824	630	12.4	88.6	499	4	CNS091LY	CNS091LY	Single re
558	12.4	88.6	459	6	CA584142	CA584142	631	12.4	88.6	499	11	CR211283	CR211283	Reverse s
559	12.4	88.6	460	3	BM534122	BM534122	632	12.4	88.6	500	3	BI195422	BI195422	RST70016
560	12.4	88.6	461	3	BI569021	BI569021	633	12.4	88.6	500	6	CA110921	CA110921	wdx2c.pk0
561	12.4	88.6	461	6	CD229678	CD229678	634	12.4	88.6	500	6	CNS61268	CNS61268	taf80h08.
562	12.4	88.6	463	5	BY560253	BY560253	635	12.4	88.6	500	11	TA94B01Q	TA94B01Q	bruce1
563	12.4	88.6	463	8	CN910725	CN910725	636	12.4	88.6	501	6	CA099463	CA099463	SCURFL603
564	12.4	88.6	463	8	DN972346	DN972346	637	12.4	88.6	501	1	AM476659	AM476659	GA38B08.Y
565	12.4	88.6	464	8	CX593005	CX593005	638	12.4	88.6	502	1	CB865195	CB865195	NL17_H07
566	12.4	88.6	464	10	CM739878	CM739878	639	12.4	88.6	502	6	CB333926	CB333926	EL01N0316
567	12.4	88.6	465	7	CK035932	CK035932	640	12.4	88.6	502	8	CB041291	CB041291	gd20C03.Y
568	12.4	88.6	468	6	CD736149	CD736149	641	12.4	88.6	503	1	AI438438	AI438438	486006A12
569	12.4	88.6	468	6	CF599032	CF599032	642	12.4	88.6	503	9	AT138438	AT138438	SCERFL403
570	12.4	88.6	468	7	CN891632	CN891632	643	12.4	88.6	503	6	CB222793	CB222793	SCERFL403
571	12.4	88.6	468	7	AM000587	AM000587	644	12.4	88.6	503	6	CB222793	CB222793	12B22029
572	12.4	88.6	471	6	CF079914	CF079914	645	12.4	88.6	503	6	CB295107	CB295107	BT162386
573	12.4	88.6	471	6	QK8A18.Y	QK8A18.Y	646	12.4	88.6	504	3	BM041291	BM041291	gd20C03.Y
574	12.4	88.6	472	3	BM634390	BM634390	647	12.4	88.6	504	7	CNS68692	CNS68692	taf96e05.
575	12.4	88.6	472	3	BQ088433	BQ088433	648	12.4	88.6	504	8	CX535829	CX535829	TUASLWMSu
576	12.4	88.6	472	3	CN244510	CN244510	649	12.4	88.6	504	9	BM032189	BM032189	LMARJVL_1
577	12.4	88.6	473	3	BM601956	BM601956	650	12.4	88.6	505	3	BM032189	BM032189	kh60906.Y
578	12.4	88.6	473	3	CD220332	CD220332	651	12.4	88.6	505	6	CF015164	CF015164	QBL21H01.
579	12.4	88.6	473	6	CD220332	CD220332	652	12.4	88.6	505	6	AC0209308	AC0209308	HS_3237_B
580	12.4	88.6	473	7	CN659372	CN659372	653	12.4	88.6	506	2	BE481549	BE481549	167048_BA
581	12.4	88.6	475	5	BM913534	BM913534	654	12.4	88.6	506	6	CD223335	CD223335	CCCL_26_B
582	12.4	88.6	475	10	EX698630	EX698630	655	12.4	88.6	506	6	CB239184	CB239184	TG8STZY5
583	12.4	88.6	476	7	CK593625	CK593625	656	12.4	88.6	507	8	CB538537	CB538537	TUASLWMSu
584	12.4	88.6	476	9	BZ164075	BZ164075	657	12.4	88.6	507	10	CL920847	CL920847	Reverse s
585	12.4	88.6	478	2	BF393562	BF393562	658	12.4	88.6	507	11	CR127183	CR127183	BU758071
586	12.4	88.6	479	2	BG355564	BG355564	659	12.4	88.6	508	3	BM361126	BM361126	BM361126
587	12.4	88.6	479	7	CF928552	CF928552	660	12.4	88.6	508	9	CR897951	CR897951	AO232B04-
588	12.4	88.6	479	7	CNS66990	CNS66990	661	12.4	88.6	508	7	BH260596	BH260596	CH230-75E
589	12.4	88.6	480	7	BM669010	BM669010	662	12.4	88.6	509	6	CB416248	CB416248	SCAB_6341
590	12.4	88.6	480	7	CO309880	CO309880	663	12.4	88.6	509	6	AO661119	AO661119	Sheared D
591	12.4	88.6	481	8	DN851142	DN851142	664	12.4	88.6	510	1	AU140068	AU140068	AU140068
592	12.4	88.6	482	1	AI1530525	AI1530525	665	12.4	88.6	510	3	BM361126	BM361126	AO0490-R
593	12.4	88.6	482	1	AM123712	AM123712	666	12.4	88.6	511	6	CD224564	CD224564	CCCL_34_F
594	12.4	88.6	482	8	CN897580	CN897580	667	12.4	88.6	511	7	CY129430	CY129430	Mdbf600K
595	12.4	88.6	482	8	CX535904	CX535904	668	12.4	88.6	512	5	BQ809132	BQ809132	1030009B0
596	12.4	88.6	483	3	BM360227	BM360227	669	12.4	88.6	512	7	CO343904	CO343904	EP18326.3
597	12.4	88.6	484	7	AV643342	AV643342	670	12.4	88.6	513	10	CL534691	CL534691	tr1b012xp
598	12.4	88.6	486	7	CNS66263	CNS66263	671	12.4	88.6	513	8	CX535828	CX535828	TUASLWMSu
599	12.4	88.6	487	1	AM258138	AM258138	672	12.4	88.6	513	10	CM041621	CM041621	104_275_1
600	12.4	88.6	487	2	BG355443	BG355443	673	12.4	88.6	514	3	BM642224	BM642224	170006873
601	12.4	88.6	487	2	BM369291	BM369291	674	12.4	88.6	514	3	CN137199	CN137199	OX1_18_HI
602	12.4	88.6	487	8	CV952126	CV952126	675	12.4	88.6	515	6	CA232784	CA232784	SCRFL306
603	12.4	88.6	487	9	BH899362	BH899362	676	12.4	88.6	515	6	CD155416	CD155416	ML1_004IU
604	12.4	88.6	488	2	BF413852	BF413852	677	12.4	88.6	517	1	AM244188	AM244188	687050D10
605	12.4	88.6	489	1	AJ737889	AJ737889	678	12.4	88.6					
606	12.4	88.6	489	1	AJ737889	AJ737889	679	12.4	88.6					

C 680	12.4	88.6	517	6	CA214502	CA214502	SCURFL105	C 753	12.4	88.6	546	9	AQ048055	AQ048055	CLM-5a9-t
C 681	12.4	88.6	517	6	CA829247	CA829247	1114040E0	C 754	12.4	88.6	546	9	BZ656892	BZ656892	OGCCU68TM
C 682	12.4	88.6	518	7	BO164222	BO164222	10910107H0	C 755	12.4	88.6	547	3	BJS521139	BJS521139	BU521139
C 683	12.4	88.6	518	7	CK341281	CK341281	K0228E03-	C 756	12.4	88.6	547	7	CV013589	CV013589	TL001H02
C 684	12.4	88.6	518	7	CK371872	CK371872	1a120B11.	C 757	12.4	88.6	547	10	CM575138	CM575138	OA ABA010
C 685	12.4	88.6	518	7	AC0398309	AC0398309	mgx00017K	C 758	12.4	88.6	548	1	AW787862	AW787862	945704H08
C 686	12.4	88.6	519	6	BJ752012	BJ752012	CA274004	C 759	12.4	88.6	548	4	AY431329	AY431329	Aedex Reg
C 687	12.4	88.6	519	6	CA274004	CA274004	SCRLSD101	C 760	12.4	88.6	548	4	CA249126	CA249126	SCSBLFL110
C 688	12.4	88.6	519	8	CX664955	CX664955	db2revw0	C 761	12.4	88.6	548	6	CB099667	CB099667	py15d06.y
C 689	12.4	88.6	521	3	BJ505268	BJ505268	BM505268	C 762	12.4	88.6	548	6	CB099667	CB099667	OGQA519TH
C 690	12.4	88.6	521	3	BO340075	BO340075	MM4-NN119	C 763	12.4	88.6	548	9	CB689919	CB689919	RE74757.5
C 691	12.4	88.6	522	1	AU235114	AU235114	lad51f10.	C 764	12.4	88.6	549	3	BI580761	BI580761	RH26628.5
C 692	12.4	88.6	522	7	CK721684	CK721684	RIH22.60	C 765	12.4	88.6	549	3	BI587761	BI587761	py170227
C 693	12.4	88.6	523	6	BG487867	BG487867	SCMCP1500	C 766	12.4	88.6	549	6	CB191570	CB191570	py34a04.y
C 694	12.4	88.6	523	6	CA238099	CA238099	daa35c10.	C 767	12.4	88.6	549	6	CF597644	CF597644	NCEST3e01
C 695	12.4	88.6	524	2	BG264187	BG264187	BM192988	C 768	12.4	88.6	549	8	CV909566	CV909566	PE003E11
C 696	12.4	88.6	524	3	BU192988	BU192988	MD1x30249	C 769	12.4	88.6	550	2	BC103716	BC103716	Single re
C 697	12.4	88.6	524	7	CO752355	CO752355	TUASLW6SU	C 770	12.4	88.6	550	7	CV209016	CV209016	FTM003800
C 698	12.4	88.6	524	8	CX535959	CX535959	dp2revw0	C 771	12.4	88.6	550	6	CD378631	CD378631	DKF2P459F
C 699	12.4	88.6	524	8	CX864671	CX864671	yc96e09.r1	C 772	12.4	88.6	550	6	CD378631	CD378631	BS7688726
C 700	12.4	88.6	524	8	T78819	T78819	Branch108	C 773	12.4	88.6	550	7	CV209016	CV209016	PE025E10
C 701	12.4	88.6	524	11	DB019678	DB019678	leg17B05.	C 774	12.4	88.6	550	8	CV911329	CV911329	py2PCY.32
C 702	12.4	88.6	525	7	CN564423	CN564423	NAKPI2.01	C 775	12.4	88.6	550	8	CV962541	CV962541	fp23508.x
C 703	12.4	88.6	525	9	BZ895555	BZ895555	CCCL.28.B	C 776	12.4	88.6	551	2	BG883885	BG883885	km14_a272
C 704	12.4	88.6	527	6	CD223511	CD223511	BST007650	C 777	12.4	88.6	551	8	DN481950	DN481950	IM0438G13
C 705	12.4	88.6	528	9	CN241823	CN241823	fma00340	C 778	12.4	88.6	551	9	AZ612050	AZ612050	CCCL.37.G
C 706	12.4	88.6	528	9	CO663690	CO663690	BP262997	C 779	12.4	88.6	552	6	CD225046	CD225046	py2PCY.58
C 707	12.4	88.6	529	3	BP262997	BP262997	PR101444	C 780	12.4	88.6	552	8	CV961954	CV961954	Single re
C 708	12.4	88.6	530	10	CL636320	CL636320	PR101444	C 781	12.4	88.6	552	11	DR111145	DR111145	Single re
C 709	12.4	88.6	531	7	CN845976	CN845976	DFZPD459H	C 782	12.4	88.6	553	4	CNS09NKN	CNS09NKN	Single re
C 710	12.4	88.6	531	7	CR537496	CR537496	OVL.25.H0	C 783	12.4	88.6	553	4	CNS09NKN	CNS09NKN	Single re
C 711	12.4	88.6	532	2	BG047595	BG047595	PG112501	C 784	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 712	12.4	88.6	532	2	BG172501	BG172501	PG112501	C 785	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 713	12.4	88.6	532	2	BH772427	BH772427	PG112501	C 786	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 714	12.4	88.6	532	3	BJ752011	BJ752011	PG112501	C 787	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 715	12.4	88.6	532	7	CO392394	CO392394	PG112501	C 788	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 716	12.4	88.6	533	8	CV788778	CV788778	PG112501	C 789	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 717	12.4	88.6	533	11	TA315A020	TA315A020	PG112501	C 790	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 718	12.4	88.6	533	11	TA315A020	TA315A020	PG112501	C 791	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 719	12.4	88.6	534	3	BM743732	BM743732	PG112501	C 792	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 720	12.4	88.6	534	9	BZ732243	BZ732243	PG112501	C 793	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 721	12.4	88.6	535	3	BJ603162	BJ603162	PG112501	C 794	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 722	12.4	88.6	536	8	CV931712	CV931712	PG112501	C 795	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 723	12.4	88.6	536	8	BH387291	BH387291	PG112501	C 796	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 724	12.4	88.6	536	10	CZ306562	CZ306562	PG112501	C 797	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 725	12.4	88.6	536	11	CR147509	CR147509	PG112501	C 798	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 726	12.4	88.6	537	9	CV014734	CV014734	PG112501	C 799	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 727	12.4	88.6	537	9	AZ145267	AZ145267	PG112501	C 800	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 728	12.4	88.6	538	8	CV961982	CV961982	PG112501	C 801	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 729	12.4	88.6	539	6	CD227029	CD227029	PG112501	C 802	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 730	12.4	88.6	540	3	BI346270	BI346270	PG112501	C 803	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 731	12.4	88.6	540	6	CB295108	CB295108	PG112501	C 804	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 732	12.4	88.6	540	6	CB295108	CB295108	PG112501	C 805	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 733	12.4	88.6	540	9	AV299351	AV299351	PG112501	C 806	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 734	12.4	88.6	541	1	AV631565	AV631565	PG112501	C 807	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 735	12.4	88.6	541	7	CN563844	CN563844	PG112501	C 808	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 736	12.4	88.6	541	7	CN563844	CN563844	PG112501	C 809	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 737	12.4	88.6	543	2	BG696688	BG696688	PG112501	C 810	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 738	12.4	88.6	543	3	BO606154	BO606154	PG112501	C 811	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 739	12.4	88.6	543	3	DR064150	DR064150	PG112501	C 812	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 740	12.4	88.6	544	2	BG548151	BG548151	PG112501	C 813	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 741	12.4	88.6	544	2	BG548151	BG548151	PG112501	C 814	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 742	12.4	88.6	544	10	BZ511160	BZ511160	PG112501	C 815	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 743	12.4	88.6	544	10	AG919210	AG919210	PG112501	C 816	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 744	12.4	88.6	545	3	BO954996	BO954996	PG112501	C 817	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 745	12.4	88.6	545	6	CA143837	CA143837	PG112501	C 818	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 746	12.4	88.6	545	7	CNS66485	CNS66485	PG112501	C 819	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 747	12.4	88.6	545	7	CNS66485	CNS66485	PG112501	C 820	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 748	12.4	88.6	545	7	CO984897	CO984897	PG112501	C 821	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 749	12.4	88.6	545	8	CNS35953	CNS35953	PG112501	C 822	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 750	12.4	88.6	546	6	BU591453	BU591453	PG112501	C 823	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 751	12.4	88.6	546	6	CD219762	CD219762	PG112501	C 824	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re
C 752	12.4	88.6	546	7	CM909427	CM909427	PG112501	C 825	12.4	88.6	553	10	CNS09NKN	CNS09NKN	Single re

826	12.4	88.6	567	7	CN239033	EST004889	899	12.4	88.6	582	7	CN244773	EST010652
827	12.4	88.6	568	1	AM024855	AM024855	900	12.4	88.6	582	9	AO99555	RPCI-23-3
828	12.4	88.6	568	2	BE139318	BE139318	901	12.4	88.6	582	10	CL312785	mth2-126N
829	12.4	88.6	568	6	CF643871	ELI0N0432	902	12.4	88.6	583	3	BP200862	BP200862
830	12.4	88.6	568	6	CF642391	DS1_B04_F	903	12.4	88.6	583	3	BP336367	BP336367
831	12.4	88.6	568	8	CN249959	EST015880	904	12.4	88.6	583	3	BP353305	BP353305
832	12.4	88.6	568	7	CN562850	taef78a11.	905	12.4	88.6	583	3	BP362061	BP362061
833	12.4	88.6	568	8	CN897074	PA048H4.m	906	12.4	88.6	583	8	CV914265	CV914265
834	12.4	88.6	569	6	CD275020	CD275020	907	12.4	88.6	583	9	AO158861	AO158861
835	12.4	88.6	569	7	CN367867	taef78a103.	908	12.4	88.6	584	3	BP542502	BP542502
836	12.4	88.6	570	2	BG699547	602679252	909	12.4	88.6	584	3	BP217354	BP217354
837	12.4	88.6	570	6	CN50G039	CR713488	910	12.4	88.6	584	3	BP345209	BP345209
838	12.4	88.6	570	4	CN615783	AMGNVC:N	911	12.4	88.6	584	9	AZ212340	AZ212340
839	12.4	88.6	570	7	CV468538	est_1_van	912	12.4	88.6	585	6	CF619753	CF619753
840	12.4	88.6	571	6	CB335028	TC02H02R	913	12.4	88.6	586	2	BC646063	BC646063
841	12.4	88.6	571	6	CN614462	CN614462	914	12.4	88.6	586	2	BP607847	BP607847
842	12.4	88.6	571	7	CO613353	CO613353	915	12.4	88.6	586	3	BM361570	BM361570
843	12.4	88.6	572	5	BQ594687	DG9-124J8	916	12.4	88.6	586	3	BQ279493	BQ279493
844	12.4	88.6	572	5	BQ784111	BO784111	917	12.4	88.6	586	5	BUE64473	BUE64473
845	12.4	88.6	572	6	CD918656	CD918656	918	12.4	88.6	587	5	BM51877	BM51877
846	12.4	88.6	572	6	CF248923	CF248923	919	12.4	88.6	587	5	BM51877	BM51877
847	12.4	88.6	572	7	CF942011	CF942011	920	12.4	88.6	587	5	BM51877	BM51877
848	12.4	88.6	572	8	CX195317	CX195317	921	12.4	88.6	588	3	CL333405	CL333405
849	12.4	88.6	572	8	CX535935	CX535935	922	12.4	88.6	588	3	BP282010	BP282010
850	12.4	88.6	572	11	TA164050	TA164050	923	12.4	88.6	588	10	CG047050	CG047050
851	12.4	88.6	573	2	BG720399	BG720399	924	12.4	88.6	588	10	CG047050	CG047050
852	12.4	88.6	573	3	BI511796	BI511796	925	12.4	88.6	590	7	CN563109	CN563109
853	12.4	88.6	573	3	BM636573	BM636573	926	12.4	88.6	590	7	CV173780	CV173780
854	12.4	88.6	573	3	BP366764	BP366764	927	12.4	88.6	591	10	CF266418	CF266418
855	12.4	88.6	574	1	AI403567	AI403567	928	12.4	88.6	591	7	CF371584	CF371584
856	12.4	88.6	574	3	BJ607785	BJ607785	929	12.4	88.6	591	7	CN565950	CN565950
857	12.4	88.6	574	10	CL858920	CL858920	930	12.4	88.6	591	8	CV915976	CV915976
858	12.4	88.6	574	11	LEBP009H09	LEBP009H09	931	12.4	88.6	591	8	CV915976	CV915976
859	12.4	88.6	575	1	AA438781	AA438781	932	12.4	88.6	592	1	AI977188	AI977188
860	12.4	88.6	575	3	BM318333	BM318333	933	12.4	88.6	592	3	BM604155	BM604155
861	12.4	88.6	575	6	CF261256	CF261256	934	12.4	88.6	592	3	CR393106	CR393106
862	12.4	88.6	575	7	CF841714	CF841714	935	12.4	88.6	592	7	CV029023	CV029023
863	12.4	88.6	575	8	CV915806	CV915806	936	12.4	88.6	592	7	CV029023	CV029023
864	12.4	88.6	575	8	DR794621	DR794621	937	12.4	88.6	592	8	CV915806	CV915806
865	12.4	88.6	575	8	DR794621	DR794621	938	12.4	88.6	592	8	CV915806	CV915806
866	12.4	88.6	575	10	AQ163656	AQ163656	939	12.4	88.6	592	3	CC681110	CC681110
867	12.4	88.6	576	5	BM491747	BM491747	940	12.4	88.6	593	3	BP236830	BP236830
868	12.4	88.6	576	5	BK490839	BK490839	941	12.4	88.6	593	3	BP242569	BP242569
869	12.4	88.6	576	5	CR540620	CR540620	942	12.4	88.6	593	6	CD444142	CD444142
870	12.4	88.6	576	7	CR540620	CR540620	943	12.4	88.6	593	8	CV930638	CV930638
871	12.4	88.6	576	11	CR072024	CR072024	944	12.4	88.6	593	11	CR082194	CR082194
872	12.4	88.6	577	7	CK604435	CK604435	945	12.4	88.6	594	1	AV383406	AV383406
873	12.4	88.6	577	7	CN251557	CN251557	946	12.4	88.6	594	5	BI545505	BI545505
874	12.4	88.6	579	7	CV209017	CV209017	947	12.4	88.6	594	5	BM572369	BM572369
875	12.4	88.6	579	8	CV933540	CV933540	948	12.4	88.6	594	5	CA015360	CA015360
876	12.4	88.6	580	3	BJ199716	BJ199716	949	12.4	88.6	594	7	CN565962	CN565962
877	12.4	88.6	580	3	BP234102	BP234102	950	12.4	88.6	594	7	CN565962	CN565962
878	12.4	88.6	580	3	BP234102	BP234102	951	12.4	88.6	595	3	BP201702	BP201702
879	12.4	88.6	580	3	BP234102	BP234102	952	12.4	88.6	595	3	BP201702	BP201702
880	12.4	88.6	580	5	BK274681	BK274681	953	12.4	88.6	595	3	BP271792	BP271792
881	12.4	88.6	580	7	CN563228	CN563228	954	12.4	88.6	595	6	CD442854	CD442854
882	12.4	88.6	580	7	CN563228	CN563228	955	12.4	88.6	595	6	CD442854	CD442854
883	12.4	88.6	581	3	BP197073	BP197073	956	12.4	88.6	595	10	CM167015	CM167015
884	12.4	88.6	581	3	BP197073	BP197073	957	12.4	88.6	595	10	CM167015	CM167015
885	12.4	88.6	581	6	CA648099	CA648099	958	12.4	88.6	596	7	CN565376	CN565376
886	12.4	88.6	581	9	AO948815	AO948815	959	12.4	88.6	596	7	CN566890	CN566890
887	12.4	88.6	582	1	AI640401	AI640401	960	12.4	88.6	597	1	AI0135123	AI0135123
888	12.4	88.6	582	2	BE660017	BE660017	961	12.4	88.6	597	1	AI0135123	AI0135123
889	12.4	88.6	582	2	BP200561	BP200561	962	12.4	88.6	597	7	BP336337	BP336337
890	12.4	88.6	582	3	BP200753	BP200753	963	12.4	88.6	597	10	AG917645	AG917645
891	12.4	88.6	582	3	BP245575	BP245575	964	12.4	88.6	598	3	BI473755	BI473755
892	12.4	88.6	582	3	BP260595	BP260595	965	12.4	88.6	598	3	BI637902	BI637902
893	12.4	88.6	582	3	BP261041	BP261041	966	12.4	88.6	598	5	BM557153	BM557153
894	12.4	88.6	582	3	BP261286	BP261286	967	12.4	88.6	599	3	BM557153	BM557153
895	12.4	88.6	582	3	BP262990	BP262990	968	12.4	88.6	599	6	CD433382	CD433382
896	12.4	88.6	582	3	BP353891	BP353891	969	12.4	88.6	599	6	CD609041	CD609041
897	12.4	88.6	582	3	BP361981	BP361981	970	12.4	88.6	599	7	CV667947	CV667947
898	12.4	88.6	582	6	CB076669	CB076669	971	12.4	88.6	599	10	AG923105	AG923105

972	12.4	88.6	600	3	BM439485	BM439485	partc.pko
973	12.4	88.6	600	6	CF644282	CF644282	kl8_h12_F
974	12.4	88.6	601	6	CD696157	CD696157	EST3690
975	12.4	88.6	601	9	CC822319	CC822319	MBSF14D8
976	12.4	88.6	601	10	CM0806386	CM0806386	104_430_1
977	12.4	88.6	602	3	BI580376	BI580376	RB74560.5
978	12.4	88.6	602	3	BM599560	BM599560	170006870
979	12.4	88.6	602	3	CK134865	CK134865	RH05209.3
980	12.4	88.6	602	8	CV961872	CV961872	PRPCPY.59
981	12.4	88.6	602	10	CG161459	CG161459	PUDZ10TD
982	12.4	88.6	603	3	BI878368	BI878368	FL17405.X
983	12.4	88.6	603	6	BJ041252	BJ041252	BJ041252
984	12.4	88.6	603	6	CA118295	CA118295	SCBGR109
985	12.4	88.6	603	7	CN567453	CN567453	tag09e09.
986	12.4	88.6	603	7	CO868232	CO868232	MAFRT3040
987	12.4	88.6	604	2	BB346469	BB346469	BB346469
988	12.4	88.6	604	5	BQ875869	BQ875869	QGI9F17.Y
989	12.4	88.6	604	5	BX621452	BX621452	BX621452
990	12.4	88.6	604	6	CD442696	CD442696	BT01N0414
991	12.4	88.6	604	6	CV014619	CV014619	TL025F01
992	12.4	88.6	604	8	CV958846	CV958846	PRTPXC.65
993	12.4	88.6	605	2	BI294829	BI294829	UI-R-DKO-
994	12.4	88.6	605	6	CD434360	CD434360	EL01N0323
995	12.4	88.6	606	6	CD212733	CD212733	HS1.16_B0
996	12.4	88.6	606	7	CN306622	CN306622	170004243
997	12.4	88.6	606	7	CN562993	CN562993	taf80h08.
998	12.4	88.6	607	2	BI097451	BI097451	949008B03
999	12.4	88.6	607	3	BJ604569	BJ604569	BJ604569
1000	12.4	88.6	607	5	BU462915	BU462915	603774781

## ALIGNMENTS

RESULT 1  
LOCUS BF764590 353 bp mRNA linear EST 12-JAN-2001  
DEFINITION CM3-CS0043-041100-464-all CS0043 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF764590  
VERSION BF764590.1 GI:12112490  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS  
Dias Neto,R., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Bruneir,A., deOliveira,P.S., Bucher,F., Jongeneel,C.V.,  
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
JOURNAL  
PUBMED 10737800  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&ct=CM3-CS0043-  
041100-464-all&cs=2000-11-04&ct=1)  
Seq primer: puc 18 forward  
High quality sequence start: 13  
High quality sequence stop: 353.

## FEATURES

Location/Qualifiers

## source

1..353  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_id="CS0043"  
/note="Organ: colon, est; Vector: puc18; Site 1: SmaI;  
Site 2: SmaI; A mini-library was made by cloning products  
derived from ORSITES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 14; DB 2; Length 353;  
Best Local Similarity 78.6%; Pred. No. 1.6e+03;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14  
||:|||||:  
53 CTTACTGCACTCG 40

RESULT 2  
LOCUS CF849219 419 bp mRNA linear EST 30-OCT-2003  
DEFINITION pEM4009CM21f USDA-IPAFs:Expression of Phytophthora sojae genes  
during infection and propagation\_sma Phytophthora sojae cDNA clone  
sma009M21 5, mRNA sequence.  
ACCESSION CF849219  
VERSION CF849219.1 GI:38064873  
KEYWORDS EST.  
SOURCE Phytophthora sojae  
ORGANISM Phytophthora sojae  
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;  
Phytophthora.

REFERENCE  
AUTHORS  
Tyler,B.  
TITLE  
JOURNAL  
Unpublished (2003)  
COMMENT Contact: Tyler B  
Tyler lab

VBI  
1880 Pratt Dr., Blacksburg, VA 24061, USA  
Tel: 540-231-7318  
Email: bmyler@vt.edu  
PCR PRIMERS  
FORWARD: BK reverse primer  
BACKWARD: BK reverse primer  
Plate: 009 row: M column: 21  
Seq primer: BK reverse primer  
High quality sequence stop: 419.  
Location/Qualifiers

## FEATURES

## source

1..419  
/organism="Phytophthora sojae"  
/mol\_type="mRNA"  
/db\_xref="taxon:67593"  
/clone="sma009M21"  
/tissue\_type="mycelium"  
/cell\_line="P6497"  
/dev\_stage="mycelium"  
/lab\_host="synthetic medium"  
/clone\_id="USDA-IPAFs:Expression of Phytophthora sojae  
genes during infection and propagation\_sma"  
/note="Vector: pBK-CMV; Site\_1: EcoRI; Site\_2: XhoI"

## ORIGIN

Query Match 100.0%; Score 14; DB 7; Length 419;  
Best Local Similarity 78.6%; Pred. No. 1.6e+03;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14



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Db      58 CGTACTGCACTCG 71
||||:||||:||||:
RESULT 3      B1602980      525 bp      mRNA      linear      EST 07-SEP-2001
LOCUS      B1602980/c      603249479F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5301331 5',
DEFINITION      mRNA sequence.
ACCESSION      B1602980      GI:15495919
VERSION      B1602980.1
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 525)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT      Contact: Robert Strauberg, Ph.D.
Email: cga@b8-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLAM11762 row: n column: 20
High quality sequence stop: 98.
FEATURES
source
Location/Qualifiers
1..525
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5301331"
/issue_type="hypochalamus"
/lab_host="DH10B"
/clone_1b="NIH MGC 96"
/notes="Organ: brain; Vector: pBluescript (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTNN-3', size-selected for average
insert size 2.3 kb and normalized to RGT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."
ORIGIN
Query Match      100.0%; Score 14; DB 3; Length 525;
Best Local Similarity 78.6%; Pred. No. 1.6e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY      1 CGUACUGCACTCG 14
||||:||||:||||:
Db      148 CGTACTGCACTCG 135

```

```

ORGANISM      Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 547)
REFERENCE      Grossman, A., Chang, C.-W., Davies, J., Harris, B., Hauser, C.,
Lefebvre, P., McDermott, J.P., Shrago, J., Sillow, C. and Stern, D.
TITLE      Analyses of the Chlamydomonas reinhardtii Genome: A Model
JOURNAL      Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 963
Unpublished (2001)
COMMENT      Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
FEATURES
source
Location/Qualifiers
1..547
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_1b="C. reinhardtii CC-1690, stress condition I,
normalized, lambda zap II"
/notes="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP-N (30 min, 1hr, 4hr), TAP-S (30 min,
1hr, 4hr), TAP-P (4hr, 12hr, 24hr), NO3 to NH4 (30min,
1hr, 4hr) and NH4 to NO3 (30min, 1hr, 4hr). PolyA mRNA was
purified from each sample, pooled and cDNA synthesized.
The cDNA was directionally cloned into lambda zap II
(Stratagene) in the SmaI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
zap clones by superinfection with Exsist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."
ORIGIN
Query Match      100.0%; Score 14; DB 3; Length 547;
Best Local Similarity 78.6%; Pred. No. 1.6e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY      1 CGUACUGCACTCG 14
||||:||||:||||:
Db      191 CGTACTGCACTCG 204

```



found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
 Plate: LDCM370 row: d column: 05  
 High quality sequence stop: 563.  
 Location/Qualifiers

## FEATURES

source

1..564  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3684052"  
 /issue\_type="carcinoma, cell line"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NIH MGC 53"  
 /note="Organ: bladder; Vector: pDNR-LIB (Clontech);  
 Site 1: SfiI (ggcgccctggcc); Site 2: SfiI  
 (ggccattatggc); Double-stranded cDNA was prepared from  
 cell line RNA. 5' and 3' adaptors were used in cloning as  
 follows: 5' adaptor sequence: 5'-CACGCGCATTTGCGC-3' and  
 3' adaptor sequence:  
 5'-ATTCTAGAGCGCGCGCGCGCATG-AT(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size 1.55  
 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA)."

## ORIGIN

Query Match 100.0%; Score 14; DB 2; Length 564;  
 Best Local Similarity 78.6%; Pred. No. 1.6e+03;  
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGUACUGCAGCUG 14  
 ||:||||:||||:  
 Db 58 CGTACTGCACCTCG 45

## RESULT 6

CZ662415

LOCUS OM\_Ba0214P18.f OM\_Ba Oryza minuta genomic clone OM\_Ba0214P18 5',  
 DEFINITION genomic survey sequence.

ACCESSION

CZ662415

VERSION C2662415.1 GI:70240449  
 GSS.

SOURCE

ORGANISM

Oryza minuta  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzoae; Oryza.

REFERENCE 1 (bases 1 to 564)  
 Kim,H., Collura,K., Wasieleski,M., Byrne,M., Stum,D., Smart,D.,  
 Rao,K., Luo,M., Jettly,R., Kudrna,D., Miller,C., Soderlund,C. and  
 Wang,R.

OMP (Oryza Map Alignment Project) - Arizona Genomics Institute  
 Unpublished (2005)

TITLE

JOURNAL

COMMENT

Contact: Rod A. Wang  
 Arizona Genomics Institute  
 University of Arizona  
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
 Tel: 520 626 9595  
 Fax: 520 621 1259  
 Email: rtwing@genome.arizona.edu  
 Plate: 0214 row: P column: 18  
 Class: BAC ends.

FEATURES

source

Location/Qualifiers  
 1..564  
 /organism="Oryza minuta"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:53628"  
 /clone="OM\_Ba0214P18"  
 /issue\_type="leaves"  
 /lab\_host="DH10B"  
 /clone\_lib="OM\_Ba"  
 /note="Vector: pCUG1BAC1; Site\_1: HindIII; Site\_2:

## ORIGIN

HindIII"

Query Match 100.0%; Score 14; DB 10; Length 564;  
 Best Local Similarity 78.6%; Pred. No. 1.6e+03;  
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGUACUGCAGCUG 14  
 ||:||||:||||:  
 Db 282 CGTACTGCACCTCG 295

## RESULT 7

BQ456457

LOCUS ke3ja08.v1 Dicrofilaria immitis adult PAMPI v1 Dicrofilaria immitis  
 DEFINITION cDNA 5' similar to TR:Q9XTH8 Q9XTH8 Y37A1B.1 PROTEIN. [1], mRNA  
 sequence.

ACCESSION

BQ456457

VERSION BQ456457.1 GI:21259569  
 EST.

SOURCE

ORGANISM

Dicrofilaria immitis (dog heartworm nematode)  
 Dicrofilaria immitis  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
 Onchocercidae; Dicrofilaria.

REFERENCE

AUTHORS

McCartter,J., Clifton,S., Chispeili,B., Pape,D., Martin,J.,  
 Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,  
 Bowers,Y., Gibbons,M., Ritzer,E., Bennett,J., Franklin,C.,  
 Tsagarashvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,  
 Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,  
 Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
 McCann,R., Waterston,R. and Wilson,R.

The Washington Univ. Nematode EST Project, 1999  
 Unpublished (1999)

TITLE

JOURNAL

COMMENT

Contact: McCartter JP  
 The Washington Univ. Nematode EST Project, 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.edu  
 The library was constructed by Claire Murphy and Dr. James McCartter  
 at Washington University, St. Louis. Adult nematodes were harvested  
 from infected dogs by Dr. Prema Arasu of North Carolina State  
 University, Raleigh, NC (Prema.Arasu@ncsu.edu) Total RNA was  
 isolated by Merry McAlaird of Divergence, Inc., St. Louis, MO. DNA  
 sequencing by: Washington University Genome Sequencing Center  
 Seq primer: -40RP from Glibco  
 High quality sequence stop: 421.

## FEATURES

source

Location/Qualifiers  
 1..587  
 /organism="Dicrofilaria immitis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6287"  
 /dev stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="Dicrofilaria immitis adult PAMPI v1"  
 /note="Vector: PAMPI (Gibco); Site 1: NotI; Site 2: SalI;  
 The library was constructed by Claire Murphy and Dr. James  
 McCartter at Washington University, St. Louis. The cDNA was  
 made by using Dynabead oligo-dT priming (Dynal). PCR based  
 library using a modified protocol from the SMART PCR cDNA  
 Synthesis Kit from Clontech. Directionally cloned into the  
 UDG sites of PAMPI. Adult nematodes were harvested from  
 infected dogs by Dr. Prema Arasu of North Carolina State  
 University, Raleigh, NC (Prema.Arasu@ncsu.edu). Total RNA  
 was isolated by Merry McAlaird of Divergence, Inc., St.  
 Louis, MO."

## ORIGIN

Query Match 100.0%; Score 14; DB 5; Length 587;  
 Best Local Similarity 78.6%; Pred. No. 1.6e+03;

Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGUACUGAACUCG 14  
||:|||||:|  
Db 344 CCGTACTGCACCTCG 357

RESULT 8  
BF422183  
LOCUS 614 bp mRNA linear EST 28-NOV-2000  
DEFINITION BF422183.1 GI:11410172  
ACCESSION BF422183  
VERSION BF422183  
KEYWORDS Sorghum propinquum  
SOURCE Sorghum propinquum  
ORGANISM Sorghum propinquum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Sorghum.  
1 (bases 1 to 614)  
Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M., Marsala, C. and  
Pratt, L.H.  
An EST database from Sorghum: floral-induced meristems  
Unpublished (2000)  
Contact: Cordonnier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu  
Sequences have been trimmed to exclude PolyA, vector and regions  
below Phred quality 16. The threshold for highest quality sequence  
is 20.  
Seq primer: JEN REV  
High quality sequence stop: 583  
POLYA=No.

## FEATURES

1. 614 Location/Qualifiers  
/organism="Sorghum propinquum"  
/mol\_type="mRNA"  
/db\_xref="taxon:132711"  
/clone\_lib="Floral-Induced Meristem 1 (FMI)"  
/note="Organ: Floral-Induced Meristem; Vector:  
pBluescript II from Lambda Zap II; Site\_1: XhoI; Site\_2:  
BclRI; mature plants were placed in a growth chamber for  
15 days with 16 hr darkness and 8 hr light (flowering is  
induced by short-day conditions); 16 days after being  
returned to the greenhouse under natural long days during  
late April/early May, meristems were harvested. The  
library was made from poly-A RNA in the cloning vector  
lambda Zap II. Clones to be sequenced were prepared by  
mass excision."

## FEATURES

1. 614 Location/Qualifiers

Query Match 100.0%; Score 14; DB 2; Length 614;  
Best Local Similarity 78.6%; Pred. No. 1.6e+03;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

## ORIGIN

OY 1 CGUACUGAACUCG 14  
||:|||||:|  
Db 23 CCGTACTGCACCTCG 36

RESULT 9  
CZ660542  
LOCUS 640 bp DNA linear GSS 07-JUL-2005  
DEFINITION OM\_Ba0212H16.f OM\_Ba Oryza minuta genomic clone OM\_Ba0212H16 5',  
ACCESSION CZ660542  
VERSION CZ660542.1 GI:70234850  
KEYWORDS GSS.

## SOURCE

Oryza minuta  
Oryza minuta  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 640)  
Kim, H., Collura, K., Wisesoteki, M., Byrne, M., Stum, D., Smart, D.,  
Rao, K., Luo, M., Jettly, R., Kudrna, D., Muller, C., Soderlund, C. and  
Wing, R.  
OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute  
Unpublished (2005)  
Contact: Rod A. Wing  
Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: rwing@genome.arizona.edu  
Plate: 0212 row: H column: 16  
Class: BAC ends.

## TITLE

Unpublished (2005)  
Contact: Rod A. Wing  
Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: rwing@genome.arizona.edu  
Plate: 0212 row: H column: 16  
Class: BAC ends.

## FEATURES

1. 640 Location/Qualifiers  
/organism="Oryza minuta"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:63629"  
/clone="OM\_Ba0212H16"  
/rifeuse\_type="leaves"  
/lab\_host="DH10B"  
/clone\_lib="OM\_Ba"  
/note="Vector: pCUGIBAC1; Site\_1: HindIII; Site\_2:  
HindIII"

## ORIGIN

Query Match 100.0%; Score 14; DB 10; Length 640;  
Best Local Similarity 78.6%; Pred. No. 1.6e+03;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGUACUGAACUCG 14  
||:|||||:|  
Db 282 CCGTACTGCACCTCG 295

## RESULT 10

BZ563771/C  
LOCUS 670 bp DNA linear GSS 17-DEC-2002  
DEFINITION pacs2-164\_4414.x3 pacs2-164 Pseudomonas aeruginosa genomic clone  
pacs2-164\_4414, genomic survey sequence.  
BZ563771  
ACCESSION BZ563771.1 GI:27188318  
VERSION BZ563771.1 GI:27188318  
KEYWORDS GSS.

## SOURCE

Pseudomonas aeruginosa  
Pseudomonas aeruginosa  
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
Pseudomonadaceae; Pseudomonas.  
1 (bases 1 to 670)

## REFERENCE

Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,  
Burns, J.L., Kaul, R. and Olsen, M.V.  
Whole-Genome-Sequence variation among multiple isolates of  
Pseudomonas aeruginosa library  
J. Bacteriol. (2002) In press  
Contact: Chris K. Raymond  
Genome Center  
University of Washington  
Box 352145, Seattle, WA 98105-2145, USA  
Tel: 2062216954  
Fax: 2066857244  
Email: craymond@u.washington.edu  
Class: shotgun;

## JOURNAL

Genome Center  
University of Washington  
Box 352145, Seattle, WA 98105-2145, USA  
Tel: 2062216954  
Fax: 2066857244  
Email: craymond@u.washington.edu  
Class: shotgun;

## FEATURES

1. 670 Location/Qualifiers  
/organism="Pseudomonas aeruginosa"  
/mol\_type="genomic DNA"  
/strain="2-164"

## ORIGIN

/db xref="taxon:287"  
/clone="pac82-164\_4414"  
/clone\_lib="pac82-164"  
/note="clinical isolate 2-164 whole genomic shotgun library."

Query Match 100.0%; Score 14; DB 9; Length 670;  
Best Local Similarity 78.6%; Pred. No. 1.6e+03;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACUGCACTCG 14  
||:|||||:  
Db 417 CGTACTGCACTCG 404

RESULT 11  
BH565722 711 bp DNA linear GSS 14-DEC-2001  
LOCUS BH565722/c  
DEFINITION BOGFP49R BOGF Brassica oleracea genomic clone BOGFP49, genomic survey sequence.

ACCESSION BH565722 GI:17817562  
VERSION BH565722  
KEYWORDS GSS.  
SOURCE Brassica oleracea  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eustroids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 711)  
Ayele, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S., Ulteback, T.R., Mortman, J.R., White, O.R. and Town, C.D.

Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis Genome Res. 15 (4), 487-495 (2005)

JOURNAL PUBMED 15805490

COMMENT Contact: Chris Town

TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA.  
Tel: 301-838-3523  
Fax: 301-838-0208  
Email: cdtown@tigr.org  
DNA is from a doubled haploid provided by Tom Osborn.  
Seq primer: TR  
Class: sheared ends.

## FEATURES

## Source

Location/Qualifiers  
1..711  
/organism="Brassica oleracea"  
/mol\_type="genomic DNA"  
/strain="TO100DH3"  
/db\_xref="taxon:3712"  
/clone="BOGFP49"  
/clone\_lib="BOGF"  
/note="Vector: PHOS1, Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers"

## ORIGIN

Query Match 100.0%; Score 14; DB 9; Length 711;  
Best Local Similarity 78.6%; Pred. No. 1.6e+03;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CGUACUGCACTCG 14  
||:|||||:  
Db 165 CGTACTGCACTCG 152

RESULT 12  
CF849609/c 730 bp mRNA linear EST 30-OCT-2003  
LOCUS CF849609  
DEFINITION pFMA011C23f USDA-IPAFS:Expression of Phytophthora sojae genes during infection and propagation\_sma Phytophthora sojae cDNA clone BMA011C23 5, mRNA sequence.  
ACCESSION CF849609

VERSION CF849609.1 GI:38065263  
KEYWORDS EST.  
SOURCE Phytophthora sojae  
ORGANISM Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae; Phytophthora.

REFERENCE 1 (bases 1 to 730)  
AUTHORS Tyler, B.  
TITLE Tyler, B. Not Published  
JOURNAL Unpublished (2003)  
COMMENT Contact: Tyler B  
Tyler Lab

VBI  
1880 Pratt Dr., Blacksburg, VA 24061, USA  
Tel: 540-231-7318  
Email: bmtyley@vt.edu

PCR Primers  
FORWARD: BK reverse primer  
BACKWARD: BK reverse primer  
Plate: 011 row: C column: 23  
Seq primer: BK reverse primer  
High quality sequence stop: 730.

## FEATURES

## Source

Location/Qualifiers  
1..730  
/organism="Phytophthora sojae"  
/mol\_type="mRNA"  
/db\_xref="taxon:67593"  
/clone="BMA011C23"  
/tissue\_type="mycelium"  
/cell\_line="P6497"  
/dev\_stage="mycelium"  
/lab\_host="synthetic medium"  
/clone\_lib="USDA-IPAFS:Expression of Phytophthora sojae genes during infection and propagation\_sma"  
/note="Vector: pBK-CMV; Site\_1: EcoRI; Site\_2: XhoI"

## ORIGIN

Query Match 100.0%; Score 14; DB 7; Length 730;  
Best Local Similarity 78.6%; Pred. No. 1.6e+03;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACUGCACTCG 14  
||:|||||:  
Db 725 CGTACTGCACTCG 712

RESULT 13  
CM525116/c 751 bp DNA linear GSS 08-OCT-2004  
LOCUS CM525116  
DEFINITION OP\_Ba0049M10.f OP\_Ba Oryza punctata genomic clone OP\_Ba0049M10 5', genomic survey sequence.

ACCESSION CM525116 GI:53999338  
VERSION CM525116  
KEYWORDS GSS.  
SOURCE Oryza punctata  
ORGANISM Oryza punctata  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 751)  
AUTHORS SamMiguel, P., Westerman, R., Kim, H., Yu, Y., Wisotski, M., Yost, D., Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C., Wang, R. and Jackson, S.A.  
OMAP Project - Purdue University  
Unpublished (2004)  
Contact: Scott A. Jackson  
Jackson Laboratory  
Purdue University  
915 W. State St., West Lafayette, IN 47907, USA  
Tel: 7654963621  
Fax: 7654967255  
Email: sjackson@purdue.edu

Basecalling by phred version 0.020425.c. This sequence was derived

from the raw sequence read by clipping with Lucy version 1.19s.  
Bases 52-802 of the raw sequence (length 1302) were retained after  
clipping

PCR Primers  
FORWARD: TAA TAC GAC TCA CTA TAG GG  
BACKWARD: CAC TCA TTA GGC ACC CCA  
Insert Length: 161000 Std Error: 0.00  
Plate: 0049 row: M column: 10  
Seq primer: TAA TAC GAC TCA CTA TAG GG  
Class: BAC ends.

## FEATURES

## source

Location/Qualifiers  
1..751  
/organism="Oryza punctata"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:4537"  
/clone="OP\_Ba0049M10"  
/issue\_type="young leaves"  
/lab\_host="DH10B-T1 phage resistant"  
/clone\_1lb="OP\_Ba"  
/note="Vector: PACIBAC1; Site\_1: HindIII; Site\_2: HindIII"

## ORIGIN

Query Match 100.0%; Score 14; DB 10; Length 751;  
Best Local Similarity 78.6%; Pred. No. 1.6e+03;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACTCG 14  
||:|||||:  
Db 633 CGTACTGCACACTCG 620

## RESULT 14

LOCUS BH435200

DEFINITION BH435200 759 bp DNA linear GSS 12-DEC-2001  
BOGZM10TR BOGZ Brassica oleracea genomic clone BOGZM10, genomic  
survey sequence.

ACCESSION BH435200

VERSION BH435200.1 GI:117620921

KEYWORDS GSS.

SOURCE Brassica oleracea

ORGANISM Brassica oleracea

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

AUTHORS 1 (bases 1 to 759)  
Ayala, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,  
Utechtack, T.R., Wortman, J.R., White, O.R. and Town, C.D.

JOURNAL Whole genome shotgun sequencing of Brassica oleracea and its  
application to gene discovery and annotation in Arabidopsis

COMMENT Genome Res. 15 (4), 487-495 (2005)  
15805490

Other\_GSSs: BOGZM10TF

Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.  
Seq primer: TR

Class: sheared ends.

Location/Qualifiers

## FEATURES

## source

1..759  
/organism="Brassica oleracea"  
/mol\_type="genomic DNA"  
/strain="TOL000DH3"  
/db\_xref="taxon:3712"  
/clone="BOGZM10"  
/clone\_1lb="BOGZ"  
/note="Vector: PHOS1; Site 1: BstXI; 2-3 kb sheared  
genomic DNA inserted into PHOS1 using BstXI linkers"

## ORIGIN

Query Match 100.0%; Score 14; DB 9; Length 759;  
Best Local Similarity 78.6%; Pred. No. 1.6e+03;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACTCG 14  
||:|||||:  
Db 432 CGTACTGCACACTCG 445

## RESULT 15

LOCUS CW528167/c

DEFINITION CW528167 776 bp DNA linear GSS 08-OCT-2004  
OP\_Ba0029D07.r OP\_Ba Oryza punctata genomic clone OP\_Ba0029D07  
3' genomic survey sequence.

ACCESSION CW528167

VERSION CW528167.1 GI:54002389

KEYWORDS GSS.

SOURCE Oryza punctata

ORGANISM Oryza punctata

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS 1 (bases 1 to 776)  
SanMiguel, P., Westerman, R., Klm, H., Yu, Y., Misoteki, M., Yost, D.,  
Stum, D., Rao, K., Luo, M., Jettly, R., Kudrna, D., Muller, C.,  
Hatfield, J., Soderlund, C., Wing, R. and Jackson, S.A.

JOURNAL OMAF Project - Purdue University  
Unpublished (2004)

Contact: Scott A. Jackson

Jackson Laboratory

Purdue University

915 W. State St., West Lafayette, IN 47907, USA

Tel: 765/4963621

Fax: 765/4967255

Email: sjackson@purdue.edu

Basecalling by phred version 0.020425.c. This sequence was derived  
from the raw sequence read by clipping with Lucy version 1.19s.

Bases 120-895 of the raw sequence (length 1412) were retained after  
clipping.

PCR Primers  
FORWARD: TAA TAC GAC TCA CTA TAG GG  
BACKWARD: CAC TCA TTA GGC ACC CCA

Insert Length: 161000 Std Error: 0.00

Plate: 0029 row: D column: 07

Seq primer: CAC TCA TTA GGC ACC CCA

Class: BAC ends.

Location/Qualifiers

## FEATURES

## source

1..776  
/organism="Oryza punctata"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:4537"  
/clone="OP\_Ba0029D07"  
/issue\_type="young leaves"  
/lab\_host="DH10B-T1 phage resistant"  
/clone\_1lb="OP\_Ba"  
/note="Vector: PACIBAC1; Site\_1: HindIII; Site\_2: HindIII"

## ORIGIN

Query Match 100.0%; Score 14; DB 10; Length 776;  
Best Local Similarity 78.6%; Pred. No. 1.6e+03;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACTCG 14  
||:|||||:  
Db 663 CGTACTGCACACTCG 650

## RESULT 16

LOCUS CW780591/c

DEFINITION CW780591 851 bp DNA linear GSS 19-NOV-2004  
OP\_Ba0084F10.f OP\_Ba Oryza punctata genomic clone OP\_Ba0084F10  
5' genomic survey sequence.

ACCESSION CW780591

VERSION CW780591.1 GI:55849895  
 KEYWORDS GSS.  
 SOURCE Oryza punctata  
 ORGANISM Oryza punctata  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 851)  
 Sankhuyel, P., Westerman, R., Kim, H., Yu, Y., Misotski, M., Yost, D., Stum, D., Rao, K., Luo, M., Jettly, R., Kudrna, D., Miller, C., Hatfield, J., Soderlund, C., Wing, R. and Jackson, S.A.  
 OMAF Project - Purdue University  
 Unpublished (2004)  
 CONTACT: Scott A. Jackson  
 JACKSON LABORATORY  
 PURDUE UNIVERSITY  
 915 W. STATE ST., WEST LAFAYETTE, IN 47907, USA  
 TEL: 7654963621  
 FAX: 7654967255  
 EMAIL: sjackson@purdue.edu

BASECALLING BY PHRED VERSION 0.020425.C. THIS SEQUENCE WAS DERIVED FROM THE RAW SEQUENCE READ BY CLIPPING WITH JUCY VERSION 1.19S. BASES 36-886 OF THE RAW SEQUENCE (LENGTH 1035) WERE RETAINED AFTER CLIPPING.  
 PLATE: 0084 ROW: F COLUMN: 10  
 SEQ PRIMER: TAA TAC GAC TCA CTA TAG CG  
 CLASS: BAC ends.

FEATURES  
 source  
 location/Qualifiers  
 1..851  
 /organism="Oryza punctata"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:4537"  
 /clone="OP\_BA0084F10"  
 /issue\_type="young leaves"  
 /lab\_host="DH10B-T1 phage resistant"  
 /clone\_1lb="OP\_Ba"  
 /note="Vector: PACIBAC1; Site\_1: HindIII; Site\_2: HindIII"

ORIGIN  
 Query Match 100.0%; Score 14; DB 10; Length 851;  
 Best Local Similarity 78.6%; Pred. No. 1.6e+03;  
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14  
 ||:|||||:  
 662 CCGACTCGCACTCG 649

RESULT 17  
 CWS19957/c 855 bp DNA linear GSS 08-OCT-2004  
 LOCUS OP\_BA0023E10.f OP\_Ba Oryza punctata genomic clone OP\_BA0023E10  
 DEFINITION 5', genomic survey sequence.  
 ACCESSION CWS19957  
 VERSION CWS19957  
 KEYWORDS GSS.  
 SOURCE Oryza punctata  
 ORGANISM Oryza punctata  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 855)  
 Sankhuyel, P., Westerman, R., Kim, H., Yu, Y., Misotski, M., Yost, D., Stum, D., Rao, K., Luo, M., Jettly, R., Kudrna, D., Miller, C., Hatfield, J., Soderlund, C., Wing, R. and Jackson, S.A.  
 OMAF Project - Purdue University  
 Unpublished (2004)  
 CONTACT: Scott A. Jackson  
 JACKSON LABORATORY  
 PURDUE UNIVERSITY  
 915 W. STATE ST., WEST LAFAYETTE, IN 47907, USA  
 TEL: 7654963621  
 FAX: 7654967255

EMAIL: sjackson@purdue.edu  
 BASECALLING BY PHRED VERSION 0.020425.C. THIS SEQUENCE WAS DERIVED FROM THE RAW SEQUENCE READ BY CLIPPING WITH JUCY VERSION 1.19S. BASES 41-895 OF THE RAW SEQUENCE (LENGTH 1396) WERE RETAINED AFTER CLIPPING.  
 PCR PRIMERS  
 FORWARD: TAA TAC GAC TCA CTA TAG CG  
 BACKWARD: CAC TCA TTA GGC ACC CCA  
 INSERT LENGTH: 161000 Std Error: 0.00  
 PLATE: 0023 ROW: F COLUMN: 10  
 SEQ PRIMER: TAA TAC GAC TCA CTA TAG CG  
 CLASS: BAC ends.

FEATURES  
 source  
 location/Qualifiers  
 1..855  
 /organism="Oryza punctata"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:4537"  
 /clone="OP\_BA0023E10"  
 /issue\_type="young leaves"  
 /lab\_host="DH10B-T1 phage resistant"  
 /clone\_1lb="OP\_Ba"  
 /note="Vector: PACIBAC1; Site\_1: HindIII; Site\_2: HindIII"

ORIGIN  
 Query Match 100.0%; Score 14; DB 10; Length 855;  
 Best Local Similarity 78.6%; Pred. No. 1.6e+03;  
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14  
 ||:|||||:  
 661 CCGACTCGCACTCG 648

RESULT 18  
 BP031922/c 859 bp mRNA linear EST 10-OCT-2000  
 LOCUS 601559533F1 NIH\_MGC\_58 Homo sapiens CDNA clone IMAGE:3829137 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BP031922  
 VERSION BP031922.1 GI:10739634  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 859)  
 NIH-MGC <http://mgs.nci.nih.gov/>.  
 NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)  
 UNPUBLISHED (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 EMAIL: cga@bbs-remail.nih.gov  
 TISSUE PROCUREMENT: ATCC  
 CDNA LIBRARY PREPARATION: CLONTECH LABORATORIES, INC.  
 CDNA LIBRARY ARRAYED BY: THE I.M.A.G.E. CONSORTIUM (ILNL)  
 DNA SEQUENCING BY: INCYTE GENOMICS, INC.  
 CLONE DISTRIBUTION: MGC CLONE DISTRIBUTION INFORMATION CAN BE FOUND THROUGH THE I.M.A.G.E. CONSORTIUM/ILNL AT:  
<http://image.llnl.gov>  
 PLACE: DLM501 ROW: A COLUMN: 10  
 HIGH QUALITY SEQUENCE STOP: 507.

FEATURES  
 source  
 location/Qualifiers  
 1..859  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3829137"  
 /issue\_type="hypomethylation"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_1lb="NIH MGC 58"  
 /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site\_1: SfiI (ggcgcctcgcc); Site\_2: SfiI (ggcgcctcgcc);  
 Double-stranded cDNA was prepared from cell line RNA. 5'

and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGCGCATG-dT(30)BN-3' (where B = A, C or G and N = A, C, G, or T). Average insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

Query Match 100.0%; Score 14; DB 2; Length 859;  
Best Local Similarity 78.6%; Pred. No. 1.6e+03;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUCG 14  
||:|||||:|  
Db 50 CTTACTGCACTCG 37

RESULT 19 884 bp mRNA linear EST 06-NOV-2000  
BF207946/c 601862463F1 NIH\_MGC\_53 Homo sapiens cDNA clone IMAGE:4082127 5',  
LOCUS mRNA sequence.  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BF207946.1 GI:1101532  
EST.  
Homo sapiens (human)

Homo sapiens (human)  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Homo.  
1 (bases 1 to 884)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL).  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](http://image.llnl.gov)  
Plate: LLCM944 row: n column: 16  
High quality sequence stop: 664.

Location/Qualifiers  
1. 884  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4082127"  
/tissue\_type="carcinoma, cell line"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_1lb="NIH MGC 53"  
/note="Organ: bladder; Vector: pDNR-LIB (Clontech);  
Site 1: SfiI (ggcgccgcgcgc); Site 2: SfiI  
(ggccatcgcgc); Double-stranded cDNA was prepared from  
cell line RNA. 5' and 3' adaptors were used in cloning as  
follows: 5' adaptor sequence: 5'-CACGCCATTATGCGC-3' and  
3' adaptor sequence:  
5'-ATTCTAGAGCGCGCGCGCATG-dT(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.55  
kb (range 0.9-4.0 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA)."

# FEATURES

source

Query Match 100.0%; Score 14; DB 2; Length 884;  
Best Local Similarity 78.6%; Pred. No. 1.6e+03;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

## ORIGIN

Query Match 100.0%; Score 14; DB 2; Length 884;  
Best Local Similarity 78.6%; Pred. No. 1.6e+03;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUCG 14  
||:|||||:|  
Db 79 CTTACTGCACTCG 66

RESULT 20 916 bp DNA linear GSS 15-NOV-2004  
CW776517/c 5'\_\_Ba0078M13.f\_OP\_Ba Oryza punctata genomic clone OP\_\_Ba0078M13  
LOCUS 5', genomic survey sequence.  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Oryza punctata  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 916)  
Samtuel, P., Westerman, R., Kim, H., Yu, Y., Wasekaki, M., Yost, D.,  
Stum, D., Rao, K., Luo, M., Jett, R., Kudrna, D., Muller, C.,  
Hartfield, J., Soderlund, C., Wang, R., and Jackson, S.A.  
OMAP Project - Purdue University  
Unpublished (2004)  
Contact: Scott A. Jackson  
Jackson Laboratory  
Purdue University  
915 W. State St., West Lafayette, IN 47907, USA  
Tel: 7654963621  
Fax: 7654967255  
Email: [sjackson@purdue.edu](mailto:sjackson@purdue.edu)  
Basecalling by phred version 0.020425.c. This sequence was derived  
from the raw sequence read by clipping with Lucy version 1.198.  
Bases 39-954 of the raw sequence (length 967) were retained after  
clipping.  
Plate: 0078 row: M column: 13  
Seq primer: TAA TAC GAC TCA TAG GG  
Class: BAC ends.

# FEATURES

source

Location/Qualifiers  
1. 916  
/organism="Oryza punctata"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:4537"  
/clone="OP\_Ba0078M13"  
/tissue\_type="young leaves"  
/lab\_host="DH10B-T1 phage resistant"  
/clone\_1lb="OP\_Ba"  
/note="Vector: pGIBAC1, Site 1: HindIII, Site 2: HindIII"

## ORIGIN

Query Match 100.0%; Score 14; DB 10; Length 916;  
Best Local Similarity 78.6%; Pred. No. 1.6e+03;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUCG 14  
||:|||||:|  
Db 643 CTTACTGCACTCG 630

RESULT 21 943 bp DNA linear GSS 31-AUG-2000  
AZ209474 SP\_0106\_A2\_G12\_SP68 Strongylocentrotus purpuratus, purple sea  
urchin, sperm genomic BAC library Strongylocentrotus purpuratus  
genomic clone Plate=106 Col=24 Row=M, genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Strongylocentrotus purpuratus  
Strongylocentrotus purpuratus  
Bukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
Echinoidea; Euechinoidea; Echinacea; Echinoida;  
Strongylocentrotidae; Strongylocentrotus.

REFERENCE 1 (bases 1 to 943)  
 AUTHORS Cameron, R.A., Malairas, G., Rast, J.P., Martinez, P., Biondi, T.R., Swartzell, S., Wallace, J.C., Roushka, A.J., Livingston, B.T., Wray, G.A., Ettemohn, C.A., Lemach, H., Bitten, R.U., Davidson, E.H. and Hood, L.  
 A sea urchin genome project: Sequence scan, virtual map, and additional resources  
 Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)

JOURNAL  
 PUBLISHED 10920195  
 CONTACT: Cameron, R.A., Davidson, E.H., Hood, L  
 Division of Biology 156-29  
 California Institute of Technology  
 Pasadena California 91125, USA  
 Tel: (626) 395-8421  
 Fax: (626) 793-3047  
 Email: acameron@caltech.edu  
 Plate: 106 ROW: M column: 24  
 Seq primer: SP6  
 Class: BAC ends  
 High quality sequence stop: 943.  
 Location/Qualifiers

FEATURES  
 source 1..943  
 /organism="Strongylocentrotus purpuratus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7668"  
 /clone="Plate=106 Col=24 Row=M"  
 /clone\_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"  
 /note="Organ: sperm; Vector: BAC3.6; BAC Clones in E-Coli DH10B"

ORIGIN

Query Match 100.0%; Score 14; DB 9; Length 943;  
 Best Local Similarity 78.6%; Pred. No. 1.6e+03;  
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14  
 ||:|||||:  
 Db 627 CGTACTGCACTCG 614

RESULT 22  
 DN693741 1195 bp mRNA linear EST 30-MAR-2005  
 LOCUS CX90-B12 5', mRNA sequence.  
 DEFINITION CX90-B12 5', mRNA sequence.  
 ACCESSION DN693741  
 VERSION DN693741.1 GI:62050365  
 KEYWORDS EST.  
 SOURCE Gasterosteus aculeatus (three spined stickleback)  
 ORGANISM Gasterosteus aculeatus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes; Gasterosteidae; Gasterosteus.  
 1 (bases 1 to 1195)  
 REFERENCE 1 Kingsley, D.M., Pelich, C., Balabhadra, S., Grimwood, J., Dickson, M., Schmutz, J. and Myers, R.M.  
 Expressed sequence tags from Gasterosteus aculeatus  
 Unpublished (2003)  
 CONTACT: Grimwood, Jane  
 Stanford Human Genome Center  
 Stanford University School of Medicine  
 975 S California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 320 5917  
 Fax: 650 320 5801  
 Email: jane@hgc.stanford.edu  
 Plate: 90  
 High quality sequence stop: 726.  
 Location/Qualifiers

FEATURES  
 source 1..1195  
 /organism="Gasterosteus aculeatus"  
 /mol\_type="mRNA"

/strain="Conner Creek sticklebacks, WA USA"  
 /db\_xref="taxon:69293"  
 /clone="CX90-B12"  
 /sex="mixed male and female"  
 /tissue\_type="eyes"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (T1 phage resistant)"  
 /clone\_lib="SHGC-CGX"  
 /note="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: 5'-GACTGATTCGATCGAGCGCGCC(725-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxxxc' (where 'c' is ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at: [http://www.openbiosystems.com/cdna\\_library\\_construction\\_fa\\_q.php#8](http://www.openbiosystems.com/cdna_library_construction_fa_q.php#8) The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria. Clones available from Open Biosystems: <http://www.openbiosystems.com/stickleback>"

ORIGIN

Query Match 100.0%; Score 14; DB 8; Length 1195;  
 Best Local Similarity 78.6%; Pred. No. 1.6e+03;  
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14  
 ||:|||||:  
 Db 221 CGTACTGCACTCG 234

RESULT 23  
 DN663186 1200 bp mRNA linear EST 29-MAR-2005  
 LOCUS CFM12-D08 5', mRNA sequence.  
 DEFINITION CFM12-D08 5', mRNA sequence.  
 ACCESSION DN663186  
 VERSION DN663186.1 GI:61983242  
 KEYWORDS EST.  
 SOURCE Gasterosteus aculeatus (three spined stickleback)  
 ORGANISM Gasterosteus aculeatus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes; Gasterosteidae; Gasterosteus.  
 1 (bases 1 to 1200)  
 REFERENCE 1 Kingsley, D.M., Pelich, C., Balabhadra, S., Grimwood, J., Dickson, M., Schmutz, J. and Myers, R.M.  
 Expressed sequence tags from Gasterosteus aculeatus  
 Unpublished (2003)  
 CONTACT: Grimwood, Jane  
 Stanford Human Genome Center  
 Stanford University School of Medicine  
 975 S California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 320 5917  
 Fax: 650 320 5801  
 Email: jane@hgc.stanford.edu  
 Plate: 12  
 High quality sequence stop: 855.  
 Location/Qualifiers

FEATURES  
 source 1..1200  
 /organism="Gasterosteus aculeatus"  
 /mol\_type="mRNA"  
 /strain="Conner Creek sticklebacks, WA USA"  
 /db\_xref="taxon:69293"



```

/clone="CFM12-D08"
/sex="mixed male and female"
/tissue_type="gill18"
/dev_stage="adult"
/lab_host="DH10B (T1 phage resistant)"
/clone_1ib="SHGC-CFM"
/notes="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: 5'-GACTGCTTACATCGCAGCGCCGCC(T)25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5' prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxATC' (where is ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at: http://www.openbiosystems.com/cdna_library_construction_fa 9.php#8 The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria. Clones available from Open Biosystems: http://www.openbiosystems.com/stickleback"

```

## ORIGIN

Query Match 100.0%; Score 14; DB 8; Length 1200;  
 Best Local Similarity 78.6%; Pred. No. 1.6e+03;  
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14  
 ||:|||||:  
 DB 240 CGTACTGCACTCG 253

RESULT 24  
 DN738151 1211 bp mRNA linear EST 31-MAR-2005  
 LOCUS CNB96-H05.y1d-s SHGC-CNB *Gasterosteus aculeatus* cDNA clone  
 DEFINITION DN738151  
 ACCESSION DN738151  
 VERSION DN738151.1 GI:62115161  
 KEYWORDS EST.  
 SOURCE *Gasterosteus aculeatus* (three spined stickleback)  
 ORGANISM *Gasterosteus aculeatus*  
 BUKARYOTA; Metazoa; Chordata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; *Gasterosteiformes*; *Gasterosteidae*; *Gasterosteus*.  
 1 (bases 1 to 1211)  
 Kingsley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M., Schmutz,J. and Myers,R.M.  
 Expressed sequence tags from *Gasterosteus aculeatus*  
 Unpublished (2003)  
 CONTACT: Grimwood, Jane  
 Stanford Human Genome Center  
 Stanford University School of Medicine  
 975 S California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 320 5917  
 Fax: 650 320 5801  
 Email: jane@hgc.stanford.edu  
 Plate: 96  
 High quality sequence start: 2  
 High quality sequence stop: 790.  
 Location/Qualifiers  
 1..1211  
 /organism="*Gasterosteus aculeatus*"  
 /mol\_type="mRNA"  
 /strain="Conner Creek sticklebacks, WA USA"  
 /db\_xref="taxon:69293"  
 /clone="CNB96-H05"

## FEATURES

```

/sex="mixed male and female"
/tissue_type="brain"
/dev_stage="adult"
/lab_host="DH10B (T1 phage resistant)"
/clone_1ib="SHGC-CNB"
/notes="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: 5'-GACTGCTTACATCGCAGCGCCGCC(T)25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5' prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxATC' (where is ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at: http://www.openbiosystems.com/cdna_library_construction_fa 9.php#8 The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria. Clones available from Open Biosystems: http://www.openbiosystems.com/stickleback"

```

## ORIGIN

Query Match 100.0%; Score 14; DB 8; Length 1211;  
 Best Local Similarity 78.6%; Pred. No. 1.6e+03;  
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCACTCG 14  
 ||:|||||:  
 DB 237 CGTACTGCACTCG 250

RESULT 25  
 DN660653 1289 bp mRNA linear EST 28-MAR-2005  
 LOCUS CEC48-A03.y1d-s SHGC-CBC *Gasterosteus aculeatus* cDNA clone  
 DEFINITION CEC48-A03 5', mRNA sequence.  
 ACCESSION DN660653  
 VERSION DN660653.1 GI:61965902  
 KEYWORDS EST.  
 SOURCE *Gasterosteus aculeatus* (three spined stickleback)  
 ORGANISM *Gasterosteus aculeatus*  
 BUKARYOTA; Metazoa; Chordata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; *Gasterosteiformes*; *Gasterosteidae*; *Gasterosteus*.  
 1 (bases 1 to 1289)  
 Kingsley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M., Schmutz,J. and Myers,R.M.  
 Expressed sequence tags from *Gasterosteus aculeatus*  
 Unpublished (2003)  
 CONTACT: Grimwood, Jane  
 Stanford Human Genome Center  
 Stanford University School of Medicine  
 975 S California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 320 5917  
 Fax: 650 320 5801  
 Email: jane@hgc.stanford.edu  
 Plate: 48  
 High quality sequence stop: 806.  
 Location/Qualifiers  
 1..1289  
 /organism="*Gasterosteus aculeatus*"  
 /mol\_type="mRNA"  
 /strain="Conner Creek sticklebacks, WA USA"  
 /db\_xref="taxon:69293"  
 /clone="CEC48-A03"  
 /sex="mixed male and female"  
 /tissue\_type="skin"

## FEATURES

```
/dev stage="adult"  
/lab_host="DH10B (T1 phage resistant)"  
/clone_lib="SHGC-CBC"  
/note="Vector: Express 1; Total and poly A+ RNA was  
isolated from the indicated stickleback tissue, and a cDNA  
library was constructed in the Express 1 plasmid vector by  
Open Biosystems. First strand cDNA synthesis was primed  
with an 54 bp linker primer containing an oligodT sequence  
preceded by a synthetic NotI site (first strand primer:  
5'-GACTACTCTAGATCGGAGCGCCGCTT25-3'). Following  
second strand synthesis, cDNAs were made blunt at the end  
corresponding to the original 5 prime end of mRNA, and  
cloned directionally into the NotI and EcoRV sites of  
Express 1. Note that the EcoRV site is typically destroyed  
in the blunt end cloning, leaving a junction of the form  
'xxATC' (where x is ATC is the second half of the EcoRV  
site, and xxx is derived from the cDNA sequence). A map of  
the Express 1 vector is available at:  
http://www.openbiosystems.com/cdna_library_construction_fa  
q.php#8 The primary library was transformed and amplified  
in DH10B (T1 phage resistant) bacteria. Clones available  
from Open Biosystems:  
http://www.openbiosystems.com/stickleback"
```

## ORIGIN

Query Match 100.0%; Score 14; DB 8; Length 1289;  
Best Local Similarity 78.6%; Pred. No. 1.6e+03;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUCG 14  
||:|||||:  
Db 18 CCGACTCGCACTCG 31

RESULT 26  
A0661032/c 157 bp DNA linear GSS 23-JUN-1999  
LOCUS Sheared DNA-11G3.TF Sheared DNA Trypanosoma brucei genomic clone  
DEFINITION  
ACCESSION A0661032  
VERSION A0661032.1 GI:5168800  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Bukariyoca; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.  
1 (bases 1 to 157)  
El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,  
Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S.,  
Donelson,J., Fraser,C. and Adams,M.  
Determination of clone end sequences from Trypanosoma brucei GUTat  
10.1 sheared DNA library

TITLE  
JOURNAL  
COMMENT  
OTHER GSSES: Sheared DNA-11G3.TR  
Contact: Najib M. El-Sayed  
Department of Bukariyocic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: nelsayed@igir.org  
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared  
DNA library constructed at TIGR. Clones will be available for  
distribution through ATCC. Sheared DNA end sequences search page:  
http://www.tigr.org/tcdb/mbd/lbdb/.  
Seq primer: M13-Forward  
Class: shotgun.

FEATURES  
source

1..157  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927/4 GUTat 10.1"  
/db\_xref="taxon:5691"

## ORIGIN

Query Match 92.9%; Score 13; DB 9; Length 157;  
Best Local Similarity 76.9%; Pred. No. 6.3e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13  
||:|||||:  
Db 30 CCGACTCGCACTC 18

RESULT 27  
CR555866/c 205 bp mRNA linear EST 12-JUL-2004  
LOCUS DKFZp469B092\_r1 469 (synonym: pkId1) Pongo pygmaeus cDNA clone  
DEFINITION  
ACCESSION CR555866  
VERSION CR555866.1 GI:50249468  
KEYWORDS EST.  
SOURCE Pongo pygmaeus (orangutan)  
ORGANISM Pongo pygmaeus  
Bukariyoca; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Hominiidae; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Pongo.  
1 (bases 1 to 205)  
Blocker,H., Boecker,M., Brandt,P., Mewes,H.W., Weill,B., Amld,C.,  
Oanger,A., Robo,G., Han,M. and Wiemann,S.  
Pongo pygmaeus mRNA (Blocker,H., Boecker,M., Brandt,P., et al.)  
Unpublished (2004)  
Contact: MIPS

TITLE  
JOURNAL  
COMMENT  
OTHER GSSES: MIPS  
Ingolstaedter lander.1, D-85764 Neuberg, Germany  
This is the 5' sequence of the clone insert from S. Wiemann,  
Molecular Genome Analysis, German Cancer Research Center (DKFZ);  
Small S. Wiemann@dkfz-heidelberg.de; sequenced by GSF (National  
Research Centre for Biotechnology Ltd., Braunschweig/Germany)  
within the cDNA sequencing consortium of the German Genome Project.  
This clone (DKFZp469B092) is available at the RZPD in Berlin.  
Please contact the RZPD: Reesourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clonezrpd.de Further  
information about the clone and the sequencing project is available  
at http://mips.gsf.de/projects/cdna/.  
Location/Qualifiers

FEATURES  
source

1..205  
/organism="Pongo pygmaeus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9600"  
/clone="DKFZp469B092"  
/cissue\_type="kidney"  
/dev stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="469 (synonym: pkId1)"  
/note="Vector: pSPORT1\_Sfi; Site\_1: SfiIa; Site\_2: SfiIb"

## ORIGIN

Query Match 92.9%; Score 13; DB 7; Length 205;  
Best Local Similarity 76.9%; Pred. No. 6.4e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13

Db 49 CGTACTGCACTC 37

RESULT 28  
LOCUS BUE40724  
DEFINITION BUE40724 255 bp mRNA linear EST 06-MAY-2003  
griesea cDNA clone mgmk001xh17 5', mRNA sequence.

ACCESSION BUE40724 GI:30402792

VERSION BUE40724.2 GI:30402792

KEYWORDS EST.

ORGANISM Magnaporthe griesea (anamorph: Pyricularia griesea)

REFERENCE Magnaporthe griesea  
Bakayocet, Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Sordariomycetes Incertae sedis; Magnaportheaceae; Magnaporthe.

AUTHORS Bholle, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G.,  
Bhatterai, K. and Dean, R.A.

TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe

JOURNAL Unpublished (2002)  
On Sep 30, 2002 this sequence version replaced gi:23353050.

COMMENT Contact: Bholle DJ  
Department of Plant Pathology & Microbiology  
Texas A&M University  
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA  
Tel: 979 845 4831  
Fax: 979 845 6483  
Email: d-bholle@tamu.edu  
Chromatogram file of this sequence is available, see contact  
person. Best hit (April 22, 2003) ref|NP\_620661.1| AV2 [South  
African caasava mosaic virus] >gi|70...323.1

PCR PRIMERS  
FORWARD: T3 primer  
BACKWARD: T7 primer  
Plate: mgmk001 row: H column: 17  
Seq primer: T3

FEATURES  
source Location/Qualifiers

1..255  
/organism="Magnaporthe griesea"  
/mol\_type="mRNA"  
/strain="NN95"  
/db\_xref="taxon:148305"  
/clone="mgmk001xh17"  
/sex="Mati-1 hermaphrodite"  
/cell\_type="germinated conidia"  
/note="Vector: pBluescriptSK, Site\_1: EcoRI, Site\_2: XhoI;  
Conidia germinated in hydrophobic surface membrane in 27C  
for 12 hours. NN95 is a hygromycin phosphotransferase gene  
replacement of the PMK1 MAP kinase gene in the Guy11  
strain background (Xu and Hamer, 1996. Genes & Dev.  
10:2696). Sequences were processed by one of two methods.  
Where a full-length alignment to the M. griesea genome  
sequence was available, the EST sequence was trimmed  
according to the alignment, otherwise sequence quality was  
assessed using phredPhrap version 991019 and trimmed  
according to pnd files (0.05) and for vector seq."

ORIGIN  
Query Match 92.9%; Score 13; DB 5; Length 255;  
Best Local Similarity 76.9%; Pred. No. 6.4e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 224 GTCAGTCACTCG 236

RESULT 29  
LOCUS CA374069 285 bp mRNA linear EST 06-NOV-2002

DEFINITION 648371 NCCWA 1RT Oncorhynchus mykiss cDNA clone 1RT16K01\_A\_F01 5',  
mRNA sequence.

ACCESSION CA374069.1 GI:24690094

VERSION CA374069.1

KEYWORDS EST.

SOURCE Oncorhynchus mykiss (rainbow trout)

ORGANISM Oncorhynchus mykiss

REFERENCE Oncorhynchus mykiss  
Bakayocet; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
1 (bases 1 to 285)

AUTHORS Koop, B., Gahr, S.A., Palti, Y. and Quackenbush, J.  
Sequence analysis of a rainbow trout cDNA library and creation of a  
gene index

JOURNAL Cyogenet. Genome Res. 102 (1-4), 347-354 (2003)  
Contact: Rexroad CE  
USDA, ARS, National Center for Cool and Cold Water Aquaculture  
11876 Leetown Road, Kearneysville, WV 25430, USA  
Tel: 304 724 8340 x2129  
Fax: 304 725 0351

COMMENT Email: crexroad@nccwa.ars.usda.gov  
Single pass sequencing. Bases called with phred v0.020425.c and  
trimmed with the aid of the trim\_alt option. Vector identified by  
cross match v0.990329.

Seq primer: AGCGGATACCAATTTCACACAGA.  
Location/Qualifiers

1..285  
/organism="Oncorhynchus mykiss"  
/mol\_type="mRNA"  
/db\_xref="taxon:8022"  
/clone="1RT16K01\_A\_F01"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_1lb="NCCWA 1RT"  
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;  
library made from pooled tissue from brain, gill, liver,  
spleen, muscle, and kidney."

ORIGIN  
Query Match 92.9%; Score 13; DB 6; Length 285;  
Best Local Similarity 76.9%; Pred. No. 6.5e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 1 CGUACUGCACTC 13  
229 GTCAGTCACTCG 241

RESULT 30  
LOCUS CW452335 290 bp DNA linear GSS 02-NOV-2004  
DEFINITION fbb0001f192n03k0 Sorghum methylation filtered library (libid: 104)  
Sorghum bicolor genomic clone fbb0001f192n03, genomic survey  
sequence.

ACCESSION CW452335.1 GI:55200296

VERSION CW452335.1

KEYWORDS GSS.

SOURCE Sorghum bicolor (sorghum)

ORGANISM Sorghum bicolor

REFERENCE Sorghum bicolor  
Bakayocet; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Sorghum.  
1 (bases 1 to 290)

AUTHORS Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,  
Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,  
McKenamy, J., Smith, M., Holeman, H., Roe, B.A., Wiley, G., Korff, I.F.,  
Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddelton, J.A. and  
Martiniussen, R.A.  
Sorghum genome sequencing by methylation filtration  
PLOS Biol. 3 (1), e13 (2005)  
15660154  
Contact: Bedell JA

Orion Genomics, LLC  
4041 Forest Park Ave., St. Louis, MO 63108, USA  
Tel: 314 615 6979  
Fax: 314 615 5975

## ORIGIN

Query Match	92.9%	Score 13	DB 10	Length 230
Best Local Similarity	76.9%	Pred. No. 6.5e+03		
Matches 10	Conservative 3	Mismatches 0	Indels 0	Gaps 0

```

QY      1 CGUACUGCACTUC 13
         ||:|||||:|
Db      164 CGTACTGCAACTC 176

```

RESULT	31
CM772355	
LOCUS	292 bp DNA linear GSS 12-NOV-2004
DEFINITION	CG_BBA008B23.f CG_BBA Oryza glaberrima genomic clone CG_BBA0089B23 5' genomic survey sequence.

## FEATURES

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source
1. .292
/organism="Oryza glaberrima"
/mol_type="genomic DNA"
/db_xref="taxon:4538"
/clone="OG_BB40089B23"
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```

/tissue_type="young leaves"
/lab_host="DH10B T1 phage resistant"
/clone_idb="OG_BBA"
/note="Vector: pGIRAC1; Site_1: HindIII; Site_2: HindIII

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## ORIGIN

Query Match	92.9%	Score 13;	DB 10;	Length 292;
Best Local Similarity	76.9%	Pred. No. 6.5e+03;		
Matches 10;	Conservative 3;	Mismatches 0;	Indels 0;	Gaps 0;

QY	2	GUACUGCAACUCG	14
		: : : : : :	
Db	55	GTA CTGCAACTCG	67

RESULT 32					
AJ578024					
LOCUS					
DEFINITION	AJ578024	344 bp	mRNA	linear	EST 04-AUG-2001
	AJ578024		Plac1ch1y3 f1eslcs 11ver sexually		
			f1eslcs cDNA clone BR2A6, mRNA sequence.		

**JOURNAL  
COMMENT**

Biosciences  
University of Birmingham  
Edgbaston Park Road, Birmingham, B15 2TT, UNITED KINGDOM.

## FEATURES

```
source
1. .344
/organism="Platichthys fleussus"
/mol_type="mRNA"
/db_xref="taxon:8260"
/cisone="BR2A6"
/cisone_type="liver"
/dev_stage="sexually immature"
/cisone_lib="Platichthys fleussus liver sexually immature"
/note="country: Isle of Man;Port Birlin"
```

## ORIGIN

Query Match	92.9%	Score 13;	DB 1;	Length 344;
Best Local Similarity	76.9%;	Pred. No. 6.5e+03;		
Matches 10;	Conservative 3;	Mismatches 0;	Indels 0;	Gaps 0;

QY	2	GUACUGCAACTUG	14
		: : : : : :	
Db	271	GTA CTGCAACTCG	28

RESULT 33	LOCUS	DEFINITION	EST 07-DEC-2002
BY111672	BY111672	345 bp mRNA	linear
	BY111672	RIKEN full-length enriched, 15 days embryo	whole body Mus
		musculus cDNA clone U330004/G17 5', mRNA sequence.	

REFERENCE 1 (bases 1 to 345)  
 AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaio, O., Otsu, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojohori, T., Baldarelli, R., Hill, D. P., Bull, C., Hume, D. A., Quackenbush, J., Schiraldi, L. M., Kanagin, A., Masuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Brad, D., Brusic, V., Choibha, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, J. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Kongaya, A., Kurochkin, I. V., Lee, Y., Lendhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Nmatu, K., Okido, T., Pavan, W. J., Pettes, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. O., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wyszynski, B. A., Yang, I., Yang, I., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carrinchi, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E., and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)

12466851  
 CONTACT: Yoshinide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/  
 Aizawa, K., Akimura, T., Arakawa, T., Carrinchi, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Kono, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission  
 Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome 12, 673-677 (2001)  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
 RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site (http://genome.gsc.riken.go.jp) for further details.  
 Location/Qualifiers  
 1..345  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="CS7BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="1330047G17"  
 /tissue\_type="whole body"  
 /dev\_stage="15 days embryo"

ORIGIN  
 Query Match 92.9%; Score 13; DB 5; Length 345;  
 Best Local Similarity 76.9%; Pred. No. 6.5e+03;  
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

CY 2 GUDCUGCACTCG 14  
 ||:|||||:  
 Db 258 GTACTGCACTCG 270

RESULT 34  
 LOCUS DR073074 364 bp mRNA linear EST 06-JUN-2005  
 DEFINITION Ik85f03.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA sequence.  
 ACCESSION DR073074  
 VERSION DR073074.1 GI:67050923  
 KEYWORDS EST.  
 SOURCE Ginkgo biloba (maidenhair tree)  
 ORGANISM Ginkgo biloba  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.  
 1 (bases 1 to 364)  
 Brenner, E. D., A. J., Ball, J. V., Martienssen, R. A., McCombie, R. W., O'Shaughnessy, T. W., Ball, J. V., Martienssen, R. A., McCombie, R. W., Benfey, P., Coruzzi, G. and Stevenson, D.  
 Expressed tag sequences from Ginkgo female leaf (NYBG)  
 Unpublished (2005)  
 CONTACT: W. Richard McCombie  
 Lita Annenberg Hazen Genome Sequencing Center  
 Cold Spring Harbor Laboratory  
 PO Box 100, Cold Spring Harbor, NY 11724, USA  
 Tel: 516 367 8884  
 Fax: 516 367 8874  
 Email: mcombie@cshl.org  
 Seq primer: -21m1univRev.  
 Location/Qualifiers  
 1..364  
 /organism="Ginkgo biloba"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3311"  
 /sex="Female"  
 /clone\_lib="Ginkgo female leaf (NYBG)"  
 /note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Strain: ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts."

ORIGIN  
 Query Match 92.9%; Score 13; DB 8; Length 364;  
 Best Local Similarity 76.9%; Pred. No. 6.5e+03;  
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

CY 2 GUDCUGCACTCG 14  
 ||:|||||:  
 Db 258 GTACTGCACTCG 270

RESULT 35  
 LOCUS CV724006 366 bp mRNA linear EST 04-NOV-2004  
 DEFINITION root--05-105.g1 Rice root Lambda phage cDNA library (root) Oryza sativa (japonica cultivar-group) cDNA clone root--05-105, mRNA sequence.  
 ACCESSION CV724006  
 VERSION CV724006.1 GI:55411630  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Erihartoideae; Oryzeae; Oryza.  
1 (bases 1 to 366)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES  
source

1. 366  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:3947"  
/clone="root-05-105"  
/issue\_type="root"  
/dev\_stage="14 days after germination"  
/lab\_host="B.colli SOLR"  
/clone\_id="Rice root lambda phage cDNA library (root)"  
/note="Vector: pBluescript SK(+); Site 1: Scori; Site 2:  
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'  
end with Scori and 3' end with XhoI site."

ORIGIN

Query Match 92.9%; Score 13; DB 7; Length 366;  
Best Local Similarity 76.9%; Pred. No. 6.5e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCACTCG 14  
||:|||||:  
182 GTACTGCACTCG 194

RESULT 36  
LOCUS CK749390 367 bp mRNA linear EST 07-JUN-2005  
DEFINITION nad03-5c82-a03 Nuphar advena cDNA clone nad03-5c82-a03 5',  
mRNA sequence.  
ACCESSION CK749390  
VERSION CK749390.1 GI:42639813  
KEYWORDS EST.  
SOURCE Nuphar advena  
ORGANISM Nuphar advena  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; basal Magnoliophyta; Nymphaeales;  
Nymphaeaceae; Nuphar.  
1 (bases 1 to 367)  
dePamphilis,C., Carlson,J., Ma,H., Frohlich,M., Tanksey,S.,  
Leebens-Mack,J., Field,D., Arington,J., Zahn,L., Kong,H.,  
Druckemiller,M., Landherr,L., Hu,Y., Iluc,D., Wall,K.,  
Plock,S.,Chlozean,S., Albert,V., Doyle,D., Miller,W.,  
Openeimer,D., Soltis,D., Soltis,P. and Theissen,G.  
Generation of ESTs from early flower buds of Nuphar advena  
Unpublished (2002)  
Contact: Claude dePamphilis or James Leebens-Mack  
Mailier Laboratory  
Penn State University  
208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn  
State University, University Park, PA 16802, USA  
Tel: 814 863 6413  
Fax: 814 865 9131  
Email: cw43@psu.edu or jh110@psu.edu  
The sequence provided is trimmed of vector and low quality regions.  
Full sequence and original trace file are available from the Plant  
Genome Network website (<http://pgn.cornell.edu>)  
Plate: nad03-5c82 row: a column: 03  
Seq primer: M13F.

FEATURES  
source

Location/Qualifiers  
1. 367  
/organism="Nuphar advena"  
/mol\_type="mRNA"  
/db\_xref="taxon:nad03-5c82-a03"  
/db\_xref="taxon:77108"  
/clone="nad03-5c82-a03"  
/issue\_type="flower buds"  
/dev\_stage="2.5mm"  
/lab\_host="SOLR"  
/clone\_id="nad03"  
/note="Vector: pBluescript SK (+/-); Site 1: Scori;  
Site 2: XhoI; Only floral buds with diameter of 2.5 mm of  
leaves were used for RNA isolation. This is a directionally  
cloned, non-normalized library. Avg. insert length: 1134;  
primers: M13F and M13R; Antibiotic: 50 ug/ml Ampicillin;  
Primary Titer: 286 pfu total; Amplified Titer: 3.2E10  
pfu/ml; Mass Excised Titer: 5E10 total; This library has  
been generated by the Floral Genome Project (FGP). The  
Floral Genome Project is funded by NSF's Plant Genome  
Research Program (DBI-0115684). More information about the  
project can be obtained at <http://fgp.bio.psu.edu>"

ORIGIN

Query Match 92.9%; Score 13; DB 7; Length 367;  
Best Local Similarity 76.9%; Pred. No. 6.5e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUACUGCACTCG 13  
||:|||||:  
195 GTACTGCACTCG 207

RESULT 37  
LOCUS FR0030316 368 bp DNA linear GSS 25-FEB-2004  
DEFINITION Fugu rubripes GSS sequence, clone 07H20ec3, genomic survey  
sequence.  
ACCESSION AL026685  
VERSION AL026685.1 GI:3264028  
KEYWORDS GSS; genome survey sequence.  
SOURCE Takifugu rubripes (Fugu rubripes)  
ORGANISM Takifugu rubripes  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
Tetraodontidae; Tetraodontidae; Takifugu.  
1  
Bigar,G., Clark,M.S., Meek,S., Smith,S., Warner,S., Edwards,Y.J.,  
Bouchlir,N., Cottage,A., Yeo,G.S., Umranta,Y., Williams,G. and  
Brenner,S.  
Generation and analysis of 25 Mb of genomic DNA from the pufferfish  
Fugu rubripes by sequence scanning  
Genome Res. 9 (10), 960-971 (1999)  
10523524  
2 (bases 1 to 368)  
Bigar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umranta,Y.,  
Williams,G. and Brenner,S.  
Direct Submission  
Submitted (09-JUN-1998) MRC Human Genome Mapping Project Resource  
Centre, Hinxton, Cambridge, CB10 1SB, UK. Email:  
biohelp@hmp.mrc.ac.uk  
Vector: pBluescript II KS  
V type: phagemid  
PRIMER: KS  
DESCR: One pass dye-terminator sequencing of cosmid cloned genomic  
sequence.  
Location/Qualifiers  
1. 368  
/organism="Takifugu rubripes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:31033"

ORIGIN /clone="077E20EC3"  
/clone\_1b="cosmid 077E20"

Query Match 92.9%; Score 13; DB 11; Length 368;  
Best Local Similarity 76.9%; Pred. No. 6.5e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACTGCACTCG 14  
DB 293 GTACTGCACTCG 305

RESULT 38  
LOCUS CD733604/c 369 bp mRNA linear EST 26-JUN-2003  
DEFINITION 4046300 IGAL - Chicken intestinal lymphocyte Gallus gallus cDNA  
CD733604  
CD733604.1 GI:32284453

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
EST.  
Gallus gallus (chicken)  
Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 369)  
Min,W., Lillehoj,H.S., Ashwell,C.M., Matukumalli,L.K., van  
Tassel,C. and Han,J.Y.  
Chicken intestinal lymphocyte EST database as a resource for the  
analysis of mucosal immune function  
Unpublished (2003)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Contact: Hyun S. Lillehoj  
Animal Parasite Diseases Laboratory  
Animal and Natural Resources Institute, USDA  
Bldg. 1043, BARC-East, Beltsville, MD 20705, USA  
Tel: 3015048771  
Fax: 3015045103  
Email: lillehoj@ars.usda.gov  
Single pass sequencing. Bases called and trimmed with phred  
0.000925 using options -trim\_alt '' -trim\_fasta. Vector identified  
by cross match using options -mismatch 12 -minscore 12  
Plate: 50 row: F column: 07  
Seq primer: ATTGAGTGCACACTGATG  
High quality sequence stop: 369.  
Location/Qualifiers

FEATURES  
Source  
1. 369

/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="white leghorn SC"  
/db\_xref="taxon:9031"  
/clone="IGAL\_50P07"  
/sex="mixed"  
/tissue\_type="Gut"  
/cell\_type="Lymphocyte"  
/dev\_stage="Adult"  
/lab\_host="EMDH10B"  
/clone\_1b="IGAL - Chicken intestinal lymphocyte"  
/note="Organ: Intestine; Vector: PCMV-SPORT6; Site 1:  
Sal; Site 2: NotI; Normalized library from chicken gut  
infected with coccidia duodenum and middle gut."

ORIGIN  
Query Match 92.9%; Score 13; DB 6; Length 369;  
Best Local Similarity 76.9%; Pred. No. 6.5e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACTGCACTCG 14  
DB 17 GTACTGCACTCG 5

RESULT 39

B1120564/c 376 bp mRNA linear EST 31-DEC-2001  
LOCUS B1120564  
DEFINITION B1120564 Populus flower cDNA library Populus trichocarpa cDNA, mRNA  
sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Populus trichocarpa (Populus balsamifera subsp. trichocarpa)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.  
1 (bases 1 to 376)  
Hertberg,M., Aspeborg,H., Erlandsson,R., Bjorkbacka,H.,  
Nilsson,T., Karlsson,J., Teeri,T., Gustafsson,P., Bahlberg,R.,  
Jansson,S., Nilsson,O., Sundberg,B., Nilsson,P., Uhlen,M.,  
Sanderberg,G. and Lundberg,J.  
Gene expression in Populus  
Unpublished (2001)  
Contact: Erlandsson R

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Department of Biotechnology  
Royal Institute of Technology  
Teknikringen 30, Stockholm S-10044, Sweden  
Tel: 46 8 790 8287  
Fax: 46 8 245452  
Email: rikert@biochem.kth.se.  
Location/Qualifiers

FEATURES  
Source  
1. 376

/organism="Populus trichocarpa"  
/mol\_type="mRNA"  
/db\_xref="taxon:3694"  
/tissue\_type="floral buds"  
/clone\_1b="Populus flower cDNA library"  
/note="Organ: flower"

ORIGIN

Query Match 92.9%; Score 13; DB 2; Length 376;  
Best Local Similarity 76.9%; Pred. No. 6.5e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACTGCACTCG 14  
DB 175 GTACTGCACTCG 163

RESULT 40  
LOCUS A1059369/c 379 bp mRNA linear EST 05-JUL-1999  
DEFINITION UI-R-CI-1d-e-09-0-UI\_81 UI-R-CI Rattus norvegicus cDNA clone  
UI-R-CI-1d-e-09-0-UI 3', mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
A1059369  
A1059369.1 GI:3333146  
EST.  
Rattus norvegicus (Norway rat)  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae; Rattus.  
1 (bases 1 to 379)  
Bonaldo,M.F., Lennon,G. and Soares,M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
8889548  
Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBR, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@iowa.edu  
The sequence tag present in the cDNA between the NotI site and the  
oligo-dt track served to identify it as a clone from the normalized

JOURNAL  
PUBMED  
COMMENT



adult 18-day-embryo library. cDNA library Preparation: M. Fatima Bonafide, Ph.D. Clone distribution: clones will be available through Research Genetics This clone is also available through the I.M.A.G.R. Consortium at LBNL (info@image.lbnl.gov). IMAGE ID=1784760 The following repetitive elements were found in this cDNA sequence: 1-23, >AT-rich#low\_complexity 217-249, >AT-rich#low\_complexity  
Seq primer: M13 Forward  
POLYA-No.

## FEATURES

## SOURCE

## Location/Qualifiers

1..379  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="UI-R-C1-1d-e-09-0-UI"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_1lb="UI-R-C1"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; The UI-R-C1 library is a subtracted library derived from the UI-R-C0 library, which is a subtracted library derived from the UI-R-A1 and UI-R-E1 libraries. The UI-R-A1 library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The UI-R-E1 library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C1) was constructed as follows: PCR amplified cDNA inserts from UI-R-C0 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-C0 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C1 library. This procedure has been previously described (Bonafide, Lennon and Soares, Genome Research 6: 791-806, 1996)."

## ORIGIN

Query Match 92.9%; Score 13; DB 1; Length 379;  
Best Local Similarity 76.9%; Pred. No. 6.6e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

CY 2 GUACUGCAACUCG 14  
|:|||||:|  
DB 36 GTACTGCAACTCG 24

RESULT 41  
AM425513  
LOCUS AM425513 399 bp mRNA linear EST 25-APR-2001  
DEFINITION 57554 MARC 2B0V Bos taurus cDNA 5', mRNA sequence.  
VERSION AM425513  
KEYWORDS AM425513.1 GI:6953460  
SOURCE EST.  
ORGANISM Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.

REFERENCE  
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,  
Cassab,B., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,  
Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,  
Chitko-McKown,C.G., Petrea,G., Holt,I., Karaymcheva,S., Liang,F.,

TITLE Quackenbush,J. and Keele,J.W.  
JOURNAL Sequence evaluation of four pooled-tissue normalized bovine cDNA  
PUBMED libraries and construction of a gene index for cattle  
COMMENT Genome Res. 11 (4), 626-630 (2001)  
11282978  
Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called and trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 20  
and -mismatch 12 options.  
PCR primers  
FORWARD: AGGAACACGATGACCAT  
REVERSE: GTTTCGCCAGTCACGACG  
Plate: 31 row: C column: 15  
Seq primer: ATTAGGTACACTATG.  
Location/Qualifiers

## FEATURES

## SOURCE

1..399  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/issue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_1lb="MARC 2B0V"  
/note="Vector: PCMV SPORt6; Site 1: NotI; Site 2: SalI;  
library made from pooled tissue from testis, thymus,  
semiteudonous muscle, longissimus muscle, pancreas,  
adrenal, and endometrium."

## ORIGIN

Query Match 92.9%; Score 13; DB 1; Length 399;  
Best Local Similarity 76.9%; Pred. No. 6.6e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

CY 2 GUACUGCAACUCG 14  
|:|||||:|  
DB 217 GTACTGCAACTCG 229

RESULT 42  
BM032972  
LOCUS BM032972 402 bp mRNA linear EST 05-NOV-2001  
DEFINITION h616109.y1 Ascaris suum female gonad GZ pAMP1 v2 chapel11 McCarter  
ACCESSION BM032972  
VERSION BM032972.1 GI:16746543  
KEYWORDS EST.  
SOURCE Ascaris suum (pig roundworm)  
Ascaris suum  
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida;  
Ascarididae; Ascarididae; Ascaris.

REFERENCE  
AUTHORS McCarter,J., Clifton,S., Chapel11,B., Pape,D., Martin,J.,  
Wylie,T., Dante,M., Maria,M., Hillier,L., Kucaba,T., Treising,B.,  
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,  
Tragarethvill,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,  
Underwood,K., Stepcio,M., Allen,M., Peterson,B., Swaller,T.,  
Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
McCaun,R., Watson,R. and Wilson,R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)  
Contact: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
The library was constructed by Brandi Chapel11 and Dr. James  
McCarter at Washington University, St. Louis. The cDNA was made by

using Dynabead oligo-dT priming (Dyna1). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of PAMPI. Dissected nematode tissues were provided by Dr. Alan Scott (ascot@jhsph.edu) of the School of Public Hygiene and Public Health at John Hopkins University in Baltimore, MD.

## FEATURES

source

1. 402  
/organism="Ascaris suum"  
/mol\_type="mRNA"  
/db\_xref="taxon:6253"  
/sex="Female"  
/tissue\_type="Dissected female gonad (GZ=germinal zone, most distal region of gonad)"  
/dev\_stage="Adult"  
/lab\_host="DH10B"  
/clone\_lib="Ascaris suum female gonad GZ PAMPI v2  
Chapelli McCarter"  
/note="Vector: PAMPI (Gibco); Site 1: NotI; Site 2: SalI; The library was constructed by Brandi Chapelli and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dyna1). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of PAMPI. Dissected nematode tissues were provided by Dr. Alan Scott (ascot@jhsph.edu) of the School of Public Hygiene and Public Health at John Hopkins University in Baltimore, MD."

## ORIGIN

Query Match 92.9%; Score 13; DB 3; Length 402;  
Best Local Similarity 76.9%; Pred. No. 6.6e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 GUACGCAACUCG 14  
|:|:|:|:|:|:|:  
Db 243 GTACTGCAACTCG 255

RESULT 43  
LOCUS A0123512  
DEFINITION HS\_3101\_B1\_E10\_MR\_CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3101 Col=19 Row=J, genomic survey sequence.  
ACCESSION A0123512  
VERSION A0123512  
KEYWORDS GI:3500678  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 403)  
Mahaits,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
COMMENT  
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome  
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
10449764  
Contact: Mahaits GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Sequence Tagged Connector  
Plate: 3101 Row: J Column: 19  
Class: BAC ends

High quality sequence stop: 403..  
Location/Qualifiers  
1. 403  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
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/clone\_plate="Plate=3101 Col=19 Row=J"  
/sex="male"  
/clone\_lib="CIT Approved Human Genomic Sperm Library D"  
/note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in E-Coli DH10B"

## ORIGIN

Query Match 92.9%; Score 13; DB 9; Length 403;  
Best Local Similarity 76.9%; Pred. No. 6.6e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 GUACGCAACUCG 14  
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Db 380 GTACTGCAACTCG 392

RESULT 44  
LOCUS BW915405  
DEFINITION BW915405 Amphioxus Branchiostoma floridae unpublished cDNA library, neurula whole animal Branchiostoma floridae cDNA clone dbne053607 3', mRNA sequence.  
ACCESSION BW915405  
VERSION BW915405.1 GI:66541385  
KEYWORDS EST.  
SOURCE Branchiostoma floridae (Florida lancelet)  
ORGANISM Branchiostoma floridae  
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma.  
1 (bases 1 to 408)  
Yu,J., Holland,L.Z., Shin-I,T., Kohara,Y., Satou,Y. and Satoh,N.  
Expressed genes in Branchiostoma floridae  
Unpublished (2005)  
Contact: Tadashi Shin-I  
Center For Genetic Resource Information  
National Institute of Genetics  
111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6855  
Fax: 81-559-81-6855  
Email: tshin@genetics.nig.ac.jp.  
Location/Qualifiers  
1. 408  
/organism="Branchiostoma floridae"  
/mol\_type="mRNA"  
/db\_xref="taxon:7739"  
/clone="dbne053607"  
/tissue\_type="whole animal"  
/dev\_stage="neurula"  
/clone\_lib="Amphioxus Branchiostoma floridae unpublished cDNA library, neurula whole animal"

## FEATURES

source

1. 408  
/organism="Branchiostoma floridae"  
/mol\_type="mRNA"  
/db\_xref="taxon:7739"  
/clone="dbne053607"  
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/dev\_stage="neurula"  
/clone\_lib="Amphioxus Branchiostoma floridae unpublished cDNA library, neurula whole animal"

## ORIGIN

Query Match 92.9%; Score 13; DB 5; Length 408;  
Best Local Similarity 76.9%; Pred. No. 6.6e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GUACGCAACUCG 13  
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Db 70 GTACTGCAACTC 82

RESULT 45  
LOCUS B0852614/C  
DEFINITION B0852614 409 bp mRNA linear EST 14-AUG-2002  
QB18102.yg.ab1 QG ABCDI lectuca salinas lactuca sativa cDNA clone  
QB18102, mRNA sequence.  
ACCESSION B0852614

VERSION B0852614.1 GI:22238079  
 KEYWORDS EST.  
 SOURCE Lactuca sativa  
 ORGANISM Lactuca sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 asterids; campanulids; Asterales; Asteraceae; Cichorioideae;  
 Cichorieae; Lactuca.  
 1 (bases 1 to 409)  
 Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,  
 Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, D.,  
 Ellstrom, P., Kolman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,  
 Lai, Z., Church, S., Jackson, L. and Bradford, K.  
 Lecture and Sunflower ESTs from the Compositae Genome Project  
 http://compgenomics.ucdavis.edu/  
 Unpublished (2002)  
 JOURNAL Contact: Alexander Kozik (R.W.Michelmore)  
 COMMENT Department of Vegetable Crops, R.W.Michelmore Lab  
 University of California at Davis (UCD)  
 Asmundson Hall, UCD, Davis, CA 95616, USA  
 Tel: 1-(530)-742-1742  
 Fax: 1-(530)-752-9659  
 Email: akozik@ucdavis.edu [michelmore@ucdavis.edu]  
 singleton, see http://cgdb.ucdavis.edu/ for details.  
 Plate: Q8B18 row: 1 column: 02.  
 Location/Qualifiers  
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 /lab\_host="E.coli"  
 /clone\_1fb="QG ABCDI lettuce salinas"  
 /note="Vector: pBRCDMSfiAB: The library was constructed  
 from 10 different sources of RNA from a single genotype.  
 Separate cDNAs were generated using primers that  
 incorporated unique 5' and 3' tags to distinguish each  
 source of RNA. cDNAs were then pooled, size-fractionated,  
 directionally cloned into a custom medium-copy vector and  
 transformations made with four size classes to minimize  
 size bias. Details of each source of RNA and library  
 construction can be obtained at http://cgdb.ucdavis.edu/  
 TAG TISSUE=germinating seeds  
 TAG LIB=QG ABCDI lettuce salinas  
 TAG\_SEQ=TCCTGCGCGG"  
 ORIGIN  
 Query Match 92.9%; Score 13; DB 5; Length 409;  
 Best Local Similarity 76.9%; Pred. No. 6.6e+03;  
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGUACUGCACTC 13  
 DB 231 GCTACTGCAACTC 219  
 RESULT 46  
 B0646387 410 bp mRNA linear EST 07-OCT-2004  
 LOCUS B0646387 Eptaretus burgeri adult Eptaretus burgeri cDNA clone  
 DEFINITION hg106p18 5', mRNA sequence.  
 ACCESSION B0646387  
 VERSION B0646387.1 GI:53861248  
 KEYWORDS EST.  
 SOURCE Eptaretus burgeri (Inshore hagfish)  
 ORGANISM Eptaretus burgeri  
 Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;  
 Myxiniidae; Eptarettidae; Eptaretus.  
 1 (bases 1 to 410)  
 Suzuki, T., Shin-I, T., Kohara, Y. and Kasahara, M.  
 Transcription analysis of hagfish leukocytes: a framework for  
 understanding the immune system of jawless fishes

JOURNAL Dev. Comp. Immunol. 28 (10), 993-1003 (2004)  
 PUBMED 15236930  
 COMMENT Contact: Tadao Shin-I  
 Center for Genetic Resource Information  
 National Institute of Genetics  
 1111 Yata, Mishima, Shizuoka 411-8540, Japan  
 Tel: 81-559-81-6856  
 Fax: 81-559-81-6855  
 Email: tehini@genes.nig.ac.jp.  
 Location/Qualifiers  
 FEATURES  
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 /clone="hg106p18"  
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 Best Local Similarity 76.9%; Pred. No. 6.6e+03;  
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GUACUGCACTC 14  
 DB 274 GCTACTGCAACTC 262  
 RESULT 47  
 CL555282 413 bp DNA linear GSS 14-JUN-2004  
 LOCUS OB\_Ba0005124.f OB\_Ba Oryza brachyantha genomic clone  
 DEFINITION OB\_Ba0005124 5', genomic survey sequence.  
 ACCESSION CL555282  
 VERSION CL555282.1 GI:47631696  
 KEYWORDS GSS.  
 SOURCE Oryza brachyantha  
 ORGANISM Oryza brachyantha  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 413)  
 Kim, H., Yu, Y., Stum, D., Yeast, D., Rao, K., Luo, M., Jetty, R.,  
 Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.  
 OMAP Project  
 Unpublished (2004)  
 JOURNAL Contact: Rod A. Wing  
 COMMENT Arizona Genomics Institute  
 University of Arizona  
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
 Tel: 520 626 9595  
 Fax: 520 621 1259  
 Email: rwing@genome.arizona.edu  
 PCR Primers  
 FORWARD: TAA TAC GAC TCA TTA TAG GG  
 BACKWARD: CAC TCA TTA GGC ACC CCA  
 Insert Length: 145000 Std Error: 0.00  
 Plates: 0005 row: 1 column: 24  
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## REFERENCE

**TITLE**

Db

ACCESSION  
VERSION

## AUTHORS

•

**Email:** ht  
**5 prime s**

CGTACTG

CV723505  
CV723505.

**Song, S.I.  
Large-Bca.**

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/cultivar="Nackdong"
/db_xref="taxon:39947"
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/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Rice root lambda phage CDNA library (root)"
/note="Vector: pluscript SK(+); Site 1: EcoRI; Site 2:
XhoI; CDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

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ORIGIN

```

Query Match          92.9%; Score 13; DB 7; Length 459;
Best Local Similarity 76.9%; Pred. No. 6.6e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY      2 GUACUGCAACTCG 14
       ||:||:||:||
DB      356 GTACTGCAACTCG 344

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Search completed: March 18, 2006, 20:02:46  
Job time : 1384.15 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 18:34:54 ; Search time 281.346 Seconds  
(without alignments)  
331.640 Million cell updates/sec

Title: US-10-800-926-2

Perfect score: 14

Sequence: 1 cguacugcaacug 14

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 segs, 333346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 1000 summaries

Database :

N\_Geneseq\_21:\*

- 1: geneseqn19809:\*
- 2: geneseqn19808:\*
- 3: geneseqn20008:\*
- 4: geneseqn20011a:\*
- 5: geneseqn20011b:\*
- 6: geneseqn2002a:\*
- 7: geneseqn2002b:\*
- 8: geneseqn2003a:\*
- 9: geneseqn2003b:\*
- 10: geneseqn2003c:\*
- 11: geneseqn2003d:\*
- 12: geneseqn2004a:\*
- 13: geneseqn2004b:\*
- 14: geneseqn2005a:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	100.0	14	ADM79935	Adm79935 Bacterial
2	14	100.0	14	ADM60734	Adm60734 Bacterial
3	14	100.0	13	ADM49626	Adm49626 Bacterial
4	14	100.0	13	ACA25094	ACA25094 Prokaryot
5	14	100.0	13	ADM55136	Adm55136 Bacterial
6	14	100.0	13	ACA45239	ACA45239 Prokaryot
7	14	100.0	21	ADU44189	Adu44189 Knock-dow
8	13	92.9	65	ABN51005	Abn51005 Mouse spl
9	13	92.9	100	ACD68769	Acdd68769 E. coli K
10	13	92.9	100	ACD68770	Acdd68770 E. coli K
11	13	92.9	1197	3 AAC61183	Aac61183 Formate d
12	13	92.9	1306	13 ADM51056	Adm51056 Bacterial
13	13	92.9	1332	13 ADM85906	Adm85906 Aspergill
14	13	92.9	1359	5 AAS73079	Aas73079 DNA encod
15	13	92.9	1443	13 ADM85319	Adm85319 Aspergill
16	13	92.9	1488	4 AAF33074	Aaf33074 Human sec
17	13	92.9	1647	4 AAS52489	Aas52489 E. coli D
18	13	92.9	1647	8 ACA32562	ACA32562 Prokaryot
19	13	92.9	1720	6 ABK13893	Abk13893 Gene enco

20	c	13	92.9	1732	5 AAS92825	Aas92825 DNA encod
21	c	13	92.9	1919	5 AAS90081	Aas90081 DNA encod
22	c	13	92.9	1945	4 AAI14703	Aai14703 Probe #46
23	c	13	92.9	1945	4 ABM56435	Abm56435 Human foe
24	c	13	92.9	1945	4 AAI36072	Aai36072 Probe #47
25	c	13	92.9	1945	4 ABA45908	Abm45908 Human bre
26	c	13	92.9	1945	4 ABA26067	Abm26067 Probe #45
27	c	13	92.9	1945	4 ABA30108	Abm30108 Human bon
28	c	13	92.9	1945	4 AAK04600	Aak04600 Human bra
29	c	13	92.9	1945	4 ABE29757	Abm29757 Human liv
30	c	13	92.9	1945	5 AAI04509	Aai04509 Probe #45
31	c	13	92.9	1945	6 ABE04688	Abm04688 Human gen
32	c	13	92.9	2000	10 ACC61225	Acc61225 Gene sequ
33	c	13	92.9	2000	10 ADM63219	Adm63219 DNA encod
34	c	13	92.9	2133	5 AAS88191	Aas88191 DNA encod
35	c	13	92.9	2263	2 AAT93775	Aat93775 PSD-93 co
36	c	13	92.9	3222	5 AAS90082	Aas90082 DNA encod
37	c	13	92.9	3443	13 ADM84732	Adm84732 Aspergill
38	c	13	92.9	14063	2 AAX20500	Aax20500 Polynucle
39	c	13	92.9	83493	14 ADZ13310	Adz13310 Murine ca
40	c	13	92.9	84707	6 ABE67196_6	ABE67196_6
41	c	13	92.9	110000	6 ABE69245_26	ABE69245_26
42	c	13	92.9	110000	14 AEB39175_12	AEB39175_12
43	c	13	92.9	110000	14 AEB42401_12	AEB42401_12
44	c	13	92.9	110000	14 AEB42735_6	AEB42735_6
45	c	13	92.9	184368	14 AEB35722_6	AEB35722_6
46	c	13	92.9	207461	14 AEB39170	AEB39170
47	c	12.6	90.0	201	13 ADS37261	ADS37261
48	c	12.6	90.0	201	13 ADS40621	ADS40621
49	c	12.6	90.0	2290	3 AAA28552	AAA28552
50	c	12.6	90.0	29871	13 ADS36480	ADS36480
51	c	12.6	90.0	321019	13 ADS36450	ADS36450
52	c	12.6	88.6	100	8 ACD68918	ACD68918
53	c	12.4	88.6	100	8 ACD71764	ACD71764
54	c	12.4	88.6	100	8 ACD68919	ACD68919
55	c	12.4	88.6	283	6 ABN16733	ABN16733
56	c	12.4	88.6	323	3 AAC02301	AAC02301
57	c	12.4	88.6	339	13 ADT71332	ADT71332
58	c	12.4	88.6	349	2 AAT78164	AAT78164
59	c	12.4	88.6	349	3 AAS59127	AAS59127
60	c	12.4	88.6	365	12 ADP92282	ADP92282
61	c	12.4	88.6	373	5 ABS72705	ABS72705
62	c	12.4	88.6	375	5 ABA18180	ABA18180
63	c	12.4	88.6	381	4 AAK73289	AAK73289
64	c	12.4	88.6	386	2 AAT29011	AAT29011
65	c	12.4	88.6	435	11 ABD01475	ABD01475
66	c	12.4	88.6	438	6 ABR16449	ABR16449
67	c	12.4	88.6	478	9 ACH41779	ACH41779
68	c	12.4	88.6	504	11 ABD02722	ABD02722
69	c	12.4	88.6	515	13 ABO83881	ABO83881
70	c	12.4	88.6	535	4 AAK91915	AAK91915
71	c	12.4	88.6	535	4 AAK93946	AAK93946
72	c	12.4	88.6	535	12 ADL28342	ADL28342
73	c	12.4	88.6	535	12 ADL30373	ADL30373
74	c	12.4	88.6	543	11 ABD09101	ABD09101
75	c	12.4	88.6	543	11 ABD01629	ABD01629
76	c	12.4	88.6	557	2 AAG13766	AAG13766
77	c	12.4	88.6	558	4 AAF86562	Aaf86562 Vibrio pa
78	c	12.4	88.6	558	4 AAS52309	E. coli D
79	c	12.4	88.6	570	8 ACA32370	Prokaryot
80	c	12.4	88.6	570	8 ABO46119	ABO46119
81	c	12.4	88.6	570	6 ABO46118	ABO46118
82	c	12.4	88.6	594	6 ABO44926	ABO44926
83	c	12.4	88.6	594	6 ABO14927	ABO14927
84	c	12.4	88.6	630	8 ACA42760	ACA42760
85	c	12.4	88.6	645	4 ABL14295	ABL14295
86	c	12.4	88.6	648	4 AAK93254	AAK93254
87	c	12.4	88.6	648	12 ADL29681	ADL29681
88	c	12.4	88.6	669	11 ABD01496	ABD01496
89	c	12.4	88.6	696	11 ABD11114	ABD11114
90	c	12.4	88.6	726	11 ABD15493	ABD15493
91	c	12.4	88.6	743	4 AAK91935	AAK91935
92	c	12.4	88.6	743	4 AAK93345	AAK93345

Aas92825	DNA encod
Aas90081	DNA encod
Aai14703	Probe #46
Abm56435	Human foe
Aai36072	Probe #47
Abm45908	Human bre
Abm26067	Probe #45
Abm30108	Human bon
Aak04600	Human bra
Abm29757	Human liv
Aai04509	Probe #45
Abm04688	Human gen
Acc61225	Gene sequ
Adm63219	DNA encod
Aas88191	DNA encod
Aat93775	PSD-93 co
Aas90082	DNA encod
Adm84732	Aspergill
Aax20500	Polynucle
Adz13310	Murine ca
ABE67196_6	Continuation (7 of
ABE69245_26	Continuation (27 o
AEB39175_12	Continuation (13 o
AEB42401_12	Continuation (13 o
AEB42735_6	Continuation (7 of
AEB35722_6	Continuation (7 of
AEB39170	Continuation (7 of
ADS37261	Continuation (7 of
ADS40621	Continuation (7 of
AAA28552	Continuation (7 of
ADS36480	Continuation (7 of
ADS36450	Continuation (7 of
ACD68918	Continuation (7 of
ACD71764	Continuation (7 of
ACD68919	Continuation (7 of
ABN16733	Continuation (7 of
AAC02301	Continuation (7 of
ADT71332	Continuation (7 of
AAT78164	Continuation (7 of
AAS59127	Continuation (7 of
ADP92282	Continuation (7 of
ABS72705	Continuation (7 of
ABA18180	Continuation (7 of
AAK73289	Continuation (7 of
AAT29011	Continuation (7 of
ABD01475	Continuation (7 of
ABR16449	Continuation (7 of
ACH41779	Continuation (7 of
ABD02722	Continuation (7 of
ABO83881	Continuation (7 of
AAK91915	Continuation (7 of
AAK93946	Continuation (7 of
ADL28342	Continuation (7 of
ADL30373	Continuation (7 of
ABD09101	Continuation (7 of
ABD01629	Continuation (7 of
AAG13766	Continuation (7 of
Aaf86562	Continuation (7 of
AAS52309	Continuation (7 of
ACA32370	Continuation (7 of
ABO46119	Continuation (7 of
ABO46118	Continuation (7 of
ABO44926	Continuation (7 of
ABO14927	Continuation (7 of
ACA42760	Continuation (7 of
ABL14295	Continuation (7 of
AAK93254	Continuation (7 of
ADL29681	Continuation (7 of
ABD01496	Continuation (7 of
ABD11114	Continuation (7 of
ABD15493	Continuation (7 of
AAK91935	Continuation (7 of
AAK93345	Continuation (7 of

C 93	12.4	88.6	743	12	ADL29772	Adl29772 5' end of	166	12.4	88.6	1392	8	ACA25081	ACA25081 Prokaryot
C 94	12.4	88.6	743	12	ADL28362	Adl28362 5' end of	167	12.4	88.6	1397	13	ADL48052	ADL48052 Plant full
C 95	12.4	88.6	756	11	ABD01490	Abd01490 Pseudomon	168	12.4	88.6	1411	13	ADL49753	ADL49753 Plant full
C 96	12.4	88.6	783	5	AAS65673	Aas65673 DNA encod	C 169	12.4	88.6	1498	13	ADL48587	ADL48587 Plant full
C 97	12.4	88.6	798	4	AAK92066	Aak92066 Human CDN	C 170	12.4	88.6	1541	13	ADL49585	ADL49585 Plant full
C 98	12.4	88.6	798	4	AAK94005	Aak94005 Human CDN	C 171	12.4	88.6	1557	13	ADL491743	ADL491743 Polyetid
C 99	12.4	88.6	798	12	ADL30432	Adl30432 3' end of	C 172	12.4	88.6	1557	13	ASB87035	ASB87035 Streptom
C 100	12.4	88.6	798	12	ADL28493	Adl28493 3' end of	C 173	12.4	88.6	1557	13	ASB86832	ASB86832 Streptom
C 101	12.4	88.6	819	14	AEA20721	Aea20721 Novel hum	C 174	12.4	88.6	1563	11	ADL4296	ADL4296 Pseudom
C 102	12.4	88.6	832	14	ADVE0576	Adve0576 Muscari a	C 175	12.4	88.6	1572	4	AAS54183	AAS54183 Prokaryot
C 103	12.4	88.6	834	11	ABD07843	Abd07843 Pseudomon	C 176	12.4	88.6	1572	8	ACA42427	ACA42427 Prokaryot
C 104	12.4	88.6	867	11	ACLE69342	Ac169342 M. xanthu	C 177	12.4	88.6	1583	13	ADL11789	ADL11789 Plant full
C 105	12.4	88.6	879	13	ADT141605	Adt141605 Bacterial	C 178	12.4	88.6	1584	6	ABR6019	ABR6019 S. coelic
C 106	12.4	88.6	879	13	ADSE64017	Adse64017 Bacterial	C 179	12.4	88.6	1584	10	ADH10706	ADH10706 Streptom
C 107	12.4	88.6	889	6	ABO68459	Abog68459 Listeria	C 180	12.4	88.6	1624	13	ADL48472	ADL48472 Plant full
C 108	12.4	88.6	906	4	AAK93936	Aak93936 Human CDN	C 181	12.4	88.6	1627	13	ADL484726	ADL484726 Plant full
C 109	12.4	88.6	906	4	AAK93235	Aak93235 Human CDN	C 182	12.4	88.6	1629	11	ABD01500	ABD01500 Pseudom
C 110	12.4	88.6	906	4	AAK91977	Aak91977 Human CDN	C 183	12.4	88.6	1645	13	ADL60467	ADL60467 Bacterial
C 111	12.4	88.6	906	12	ADL29662	Adl29662 5' end of	C 184	12.4	88.6	1707	8	ACA25819	ACA25819 Prokaryot
C 112	12.4	88.6	906	12	ADL28404	Adl28404 5' end of	C 185	12.4	88.6	1713	2	AAK20661	AAK20661 Polynucle
C 113	12.4	88.6	906	12	ADL30363	Adl30363 5' end of	C 186	12.4	88.6	1737	11	ABD01648	ABD01648 Pseudom
C 114	12.4	88.6	915	13	ADSE63257	Adse63257 Bacterial	C 187	12.4	88.6	1737	11	ABD01675	ABD01675 Pseudom
C 115	12.4	88.6	915	13	ADSE59546	Adse59546 Bacterial	C 188	12.4	88.6	1743	8	ACA36283	ACA36283 Prokaryot
C 116	12.4	88.6	915	13	ADSE62456	Adse62456 Bacterial	C 189	12.4	88.6	1770	9	ADL75639	ADL75639 Rhodococ
C 117	12.4	88.6	927	13	ADSE62777	Adse62777 Bacterial	C 190	12.4	88.6	1776	11	ABD13585	ABD13585 Pseudom
C 118	12.4	88.6	927	13	ADSE63642	Adse63642 Bacterial	C 191	12.4	88.6	1782	9	ADL48275	ADL48275 Rice gene
C 119	12.4	88.6	930	11	ABD07499	Abd07499 Pseudomon	C 192	12.4	88.6	1800	11	ABD05548	ABD05548 Pseudom
C 120	12.4	88.6	960	4	ABL08433	Ab108433 Drosophill	C 193	12.4	88.6	1827	11	ABD02771	ABD02771 Pseudom
C 121	12.4	88.6	1005	14	ACI70878	Ac170878 M. xanthu	C 194	12.4	88.6	1925	11	AAH72967	AAH72967 Human cer
C 122	12.4	88.6	1007	14	ACLE63607	Ac163607 M. xanthu	C 195	12.4	88.6	1926	5	AAH80027	AAH80027 DNA encod
C 123	12.4	88.6	1017	10	ADL32538	Adl32538 R. faeciu	C 196	12.4	88.6	1959	13	ADL49381	ADL49381 Bacterial
C 124	12.4	88.6	1028	8	ABZ37536	Abz37536 Drosophill	C 197	12.4	88.6	2160	14	ADL210724	ADL210724 DNA encod
C 125	12.4	88.6	1032	8	ABZ37536	Abz37536 Streptom	C 198	12.4	88.6	2262	11	ABD02812	ABD02812 Pseudom
C 126	12.4	88.6	1035	10	ABZ66710	Abz66710 Orthosomy	C 199	12.4	88.6	2262	4	AAH23076	AAH23076 Pseudom
C 127	12.4	88.6	1065	5	AAK78324	Aak78324 DNA encod	C 200	12.4	88.6	2288	11	ABD13650	ABD13650 Pseudom
C 128	12.4	88.6	1065	11	ABD01466	Abd01466 Pseudomon	C 201	12.4	88.6	2302	4	AAH34939	AAH34939 Human col
C 129	12.4	88.6	1080	10	ABZ39803	Abz39803 N. gonorr	C 202	12.4	88.6	2346	11	ABD11032	ABD11032 Pseudom
C 130	12.4	88.6	1092	13	ADSE91348	Adse91348 Maize ear	C 203	12.4	88.6	2346	11	ABD13751	ABD13751 Pseudom
C 131	12.4	88.6	1104	11	ACH97088	Ach97088 Klebsiell	C 204	12.4	88.6	2370	11	ACH95568	ACH95568 Klebsiell
C 132	12.4	88.6	1137	11	ABD07579	Abd07579 Pseudomon	C 205	12.4	88.6	2391	11	ABD02588	ABD02588 Pseudom
C 133	12.4	88.6	1144	8	ABZ79953	Abz79953 Mycobacte	C 206	12.4	88.6	2406	8	ABZ79958	ABZ79958 Mycobacte
C 134	12.4	88.6	1152	8	ACA41012	Ac41012 Prokaryot	C 207	12.4	88.6	2409	2	AAK34178	AAK34178 Mycobacte
C 135	12.4	88.6	1152	11	ABD14446	Abd14446 Pseudomon	C 208	12.4	88.6	2409	13	ADL16958	ADL16958 M. tuberc
C 136	12.4	88.6	1185	4	AAS54272	Aas54272 Pseudomon	C 209	12.4	88.6	2416	4	AAH57446	AAH57446 Human lun
C 137	12.4	88.6	1185	9	ACA42593	Ac42593 Prokaryot	C 210	12.4	88.6	2451	2	AAK34179	AAK34179 Mycobacte
C 138	12.4	88.6	1195	9	AAI60901	Aai60901 Human com	C 211	12.4	88.6	2451	13	ADL16960	ADL16960 M. tuberc
C 139	12.4	88.6	1203	11	ABD08953	Abd08953 Pseudomon	C 212	12.4	88.6	2472	11	ABD05852	ABD05852 Pseudom
C 140	12.4	88.6	1203	11	ABD10970	Abd10970 Pseudomon	C 213	12.4	88.6	2495	4	AAI58392	AAI58392 Human pol
C 141	12.4	88.6	1206	2	AAV29010	Aav29010 Formate d	C 214	12.4	88.6	2495	5	ADL48362	ADL48362 DNA encod
C 142	12.4	88.6	1206	6	ABK86863	Abk86863 DNA encod	C 215	12.4	88.6	2495	5	ADL48362	ADL48362 Novel hum
C 143	12.4	88.6	1206	12	ADL15943	Adl15943 Coenzyme-	C 216	12.4	88.6	2502	5	AAH82516	AAH82516 DNA encod
C 144	12.4	88.6	1206	12	ADOS7977	Ados7977 Mycobacte	C 217	12.4	88.6	2508	8	ACA45230	ACA45230 Prokaryot
C 145	12.4	88.6	1233	11	ABD14621	Abd14621 Pseudomon	C 218	12.4	88.6	2520	4	AAK4335	AAK4335 Human full
C 146	12.4	88.6	1254	11	ABD081753	Abd081753 Pseudomon	C 219	12.4	88.6	2520	12	ADL30994	ADL30994 Full leng
C 147	12.4	88.6	1264	8	ACC70828	Acc70828 Thiolacil	C 220	12.4	88.6	2543	4	AAK94301	AAK94301 Human full
C 148	12.4	88.6	1278	13	ADK62241	Adk62241 Plant full	C 221	12.4	88.6	2543	12	ADL30927	ADL30927 Full leng
C 149	12.4	88.6	1287	13	ADK64465	Adk64465 Plant full	C 222	12.4	88.6	2547	4	AAK94315	AAK94315 Human full
C 150	12.4	88.6	1287	4	AAS54131	Aas54131 Pseudomon	C 223	12.4	88.6	2547	12	ADL30954	ADL30954 Full leng
C 151	12.4	88.6	1287	8	ACA42311	Ac42311 Prokaryot	C 224	12.4	88.6	2553	13	ADSE61579	ADSE61579 Bacterial
C 152	12.4	88.6	1287	12	ADH97101	Adh97101 P. aerugi	C 225	12.4	88.6	2556	6	ABQ70793	ABQ70793 Listeria
C 153	12.4	88.6	1287	12	ADH97103	Adh97103 P. aerugi	C 226	12.4	88.6	2563	4	AAK94914	AAK94914 Human full
C 154	12.4	88.6	1287	14	AEC13456	Aec13456 P. aerugi	C 227	12.4	88.6	2563	12	ADL32107	ADL32107 Full leng
C 155	12.4	88.6	1287	14	AEC13458	Aec13458 P. aerugi	C 228	12.4	88.6	2571	8	ACA35386	ACA35386 Prokaryot
C 156	12.4	88.6	1302	14	ADV11962	Adv11962 Plant full	C 229	12.4	88.6	2595	8	ACA23758	ACA23758 Prokaryot
C 157	12.4	88.6	1302	14	ADV11962	Adv11962 A. fumigat	C 230	12.4	88.6	2595	8	ACA26262	ACA26262 Prokaryot
C 158	12.4	88.6	1314	11	ABD09160	Abd09160 Pseudomon	C 231	12.4	88.6	2604	4	AAI60178	AAI60178 Human pol
C 159	12.4	88.6	1324	11	ACI27663	Ac127663 Rice abio	C 232	12.4	88.6	2622	11	ACH98789	ACH98789 Klebsiell
C 160	12.4	88.6	1324	11	ADK09661	Adk09661 Plant full	C 233	12.4	88.6	2634	13	ADL43081	ADL43081 Bacterial
C 161	12.4	88.6	1326	8	ACA23850	Ac23850 Prokaryot	C 234	12.4	88.6	2645	4	ABL05493	ABL05493 Drosophill
C 162	12.4	88.6	1359	11	ACH98649	Ach98649 Klebsiell	C 235	12.4	88.6	2645	10	ADL11404	ADL11404 Bacterial
C 163	12.4	88.6	1363	13	ADK34937	Adk34937 Plant full	C 236	12.4	88.6	2721	13	ADL46438	ADL46438 Bacterial
C 164	12.4	88.6	1365	13	ADT141687	Adt141687 Bacterial	C 237	12.4	88.6	2806	8	ABZ79957	ABZ79957 Mycobacte
C 165	12.4	88.6	1374	13	ADL11685	Adl11685 Plant full	C 238	12.4	88.6	2838	11	ABD15524	ABD15524 Pseudomon



C 239	12.4	88.6	2841	13	ADR40446	Adi40446 Human lino	C 312	12.4	88.6	110000	12	ADN46123_11	Continuation (12 o
C 240	12.4	88.6	2852	4	ABL14294	Abli14294 Drosophill	C 313	12.4	88.6	110000	12	ADN47209_09	Continuation (10 o
C 241	12.4	88.6	2861	4	ABL15226	Abli15226 Drosophill	C 314	12.4	88.6	110000	12	ADN46464_10	Continuation (11 o
C 242	12.4	88.6	2874	4	ABL11169	Abli11169 Drosophill	C 315	12.4	88.6	110000	12	ADN46464_11	Continuation (12 o
C 243	12.4	88.6	2927	13	ACN41952	Acn41952 Human dia	C 316	12.4	88.6	110000	12	ADN46464_11	Continuation (10 o
C 244	12.4	88.6	2934	11	ABD01480	Abd01480 Pseudomon	C 317	12.4	88.6	117213	2	AAV62176	AAV62176 HSV-2 str
C 245	12.4	88.6	2992	13	ACN41953	Acn41953 Human dia	C 318	12.4	88.6	156051	13	ABQ81850	Abq81850 Bifidobac
C 246	12.4	88.6	3010	14	AE887633	AE887633 Human lino	C 319	12.4	88.6	164051	13	ADQ091695	Adq091695 Polyketid
C 247	12.4	88.6	3148	4	ABL25824	Abli25824 Drosophill	C 320	12.4	88.6	164051	13	AE866862	AE866862 Streptomy
C 248	12.4	88.6	3244	4	ABL08432	Abli08432 Drosophill	C 321	12.4	88.6	164051	13	AE866862	AE866862 Streptomy
C 249	12.4	88.6	3244	6	ABL19730	Abli19730 Mouse isc	C 322	12.4	88.6	170170	10	ADL13643	Adl13643 Osteoarth
C 250	12.4	88.6	3398	4	ABL05964	Abli05964 Drosophill	C 323	12.4	88.6	326002	13	ABD32843	ABD32843
C 251	12.4	88.6	3468	5	AA594247	AA594247 DNA encod	C 324	12.4	88.6	349980	5	AAV21610	AAV21610
C 252	12.4	88.6	3472	4	ABL07626	Abli07626 Drosophill	C 325	12.4	88.6	349980	5	AAV21610	AAV21610
C 253	12.4	88.6	3490	14	ADV11961	Adv11961 A fumigat	C 326	12.4	88.6	349980	5	AAV21610	AAV21610
C 254	12.4	88.6	3507	4	ABL13699	Abli13699 Drosophill	C 327	12.4	88.6	349980	6	ABQ81845	Abq81845 Bifidobac
C 255	12.4	88.6	3710	4	ABL13193	Abli13193 Drosophill	C 328	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 256	12.4	88.6	3773	4	ABL07215	Abli07215 Drosophill	C 329	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 257	12.4	88.6	3812	5	AA593388	AA593388 DNA encod	C 330	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 258	12.4	88.6	3897	11	ABD15404	ABD15404 Pseudomon	C 331	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 259	12.4	88.6	3939	5	ABD08638	ABD08638 Human kin	C 332	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 260	12.4	88.6	4029	8	ACA51034	ACA51034 Prokaryot	C 333	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 261	12.4	88.6	4029	8	ACA51034	ACA51034 Prokaryot	C 334	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 262	12.4	88.6	4143	4	AA56308	AA56308 Salmonell	C 335	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 263	12.4	88.6	4251	5	AA589655	AA589655 DNA encod	C 336	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 264	12.4	88.6	4285	8	ABT17985	ABT17985 Aspergill	C 337	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 265	12.4	88.6	4357	12	AD145254	Ad145254 Rice isop	C 338	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 266	12.4	88.6	4525	10	ADF74213	Adf74213 Human mov	C 339	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 267	12.4	88.6	4651	8	ABT19799	ABT19799 Aspergill	C 340	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 268	12.4	88.6	4859	4	AA103936	AA103936 Human rep	C 341	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 269	12.4	88.6	4859	5	AA540336	AA540336 DNA encod	C 342	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 270	12.4	88.6	4859	11	ADT09542	ADT09542 Human pro	C 343	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 271	12.4	88.6	5188	4	ABL11168	Abli11168 Drosophill	C 344	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 272	12.4	88.6	5188	4	ABL11168	Abli11168 Drosophill	C 345	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 273	12.4	88.6	5773	12	ABE87631	ABE87631 Human lino	C 346	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 274	12.4	88.6	5875	14	ABE87631	ABE87631 Human lino	C 347	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 275	12.4	88.6	6203	16	AC164348	AC164348 M. xanthu	C 348	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 276	12.4	88.6	6239	8	ABK93553	ABK93553 Human bre	C 349	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 277	12.4	88.6	6465	8	ACA42641	ACA42641 Prokaryot	C 350	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 278	12.4	88.6	7114	4	ABL07214	Abli07214 Drosophill	C 351	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 279	12.4	88.6	7355	4	ABL07154	Abli07154 Drosophill	C 352	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 280	12.4	88.6	8544	4	ABL07154	Abli07154 Drosophill	C 353	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 281	12.4	88.6	8802	4	ABL13698	Abli13698 Drosophill	C 354	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 282	12.4	88.6	11204	4	AA546245	AA546245 DNA encod	C 355	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 283	12.4	88.6	14283	4	ABL05492	Abli05492 Drosophill	C 356	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 284	12.4	88.6	15042	4	ABL22246	Abli22246 Drosophill	C 357	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 285	12.4	88.6	15711	4	ABL26112	Abli26112 Drosophill	C 358	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 286	12.4	88.6	16141	4	AAK91491	AAK91491 Human dig	C 359	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 287	12.4	88.6	16141	4	AAK91491	AAK91491 Human dig	C 360	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 288	12.4	88.6	16439	4	ABL13192	Abli13192 Drosophill	C 361	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 289	12.4	88.6	22118	8	ADA14746	Ada14746 Mouse 455	C 362	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 290	12.4	88.6	22118	9	ADA37415	Ada37415 Origin of	C 363	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 291	12.4	88.6	22118	10	ADP10518	Adp10518 Mouse rib	C 364	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 292	12.4	88.6	22118	10	ADP10518	Adp10518 Mouse rib	C 365	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 293	12.4	88.6	22118	13	ADR43998	Adr43998 Mouse pre	C 366	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 294	12.4	88.6	22118	13	ADR43998	Adr43998 Mouse pre	C 367	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 295	12.4	88.6	22118	14	AE825474	AE825474 Mouse 455	C 368	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 296	12.4	88.6	28432	4	ABL05010	Abli05010 Drosophill	C 369	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 297	12.4	88.6	59816	8	ABZ37516	ABZ37516 Streptomy	C 370	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 298	12.4	88.6	59816	8	ABZ37516	ABZ37516 Streptomy	C 371	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 299	12.4	88.6	60873	12	AAA81469	AAA81469 N. mening	C 372	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 300	12.4	88.6	64482	12	ADQ59515	Adq59515 Human can	C 373	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 301	12.4	88.6	64482	14	ADZ13896	Adz13896 Murine ca	C 374	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 302	12.4	88.6	72704	14	ACL64810	ACL64810 M. xanthu	C 375	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 303	12.4	88.6	103765	3	AA196883_43	AA196883_43	C 376	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 304	12.4	88.6	103765	3	AA196883_43	AA196883_43	C 377	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 305	12.4	88.6	110000	6	AA196883_43	AA196883_43	C 378	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 306	12.4	88.6	110000	6	AA196883_43	AA196883_43	C 379	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 307	12.4	88.6	110000	11	ADN27081_12	ADN27081_12	C 380	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 308	12.4	88.6	110000	12	ADN46845_11	ADN46845_11	C 381	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 309	12.4	88.6	110000	12	ADN46845_11	ADN46845_11	C 382	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 310	12.4	88.6	110000	12	ADN47591_09	ADN47591_09	C 383	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac
C 311	12.4	88.6	110000	12	ADN46123_10	ADN46123_10	C 384	12.4	88.6	349980	6	ABQ81849	Abq81849 Bifidobac

385	12	85.7	995	14	ABE66688	Abb66688 Rice geno	458	12	85.7	2288	4	ABU27079	AbU27079 Drosophill
C 386	12	85.7	1039	13	ADX11555	Adx11555 Plant full	C 459	12	85.7	2289	6	ABK28655	AbK28655 Human cDN
C 387	12	85.7	1079	2	AAx20676	Aax20676 Polynucle	C 460	12	85.7	2311	3	AAx38012	Aax38012 Rat WAR-1
C 388	12	85.7	1092	4	AAf74781	Aaf74781 Rat WAR-1	C 461	12	85.7	2315	4	AAH15998	Aah15998 Human cDN
C 389	12	85.7	1146	8	ACA37829	Aca37829 Prokaryot	C 462	12	85.7	2394	10	ADC89717	Adc89717 L. johnso
C 390	12	85.7	1168	13	ADX46327	Adx46327 Plant full	C 463	12	85.7	2419	4	AAH14594	Aah14594 Human cDN
C 391	12	85.7	1179	4	ABU04417	AbU04417 Drosophill	C 464	12	85.7	2419	6	ABV77974	Abv77974 Hypoxia-r
C 392	12	85.7	1179	13	ADS96589	AdS96589 Drosophill	C 465	12	85.7	2425	13	ADX61617	Adx61617 Plant full
C 393	12	85.7	1185	3	AAZ56367	Aaz56367 Bacterich	C 466	12	85.7	2460	2	AAZ23692	Aaz23692 D. melano
C 394	12	85.7	1293	4	ABA88909	AbA88909 Bacterich	C 467	12	85.7	2460	2	AAZ88270	Aaz88270 Drosophill
C 395	12	85.7	1338	4	AAH52950	Aah52950 S. epider	C 468	12	85.7	2472	11	ACT28203	Act28203 Rice abio
C 396	12	85.7	1341	13	ADX61915	Adx61915 Plant full	C 469	12	85.7	2501	4	ABU06799	AbU06799 Drosophill
C 397	12	85.7	1356	6	ABN92161	Abn92161 Staphyloc	C 470	12	85.7	2551	4	ABU27080	AbU27080 Drosophill
C 398	12	85.7	1356	13	ADSO1882	Adso1882 Staphyloc	C 471	12	85.7	2567	10	ADG16967	Adg16967 Oncorhync
C 399	12	85.7	1362	13	ADX47723	Adx47723 Plant full	C 472	12	85.7	2571	4	AAI26650	Aai26650 Human bre
C 400	12	85.7	1368	9	ACD19166	Acd19166 B. coli 0	C 473	12	85.7	2584	13	ADO82147	Ado82147 Plant full
C 401	12	85.7	1368	10	ADC01591	Adc01591 Enterobac	C 474	12	85.7	2602	10	ADB64196	Adb64196 Human gen
C 402	12	85.7	1378	4	ABA88908	AbA88908 Bacterich	C 475	12	85.7	2724	5	AA578437	Aa578437 DNA encod
C 403	12	85.7	1413	10	ADP58398	Adp58398 Human pol	C 476	12	85.7	2724	5	AA568040	Aa68040 DNA encod
C 404	12	85.7	1431	2	AAT85635	Aat85635 Balanus a	C 477	12	85.7	2793	12	ADP22447	Adp22447 Sea-squid
C 405	12	85.7	1434	9	ADAJ2352	Adaj2352 DNA encod	C 478	12	85.7	2818	8	AAH54648	Aah54648 S. epider
C 406	12	85.7	1453	8	ABX63157	Abx63157 Human cDN	C 479	12	85.7	2850	8	ACC42476	Acc42476 Human C1Q
C 407	12	85.7	1457	2	AAZ06764	Aaz06764 Phosphodi	C 480	12	85.7	2900	10	ADC89716	Adc89716 L. johnso
C 408	12	85.7	1523	6	AB579007	Ab579007 B. coli C	C 481	12	85.7	2960	6	ABK92144	Abk92144 Prostate
C 409	12	85.7	1523	10	ADH80574	Adh80574 Bacterich	C 482	12	85.7	2960	14	ADK07065	Adk07065 Cyclin-de
C 410	12	85.7	1537	4	AAI58673	Aai58673 Human pol	C 483	12	85.7	2978	12	ADP16891	Adp16891 Acremoniu
C 411	12	85.7	1537	5	ADQ98891	Adq98891 DNA encod	C 484	12	85.7	3030	3	AAH54637	Aah54637 S. epider
C 412	12	85.7	1537	9	ADB48651	Adb48651 Novel hum	C 485	12	85.7	3108	3	AAH97632	Aah97632 Mouse neu
C 413	12	85.7	1560	8	ABZ75094	Abz75094 Mouse emb	C 486	12	85.7	3150	4	AAH54529	Aah54529 S. epider
C 414	12	85.7	1602	12	ADO26194	Ado26194 Human pho	C 487	12	85.7	3348	6	ABZ11420	Abz11420 Human pol
C 415	12	85.7	1636	2	AAK97992	Aak97992 Human sec	C 488	12	85.7	3348	5	ADM43938	Adm43938 Novel hum
C 416	12	85.7	1636	8	ADAA40396	Ada40396 Human sec	C 489	12	85.7	3353	2	ABX71421	Abx71421 Human tes
C 417	12	85.7	1636	8	ACCS0766	Accs0766 Human sec	C 490	12	85.7	3387	2	AAK55540	Aak55540 Invertebr
C 418	12	85.7	1636	9	ADAI11488	Adai11488 Human cDN	C 491	12	85.7	3437	4	ABL18960	AbL18960 Drosophill
C 419	12	85.7	1653	10	ADJ95081	Adj95081 Novel NOV	C 492	12	85.7	3511	6	ABZ11574	Abz11574 Human pol
C 420	12	85.7	1676	11	ACL29320	Acl29320 Rice abio	C 493	12	85.7	3511	5	ADM44092	Adm44092 Novel hum
C 421	12	85.7	1677	14	ACL71310	Acl71310 M. xanthu	C 494	12	85.7	3523	5	ABV24226	Abv24226 Human pro
C 422	12	85.7	1702	6	ABN59709	Abn59709 Novel hum	C 495	12	85.7	3523	3	ABV25694	Abv25694 Human pro
C 423	12	85.7	1728	4	ABL28131	AbL28131 Drosophill	C 496	12	85.7	3546	11	ACN88654	Acn88654 Breast ca
C 424	12	85.7	1730	4	AAI60459	Aai60459 Human pol	C 497	12	85.7	3562	4	ABU04416	AbU04416 Drosophill
C 425	12	85.7	1770	2	AAK98028	Aak98028 Human sec	C 498	12	85.7	3615	4	ABU20427	AbU20427 Drosophill
C 426	12	85.7	1770	8	AAH14148	Aah14148 Human cDN	C 499	12	85.7	3668	10	ABD24893	Abd24893 DNA encod
C 427	12	85.7	1770	8	ADA39936	Ada39936 Human sec	C 500	12	85.7	3699	3	AAZ89623	Aaz89623 A. gossyp
C 428	12	85.7	1770	8	ACCS0515	Accs0515 Human sec	C 501	12	85.7	3747	13	ACN42292	Acn42292 Human dia
C 429	12	85.7	1770	9	ADAI11593	Adai11593 Human cDN	C 502	12	85.7	3828	4	AAH18018	Aah18018 Human cDN
C 430	12	85.7	1782	12	ADQ25930	Adq25930 Human pho	C 503	12	85.7	3828	10	ABX08753	Abx08753 Angiogene
C 431	12	85.7	1782	13	ADR46215	Adr46215 Human pho	C 504	12	85.7	3828	13	ADP56190	Adp56190 Human PRO
C 432	12	85.7	1852	3	AACT7519	Aact7519 Human ORF	C 505	12	85.7	3828	14	AEA36243	Aea36243 Human nuc
C 433	12	85.7	1872	10	ADJ95079	Adj95079 Novel NOV	C 506	12	85.7	3881	6	ABU58814	AbU58814 Fungal me
C 434	12	85.7	1887	2	AAZ06762	Aaz06762 Phosphodi	C 507	12	85.7	4121	2	AAK29140	Aak29140 Hypoxia-r
C 435	12	85.7	1892	10	ABX78371	Abx78371 Corn stre	C 508	12	85.7	4121	9	ACH00173	Ach00173 Rat cDNA
C 436	12	85.7	1917	13	ADRS5506	Adrs5506 Aspergill	C 509	12	85.7	4121	10	ADC69803	Adc69803 Rat R7P22
C 437	12	85.7	1929	14	ADZ62678	Adz62678 Murine pd	C 510	12	85.7	4121	10	AAZ62296	Aaz62296 Hypoxia-r
C 438	12	85.7	1929	14	ADZ85826	Adz85826 Full leng	C 511	12	85.7	4290	4	ABU23008	AbU23008 Drosophill
C 439	12	85.7	1931	4	AAH17375	Aah17375 Human cDN	C 512	12	85.7	4343	4	ABU03429	AbU03429 Drosophill
C 440	12	85.7	1936	13	ADK64838	Adk64838 Plant full	C 513	12	85.7	4343	11	ADM02716	Adm02716 Human cDN
C 441	12	85.7	1967	2	AAZ06763	Aaz06763 Phosphodi	C 514	12	85.7	4482	4	ABU30306	AbU30306 Drosophill
C 442	12	85.7	1991	6	ABK92161	Abk92161 Prostate	C 515	12	85.7	4513	13	ADR07846	Adr07846 Full leng
C 443	12	85.7	1991	12	ADO58106	Ado58106 Human pho	C 516	12	85.7	4513	13	ADR07846	Adr07846 Full leng
C 444	12	85.7	1991	13	ACN40846	Acn40846 Timour-as	C 517	12	85.7	4562	12	ADK60429	Adk60429 Angiogene
C 445	12	85.7	1997	2	AAZ09086	Aaz09086 Cyclic-GM	C 518	12	85.7	4562	14	ADK98490	Adk98490 Human bol
C 446	12	85.7	2000	8	ADA72637	Ada72637 Rice gene	C 519	12	85.7	4835	3	AAA97635	Aaa97635 Mouse neu
C 447	12	85.7	2000	8	ADA72872	Ada72872 Rice gene	C 520	12	85.7	4900	4	ABU22188	AbU22188 Drosophill
C 448	12	85.7	2000	8	ADA73231	Ada73231 Rice gene	C 521	12	85.7	4900	4	AA557166	Aa557166 DNA encod
C 449	12	85.7	2000	11	ACL35285	Acl35285 Rice stre	C 522	12	85.7	4900	10	ADC35890	Adc35890 Drosophill
C 450	12	85.7	2000	11	ACL36121	Acl36121 Rice stre	C 523	12	85.7	5242	12	ADK60429	Adk60429 Angiogene
C 451	12	85.7	2000	11	ACL36274	Acl36274 Rice stre	C 524	12	85.7	5242	12	ADK60730	Adk60730 Angiogene
C 452	12	85.7	2022	6	ABN66286	Abn66286 Streptoco	C 525	12	85.7	5242	12	ADP73052	Adp73052 Angiogene
C 453	12	85.7	2060	6	ABR844919	AbR84491 Aspergill	C 526	12	85.7	5242	12	ADQ96161	Adq96161 T cell ac
C 454	12	85.7	2166	6	ABZ32442	Abz32442 Candida a	C 527	12	85.7	5736	4	ABU08443	AbU08443 Drosophill
C 455	12	85.7	2207	4	AAV29572	Aav29572 L. lactis	C 528	12	85.7	5789	13	ADP06575	Adp06575 Full leng
C 456	12	85.7	2238	4	ABU23009	AbU23009 Drosophill	C 529	12	85.7	6250	14	ACL64310	ACL64310 M. xanthu
C 457	12	85.7	2247	14	ADM11254	Adm11254 Tobacco h	C 530	12	85.7	7040	4	ABU03428	AbU03428 Drosophill

C 531	12	85.7	7176	4	ABL23012	AbL23012 Drosophila	C 604	11.4	81.4	60	6	ABN42325	Abn42325 Human sp1
C 532	12	85.7	8060	13	ADR84332	AdR84332 Aspergillus	C 605	11.4	81.4	60	6	ABN37773	Abn37773 Human sp1
C 533	12	85.7	8158	4	AAK81908	AAK81908 C. albica	C 606	11.4	81.4	65	6	ABN29477	Abn29477 Rat. sp1c
C 534	12	85.7	9291	4	ABL20426	AbL20426 Drosophila	C 607	11.4	81.4	67	6	ABQ73859	Abq73859 Yersinia
C 535	12	85.7	9577	4	ABL08442	AbL08442 Drosophila	C 608	11.4	81.4	100	8	ACD80032	AcD80032 E. coli K
C 536	12	85.7	9974	2	AAK20573	AAK20573 Polynucle	C 609	11.4	81.4	100	8	ACD71765	AcD71765 E. coli K
C 537	12	85.7	10466	4	ABL067458	AbL067458 Drosophila	C 610	11.4	81.4	100	8	ACD80031	AcD80031 E. coli K
C 538	12	85.7	10523	4	AAK87458	AAK87458 Human imm	C 611	11.4	81.4	103	2	AAO65663	AAO65663 Alkaline
C 539	12	85.7	10523	4	AAK87455	AAK87455 Human imm	C 612	11.4	81.4	110	9	ACH03348	ACH03348 Human 1at
C 540	12	85.7	12198	10	ADRS7247	AdRS7247 Rat gene	C 613	11.4	81.4	147	8	AAK73524	AAK73524 Streptomy
C 541	12	85.7	12198	10	ADRS7247	AdRS7247 Rat gene	C 614	11.4	81.4	149	2	AAQ76767	AAQ76767 Human gen
C 542	12	85.7	12677	4	AAK72352	AAK72352 Human imm	C 615	11.4	81.4	156	7	ADRS66626	ADRS66626 Corn seed
C 543	12	85.7	12677	4	AAK72351	AAK72351 Human imm	C 616	11.4	81.4	159	4	AAI55222	AAI55222 Corn seed
C 544	12	85.7	13227	4	ABL17698	AbL17698 Drosophila	C 617	11.4	81.4	159	4	ABN49880	Abn49880 Human 1iv
C 545	12	85.7	13227	4	ABL17698	AbL17698 Drosophila	C 618	11.4	81.4	159	4	ABN70072	Abn70072 Human 1iv
C 546	12	85.7	15468	12	ADN73144	AdN73144 Thale cte	C 619	11.4	81.4	162	4	ABN70072	Abn70072 Human 1iv
C 547	12	85.7	15762	4	ABL06916	AbL06916 Drosophila	C 620	11.4	81.4	162	4	AAI50188	AAI50188 Probe #18
C 548	12	85.7	17379	4	AAK71667	AAK71667 Human imm	C 621	11.4	81.4	162	4	ABN36870	Abn36870 Probe #15
C 549	12	85.7	17379	4	AAK71667	AAK71667 Human imm	C 622	11.4	81.4	162	4	AAK44181	AAK44181 Human bon
C 550	12	85.7	17379	10	ADG41623	AdG41623 Human res	C 623	11.4	81.4	162	4	AAK18283	AAK18283 Human bra
C 551	12	85.7	19278	10	ACRS7551	ACRS7551 Human fru	C 624	11.4	81.4	162	4	ABN43837	Abn43837 Human 1iv
C 552	12	85.7	20001	13	ADT77134	AdT77134 Type II d	C 625	11.4	81.4	168	2	AAQ83666	AAQ83666 Partial I
C 553	12	85.7	20001	13	ABN96527	ABN96527 Human ALD	C 626	11.4	81.4	171	2	AAQ83671	AAQ83671 Partial I
C 554	12	85.7	24081	10	AAO54223	AAO54223 Streptomy	C 627	11.4	81.4	173	4	AAI22832	AAI22832 Probe #12
C 555	12	85.7	26190	4	AAI89929	AAI89929 Human exc	C 628	11.4	81.4	173	4	ABN67922	Abn67922 Human foe
C 556	12	85.7	26190	4	AAI89929	AAI89929 Human exc	C 629	11.4	81.4	173	4	AAI48133	AAI48133 Probe #16
C 557	12	85.7	29559	14	ACR64791	ACR64791 M. xanthu	C 630	11.4	81.4	173	4	ABN49999	Abn49999 Human bre
C 558	12	85.7	36568	6	ABK50980	ABK50980 Human sol	C 631	11.4	81.4	173	4	AAK42068	AAK42068 Human bon
C 559	12	85.7	51698	12	ADQ97614	AdQ97614 Mouse can	C 632	11.4	81.4	173	4	AAK16317	AAK16317 Human bra
C 560	12	85.7	52101	10	ADQ97614	AdQ97614 Mouse can	C 633	11.4	81.4	173	4	ABN41672	Abn41672 Human 1iv
C 561	12	85.7	53122	11	ACN43998_6	ACN43998_6 Continuation (7 of	C 634	11.4	81.4	173	5	AAI08504	AAI08504 Probe #84
C 562	12	85.7	63079	14	ADZ12509	AdZ12509 Murine ca	C 635	11.4	81.4	173	5	ABN16106	Abn16106 Human gen
C 563	12	85.7	72409	13	ABD33061	ABD33061 Human can	C 636	11.4	81.4	177	4	ABN24709	Abn24709 Drosophila
C 564	12	85.7	90616	12	ADQ97596	AdQ97596 Mouse can	C 637	11.4	81.4	180	10	ADD08988	ADD08988 Human pb
C 565	12	85.7	97291	10	ACR65377	ACR65377 Phototab	C 638	11.4	81.4	183	1	AAV92471	AAV92471 Sequence
C 566	12	85.7	110000	6	ABA90521_18	ABA90521_18 Continuation (19 o	C 639	11.4	81.4	183	2	AAQ83670	AAQ83670 Partial I
C 567	12	85.7	110000	6	ADT77367_55	ADT77367_55 Continuation (56 o	C 640	11.4	81.4	189	8	ACA25428	ACA25428 Prokaryot
C 568	12	85.7	110000	13	ABD32665	ABD32665 Human can	C 641	11.4	81.4	191	4	ABN74973	Abn74973 Human foe
C 569	12	85.7	112453	13	ABD32665	ABD32665 Human can	C 642	11.4	81.4	191	4	AAI55501	AAI55501 Probe #24
C 570	12	85.7	112453	11	ACN44296	ACN44296 Human PDE	C 643	11.4	81.4	191	4	ABN39663	Abn39663 Probe #18
C 571	12	85.7	122673	14	ABE61123	ABE61123 Human s	C 644	11.4	81.4	191	4	ABN49618	Abn49618 Human bon
C 572	12	85.7	143899	6	AAI38336	AAI38336 Genomic s	C 645	11.4	81.4	191	4	AAK23477	AAK23477 Human 1iv
C 573	12	85.7	168325	11	ACN44484	ACN44484 Mouse gen	C 646	11.4	81.4	191	4	ABN49339	Abn49339 Human bra
C 574	12	85.7	235070	11	ACN45174	ACN45174 Human gen	C 647	11.4	81.4	191	4	ABN23106	Abn23106 Human gen
C 575	12	85.7	275790	14	ADZ00150	AdZ00150 Salmonell	C 648	11.4	81.4	191	6	ABN23106	Abn23106 Human gen
C 576	12	85.7	310268	13	ABD32548	ABD32548 Human can	C 649	11.4	81.4	192	4	AAH504728	AAH504728 Gene expr
C 577	11.6	82.9	33	12	ADJ66778	ADJ66778 Flea and	C 650	11.4	81.4	195	4	AAH35239	AAH35239 Human COL
C 578	11.6	82.9	2000	8	ADAT73026	ADAT73026 Rice gene	C 651	11.4	81.4	195	10	ADH85366	ADH85366 Enterococ
C 579	11.4	81.4	20	2	AAV31172	AAV31172 Bacillus	C 652	11.4	81.4	198	6	ABN76744	Abn76744 Human ORP
C 580	11.4	81.4	20	2	AAV31180	AAV31180 Bacillus	C 653	11.4	81.4	199	12	ACH83057	ACH83057 Human gen
C 581	11.4	81.4	20	6	ABK11818	ABK11818 Hybrid B.	C 654	11.4	81.4	203	7	ADN66830	ADN66830 Corn bead
C 582	11.4	81.4	20	6	ABK11826	ABK11826 5' exchan	C 655	11.4	81.4	206	14	ADY53863	ADY53863 Gordonia
C 583	11.4	81.4	20	10	ADH93897	ADH93897 Human gen	C 656	11.4	81.4	227	14	ADY53861	ADY53861 Gordonia
C 584	11.4	81.4	20	12	ADL35186	ADL35186 B. thurin	C 657	11.4	81.4	230	4	AAH57347	AAH57347 Human bra
C 585	11.4	81.4	20	12	ADL35175	ADL35175 Human bra	C 658	11.4	81.4	237	5	AAH71836	AAH71836 DNA encod
C 586	11.4	81.4	20	12	ADQ91963	ADQ91963 PCR prime	C 659	11.4	81.4	237	13	ADN50615	ADN50615 Bacteri
C 587	11.4	81.4	20	12	ADQ91960	ADQ91960 PBG1088 a	C 660	11.4	81.4	243	12	ADL02685	ADL02685 DNA encod
C 588	11.4	81.4	24	6	ABQ05350	ABQ05350 Oligonuc	C 661	11.4	81.4	244	12	ADP55119	ADP55119 Maize car
C 589	11.4	81.4	24	6	ABQ11596	ABQ11596 Oligonuc	C 662	11.4	81.4	250	4	ABN88653	ABN88653 Bacteri
C 590	11.4	81.4	24	6	ABQ05309	ABQ05309 Oligonuc	C 663	11.4	81.4	255	6	ABK87533	ABK87533 Mammalian
C 591	11.4	81.4	24	6	ABQ06675	ABQ06675 Oligonuc	C 664	11.4	81.4	258	8	ACA00790	ACA00790 C. glutam
C 592	11.4	81.4	24	6	ABQ11637	ABQ11637 Oligonuc	C 665	11.4	81.4	264	5	AAH66623	AAH66623 C. glutam
C 593	11.4	81.4	25	2	AAH04429	AAH04429 M. tuberc	C 666	11.4	81.4	269	12	ADP66217	ADP66217 Soybean c
C 594	11.4	81.4	25	6	ABQ13132	ABQ13132 Oligonuc	C 667	11.4	81.4	276	6	ABN74740	ABN74740 Corn taab
C 595	11.4	81.4	25	9	ACH56700	ACH56700 DNA targ	C 668	11.4	81.4	291	6	ABK38794	ABK38794 CDNA enco
C 596	11.4	81.4	25	9	ACH56700	ACH56700 DNA targ	C 669	11.4	81.4	291	8	ACA11123	ACA11123 Human lun
C 597	11.4	81.4	30	2	AAO10731	AAO10731 Oligonuc	C 670	11.4	81.4	291	10	ACA02309	ACA02309 Lung can
C 598	11.4	81.4	33	2	AAO83647	AAO83647 Internal	C 671	11.4	81.4	291	13	ADJ20270	ADJ20270 Human lun
C 599	11.4	81.4	50	4	AAH34522	AAH34522 Human SNP	C 672	11.4	81.4	291	13	ADJ20270	ADJ20270 Human lun
C 600	11.4	81.4	50	4	AAO30883	AAO30883 Human 95 p	C 673	11.4	81.4	292	3	AAO19158	AAO19158 Human sec
C 601	11.4	81.4	51	4	AAI78257	AAI78257 Human g1	C 674	11.4	81.4	293	12	ADP62755	ADP62755 Maize car
C 602	11.4	81.4	60	6	ABQ73883	ABQ73883 Yersinia	C 675	11.4	81.4	296	6	ABN73464	ABN73464 Corn taab
C 603	11.4	81.4	60	6	ABN49744	ABN49744 Human sp1	C 676	11.4	81.4	305	6	ABN68969	ABN68969 Novel. mur

677	11.4	81.4	307	5	ABA11517	Abal1517 Human ner	C 750	11.4	81.4	458	5	AA104872	AA104872 Probe #48
678	11.4	81.4	308	10	ABX85434	Abx85434 Corn ear-	C 751	11.4	81.4	458	5	AA103496	AA103496 Probe #34
C 679	11.4	81.4	321	10	AAT31177	Aat31177 Mutated O	C 752	11.4	81.4	458	6	AB503564	AB503564 Human gen
C 680	11.4	81.4	321	12	ADL93587	Adl93587 Human CD4	C 753	11.4	81.4	458	6	AB505136	AB505136 Human gen
681	11.4	81.4	328	3	AAA41530	Aaa41530 Human bec	C 754	11.4	81.4	458	9	ADN38400	Adn38400 Corn cinn
682	11.4	81.4	330	3	ADA49151	Ada49151 Maize gen	C 755	11.4	81.4	458	10	ADG88750	Adg88750 Corn cinn
C 683	11.4	81.4	335	2	AAV87152	Aav87152 EST clone	C 756	11.4	81.4	459	3	ACA46344	Aca46344 Arabidops
684	11.4	81.4	340	2	ACH42717	Ach42717 Human foe	C 757	11.4	81.4	459	8	ACA35048	Aca35048 Prokaryot
685	11.4	81.4	352	12	ACH93436	Ach93436 Human gen	C 758	11.4	81.4	460	4	ABA57446	Abas7446 Human foe
C 686	11.4	81.4	357	13	ACF85010	Acf85010 Human STR	C 759	11.4	81.4	460	4	ABA36994	Abas6994 Probe #56
687	11.4	81.4	358	6	ABO85712	Abog85712 Arabidops	C 760	11.4	81.4	460	4	ABA26950	Abas6950 Probe #54
688	11.4	81.4	365	4	AAK58666	Aak58666 Human imm	C 761	11.4	81.4	460	4	AAK31085	Aak31085 Human bon
C 689	11.4	81.4	369	3	AAZ45989	Aaz45989 Gene frag	C 762	11.4	81.4	460	4	AAK05484	Aak05484 Human bra
C 690	11.4	81.4	371	3	AAZ45989	Aaz45989 CDNA enco	C 763	11.4	81.4	460	4	AB530764	Abas30764 Human liv
C 691	11.4	81.4	372	14	ACL56113	Acl56113 Human col	C 764	11.4	81.4	460	6	AB505836	AB505836 Human gen
C 692	11.4	81.4	374	2	AAQ73727	Aaq73727 Retrocans	C 765	11.4	81.4	462	10	ADD08978	Add08978 Human pan
C 693	11.4	81.4	374	4	AAK73298	Aak73298 Human imm	C 766	11.4	81.4	463	5	AAH87825	Aah87825 Peppermint
C 694	11.4	81.4	375	2	AAV87184	Aav87184 EST clone	C 767	11.4	81.4	463	5	ABV46070	Abv46070 Human pro
C 695	11.4	81.4	378	10	ADD08982	Add08982 Human pan	C 768	11.4	81.4	463	9	ACH45567	Ach45567 Human foe
C 696	11.4	81.4	381	9	ACH46902	Ach46902 Human inf	C 769	11.4	81.4	465	2	AAT36688	Aat36688 Osteoclas
C 697	11.4	81.4	388	9	ACH19655	Ach19655 Human adu	C 770	11.4	81.4	465	6	ABV98307	Abv98307 Human pan
698	11.4	81.4	392	10	ADF57861	Adf57861 Human pol	C 771	11.4	81.4	469	4	AAH00970	Aah00970 Leibman
C 699	11.4	81.4	398	8	ABX36584	Abx36584 Bovine ES	C 772	11.4	81.4	469	4	AAH00972	Aah00972 Leibman
C 700	11.4	81.4	398	10	ADH42944	Adh42944 Mouse pro	C 773	11.4	81.4	469	4	ACH13531	Ach13531 Human adu
701	11.4	81.4	403	5	AA105074	AA105074 Probe #50	C 774	11.4	81.4	471	5	ABA20385	Abas20385 Human ner
702	11.4	81.4	403	10	ADL24523	Adl24523 Intestina	C 775	11.4	81.4	480	11	ABD15066	Abd15066 Pseudomon
703	11.4	81.4	404	4	AAH12660	Aah12660 Human cdn	C 776	11.4	81.4	480	11	ACH13758	Ach13758 Human adu
C 704	11.4	81.4	405	4	AAH84616	Aah84616 B. coli g	C 777	11.4	81.4	483	9	ADH50413	Adh50413 Primary r
C 705	11.4	81.4	405	4	AAH84616	Aah84616 Bovine ES	C 778	11.4	81.4	487	10	ADH50413	Adh50413 Primary r
C 706	11.4	81.4	405	8	AAH84616	Aah84616 Bovine ES	C 779	11.4	81.4	490	9	ACH33390	Ach33390 Human end
C 707	11.4	81.4	405	12	ACH83330	Ach83330 Human gen	C 780	11.4	81.4	495	13	ADH50554	Adh50554 Plant ful
C 708	11.4	81.4	408	2	AAT85950	Aat85950 Human leu	C 781	11.4	81.4	496	13	ACN50698	Acn50698 Cotton an
C 709	11.4	81.4	408	2	AAT85950	Aat85950 Human leu	C 782	11.4	81.4	497	13	ACN50784	Acn50784 Cotton an
C 710	11.4	81.4	408	8	ABX37499	Abx37499 Bovine ES	C 783	11.4	81.4	498	6	ABK55324	Abk55324 Human col
C 711	11.4	81.4	412	8	ABX37585	Abx37585 Bovine ES	C 784	11.4	81.4	498	8	ACA26394	Aca26394 Prokaryot
C 712	11.4	81.4	412	8	ABX37585	Abx37585 Bovine ES	C 785	11.4	81.4	500	12	ACH77234	Ach77234 Human gen
713	11.4	81.4	415	5	AAH8743	Aah8743 Sucrose p	C 786	11.4	81.4	501	4	ABA62449	Abas62449 Human foe
714	11.4	81.4	415	5	AAH8743	Aah8743 Sucrose p	C 787	11.4	81.4	501	4	AAI42429	AAI42429 Probe #11
715	11.4	81.4	415	10	ADBS1486	Adbs1486 Primary r	C 788	11.4	81.4	501	4	ABA29783	Abas29783 Probe #82
C 716	11.4	81.4	417	8	ABX55824	Abx55824 Bovine ES	C 789	11.4	81.4	501	4	AAK36655	Aak36655 Human bon
717	11.4	81.4	420	5	ABV16272	Abv16272 Human pro	C 790	11.4	81.4	501	4	AAK10794	Aak10794 Human bra
718	11.4	81.4	421	5	AAH67574	Aah67574 Novel hum	C 791	11.4	81.4	501	4	AB536320	AB536320 Human liv
C 719	11.4	81.4	421	6	ABQ99118	Abq99118 Human ORF	C 792	11.4	81.4	501	5	AB591635	AB591635 DNA enco
720	11.4	81.4	429	8	ABX36242	Abx36242 Bovine ES	C 793	11.4	81.4	501	6	AB510666	Abas10666 Human gen
C 721	11.4	81.4	432	2	AAT33176	Aat33176 Mutated O	C 794	11.4	81.4	504	3	AB513976	Abas13976 Neisseria
C 722	11.4	81.4	432	6	ABK62903	Abk62903 Rat seque	C 795	11.4	81.4	504	10	ADH76429	Adh76429 DNA homol
C 723	11.4	81.4	432	10	ADBS1697	Adbs1697 Toxicity-	C 796	11.4	81.4	504	10	ADH76429	Adh76429 DNA homol
C 724	11.4	81.4	432	10	ADBS1697	Adbs1697 Toxicity-	C 797	11.4	81.4	504	10	ADH76429	Adh76429 DNA homol
C 725	11.4	81.4	438	2	AAT36689	Aat36689 Osteoclas	C 798	11.4	81.4	505	12	ADJ10782	Adj10782 Recombina
C 726	11.4	81.4	438	5	ABV38586	Abv38586 Human pro	C 799	11.4	81.4	505	12	ACH69357	Ach69357 Human gen
C 727	11.4	81.4	439	6	ABK62922	Abk62922 Rat seque	C 800	11.4	81.4	510	4	AB119531	Ab119531 Drosophi
C 728	11.4	81.4	439	10	ADBS6953	Adbs6953 Toxicity-	C 801	11.4	81.4	510	11	ACH29334	Ach29334 Drosophi
C 729	11.4	81.4	443	4	AAK64488	Aak64488 Human imm	C 802	11.4	81.4	510	11	ACH29334	Ach29334 Drosophi
C 730	11.4	81.4	443	5	AAH68816	Aah68816 DNA enco	C 803	11.4	81.4	512	12	ADL84315	Adl84315 DNA up-re
C 731	11.4	81.4	446	9	ACH41471	Ach41471 Human adu	C 804	11.4	81.4	512	12	ADL84316	Adl84316 DNA up-re
C 732	11.4	81.4	448	9	ACH48739	Ach48739 Human leu	C 805	11.4	81.4	513	13	AAH11322	Aah11322 Aspergill
C 733	11.4	81.4	448	9	ACH45475	Ach45475 Human foe	C 806	11.4	81.4	513	13	ADU55363	Adu55363 Aspergill
C 734	11.4	81.4	449	13	ADH10349	Adh10349 Plant ful	C 807	11.4	81.4	513	13	ADH29336	Adh29336 Aspergill
C 735	11.4	81.4	450	8	ACA28963	Aca28963 Prokaryot	C 808	11.4	81.4	515	6	ABQ36137	Abq36137 Oligonuc
C 736	11.4	81.4	454	6	ABT11346	Abt11346 Yeast bel	C 809	11.4	81.4	515	6	ABQ36136	Abq36136 Oligonuc
C 737	11.4	81.4	458	4	AAI13609	Aai13609 Probe #35	C 810	11.4	81.4	515	6	ACH15803	Ach15803 Human adu
C 738	11.4	81.4	458	4	AAI15114	Aai15114 Probe #50	C 811	11.4	81.4	516	11	ACH96986	Ach96986 K1ebstei
C 739	11.4	81.4	458	4	ABA55319	Abas55319 Human foe	C 812	11.4	81.4	520	6	ABL01379	Ab101379 Murine ap
C 740	11.4	81.4	458	4	ABA56866	Abas6866 Human foe	C 813	11.4	81.4	520	12	ACN59750	Acn59750 Cotton gy
C 741	11.4	81.4	458	4	AAI34970	Aai34970 Probe #36	C 814	11.4	81.4	521	12	ACH79760	Ach79760 Human gen
C 742	11.4	81.4	458	4	AAI36450	Aai36450 Probe #51	C 815	11.4	81.4	522	8	ACA32316	Aca32316 Prokaryot
C 743	11.4	81.4	458	4	ABA44858	Abas44858 Human bre	C 816	11.4	81.4	525	14	AAH15942	Aah15942 Human ost
C 744	11.4	81.4	458	4	ABA46313	Abas46313 Human bre	C 817	11.4	81.4	525	14	AAH15942	Aah15942 Human ost
C 745	11.4	81.4	458	4	AAK29023	Aak29023 Human bon	C 818	11.4	81.4	528	13	ADH65644	Adh65644 DNA enco
C 746	11.4	81.4	458	4	AAK30501	Aak30501 Human bon	C 819	11.4	81.4	535	12	ADH35889	Adh35889 CDNA enco
C 747	11.4	81.4	458	4	AAK35652	Aak35652 Human bra	C 820	11.4	81.4	535	12	ADH35889	Adh35889 CDNA enco
C 748	11.4	81.4	458	4	AB530160	AB530160 Human liv	C 821	11.4	81.4	536	4	AAI63827	Aai63827 Human pol
C 749	11.4	81.4	458	4	AB528636	AB528636 Human liv	C 822	11.4	81.4	536	4	AAH31623	Aah31623 CDNA enco

823	11.4	81.4	536	4	ABK43817	Abk43817 DNA encod	c 896	11.4	81.4	618	13	ADV41756	Adv41756 Rat card1
824	11.4	81.4	536	12	AD154204	Ad154204 CDNA pnc	c 897	11.4	81.4	629	13	ACN53940	Acn53940 Cotton an
825	11.4	81.4	536	12	ADM24378	Adm24378 Human pnc	c 898	11.4	81.4	626	10	ADCT7372	Adct7372 DNA Seg I
826	11.4	81.4	537	3	AACT4530	Aact4530 Human ORF	c 899	11.4	81.4	633	3	AAZ55544	Aaz55544 Feline ma
827	11.4	81.4	537	6	ABN16615	Abn16615 Human ORF	c 900	11.4	81.4	633	3	AAZ55545	Aaz55545 Feline ma
828	11.4	81.4	538	13	ADQ48838	Adq48838 Novel can	c 901	11.4	81.4	642	10	ADCS51237	Adcs51237 Mutant P
829	11.4	81.4	539	9	ACH37731	Ach37731 Human end	c 902	11.4	81.4	647	4	ABU18861	Abu18861 Drosophill
830	11.4	81.4	542	4	AAH37189	Aah37189 Human col	c 903	11.4	81.4	649	6	ABK43351	Abk43351 Human cdn
831	11.4	81.4	543	11	ABD17593	Abd17593 Human eos	c 904	11.4	81.4	650	5	AAH90153	Aah90153 DNA encod
832	11.4	81.4	543	6	ABQ44997	Abq44997 Oligonuc1	c 906	11.4	81.4	661	10	ADK55181	Adk55181 Plant DNA
833	11.4	81.4	546	6	ABO44996	Abq44996 Oligonuc1	c 907	11.4	81.4	661	10	ADK57744	Adk57744 Plant DNA
834	11.4	81.4	546	6	ADCT6962	Adct6962 DNA homol	c 908	11.4	81.4	662	9	ACL24023	ACL24023 DNA clone
835	11.4	81.4	547	14	ABE66206	Abe66206 Rice geno	c 909	11.4	81.4	670	5	AAE93361	Aae93361 DNA encod
836	11.4	81.4	549	3	AAAC42993	Aaac42993 Arabidops	c 910	11.4	81.4	671	3	AAE13513	Aae13513 Aspergill
837	11.4	81.4	549	13	ADQ57259	Adq57259 Novel can	c 911	11.4	81.4	671	10	ADCT6220	Adct6220 DNA homol
838	11.4	81.4	554	4	AAI43036	Aai43036 Probe #11	c 912	11.4	81.4	671	10	ADK54118	Adk54118 Plant DNA
839	11.4	81.4	554	4	ABK36880	Abk36880 Human liv	c 913	11.4	81.4	671	10	ADK54118	Adk54118 Plant DNA
840	11.4	81.4	554	6	ABO32977	Abq32977 Oligonuc1	c 913	11.4	81.4	671	10	ADK54118	Adk54118 Plant DNA
841	11.4	81.4	554	6	ABO32976	Abq32976 Oligonuc1	c 914	11.4	81.4	671	10	ADK54118	Adk54118 Plant DNA
842	11.4	81.4	555	9	ACL24021	ACL24021 DNA clone	c 915	11.4	81.4	671	10	ADK54118	Adk54118 Plant DNA
843	11.4	81.4	555	9	ACL24021	ACL24021 DNA clone	c 916	11.4	81.4	672	13	ADR61857	Adr61857 Cotton cd
844	11.4	81.4	557	4	AAH10202	Aah10202 Human cdn	c 917	11.4	81.4	679	13	ADT17591	Adt17591 Plant cdn
845	11.4	81.4	558	12	ACH79736	Ach79736 Human gen	c 918	11.4	81.4	684	13	ADT17591	Adt17591 Plant cdn
846	11.4	81.4	558	12	AAAT33180	Aaat33180 Mutated O	c 919	11.4	81.4	685	4	AAK93634	Aak93634 Human cdn
847	11.4	81.4	566	13	ADQ56901	Adq56901 Novel can	c 920	11.4	81.4	685	4	AAK93634	Aak93634 Human cdn
848	11.4	81.4	567	4	ABA60765	Abaf60765 Human foe	c 921	11.4	81.4	685	12	ADL30061	Adl30061 3' end of
849	11.4	81.4	567	4	AAI40658	Aai40658 Probe #93	c 922	11.4	81.4	685	12	ADL28387	Adl28387 5' end of
850	11.4	81.4	567	4	ABA28814	Abaf28814 Probe #72	c 923	11.4	81.4	685	12	ADL28387	Adl28387 5' end of
851	11.4	81.4	567	4	AAK34942	Aak34942 Human bon	c 924	11.4	81.4	690	8	ACC47178	Acc47178 Rat APOB
852	11.4	81.4	567	4	AAK09051	Aak09051 Human bra	c 925	11.4	81.4	690	8	AAK91781	Aak91781 DNA probe
853	11.4	81.4	567	4	ABK34696	Abk34696 Human liv	c 926	11.4	81.4	705	5	AAK91529	Aak91529 DNA encod
854	11.4	81.4	567	6	ABK09443	Abk09443 Human gen	c 927	11.4	81.4	708	4	ABA89034	Abaf89034 Escherich
855	11.4	81.4	567	10	AAU56260	Aau56260 Bovine IT	c 928	11.4	81.4	710	12	ADU42783	Adu42783 Plant cdn
856	11.4	81.4	569	12	ADU44194	Adi44194 Plant cdn	c 929	11.4	81.4	714	13	ACH90889	Ach90889 Human gen
857	11.4	81.4	570	9	ACL24022	ACL24022 DNA clone	c 930	11.4	81.4	715	13	ADK48180	Adk48180 Plant ful
858	11.4	81.4	571	12	ADQ92040	Adq92040 Human aut	c 931	11.4	81.4	717	11	ABD01748	Abd01748 Pseudomon
859	11.4	81.4	575	10	ADK53242	Adk53242 Plant DNA	c 932	11.4	81.4	720	4	AAK61014	Aak61014 Human imm
860	11.4	81.4	577	9	AAPO8377	Aaf08377 Fusarium	c 933	11.4	81.4	721	12	ADN61658	Adn61658 Triticum
861	11.4	81.4	577	9	ACL24026	ACL24026 DNA clone	c 934	11.4	81.4	725	12	ADK63436	Adk63436 Transcrip
862	11.4	81.4	577	13	ADU52418	Adu52418 Fusarium	c 935	11.4	81.4	726	9	ADK31746	Adk31746 DNA encod
863	11.4	81.4	577	14	ADZ90421	Adz90421 Pseudom	c 936	11.4	81.4	734	8	ABK26782	Abk26782 Aspergill
864	11.4	81.4	579	6	ABO38415	Abq38415 Oligonuc1	c 937	11.4	81.4	735	6	ABK78568	Abk78568 Bacillu
865	11.4	81.4	579	6	ABO38414	Abq38414 Oligonuc1	c 938	11.4	81.4	738	13	ADT46477	Adt46477 Bacterial
866	11.4	81.4	579	12	ACH69630	Ach69630 Human gen	c 939	11.4	81.4	745	10	ADCT6226	Adct6226 DNA homol
867	11.4	81.4	583	4	AAK62254	Aak62254 Human imm	c 940	11.4	81.4	745	10	ADK54127	Adk54127 Plant DNA
868	11.4	81.4	583	10	ADCT5095	Adct5095 N bentham	c 941	11.4	81.4	745	12	ADU67303	Adu67303 Human ova
869	11.4	81.4	583	10	ADK52788	Adk52788 Plant DNA	c 942	11.4	81.4	746	11	ADU644898	Adu644898 Insect re
870	11.4	81.4	583	11	ACL32596	ACL32596 Rice abio	c 943	11.4	81.4	753	8	ACA25336	Acas25336 Prokaryot
871	11.4	81.4	583	13	ADQ79202	Adq79202 Novel can	c 944	11.4	81.4	754	6	ABQ34281	Abq34281 Oligonuc1
872	11.4	81.4	584	13	ADK48762	Adk48762 Plant ful	c 945	11.4	81.4	754	6	ABQ34280	Abq34280 Oligonuc1
873	11.4	81.4	586	13	ADK33248	Adk33248 Plant ful	c 946	11.4	81.4	756	4	AAH03222	Aah03222 Human cdn
874	11.4	81.4	587	13	ACN53211	Acn53211 Cotton an	c 947	11.4	81.4	756	12	ADH01257	Adh01257 Tenaxin
875	11.4	81.4	589	6	ABL38129	AbL38129 Human col	c 948	11.4	81.4	762	10	ABE252160	AbE252160 Aspergill
876	11.4	81.4	590	4	AAH03555	Aah03555 Human cdn	c 949	11.4	81.4	762	10	ADFO1339	Adfo1339 Bacterial
877	11.4	81.4	593	13	ACN54303	Acn54303 Cotton an	c 950	11.4	81.4	765	13	ADK30282	Adk30282 Plant ful
878	11.4	81.4	594	11	ACT34332	Act34332 Mutated O	c 951	11.4	81.4	767	13	ADK48221	Adk48221 Plant ful
879	11.4	81.4	594	11	ADU11089	AdU11089 Solid tum	c 952	11.4	81.4	774	11	ABD01790	Abd01790 Pseudomon
880	11.4	81.4	597	2	AAV21146	Aav21146 Internal	c 953	11.4	81.4	777	13	ADK64963	Adk64963 Cotton cd
881	11.4	81.4	598	2	AAV21170	Aav21170 Internal	c 955	11.4	81.4	779	13	AAZ55543	Aaz55543 Feline cd
882	11.4	81.4	599	13	ADRE5645	Adre5645 Cotton cd	c 956	11.4	81.4	780	3	AAZ55542	Aaz55542 Feline cd
883	11.4	81.4	600	6	ABQ66395	Abq66395 Arabidops	c 957	11.4	81.4	780	3	AAZ55542	Aaz55542 Feline cd
884	11.4	81.4	600	6	AAZ55542	Aaz55542 Feline cd	c 958	11.4	81.4	783	10	ADT90010	Adt90010 Human gen
885	11.4	81.4	600	12	ADN61660	Adn61660 Trificact	c 959	11.4	81.4	783	10	ABZ37905	Abz37905 N. gonorr
886	11.4	81.4	602	13	ACN46478	Acn46478 Cotton pr	c 960	11.4	81.4	789	2	AAK40044	Aak40044 Prostate
887	11.4	81.4	604	14	ADK16770	Adk16770 Human can	c 961	11.4	81.4	790	6	ABO52667	AbO52667 Oligonuc1
888	11.4	81.4	608	6	ABN25395	Abn25395 Human ORF	c 962	11.4	81.4	800	6	ABO52666	AbO52666 Oligonuc1
889	11.4	81.4	609	10	ABZ41453	Abz41453 N. gonorr	c 963	11.4	81.4	802	2	AAK40045	Aak40045 Prostate
890	11.4	81.4	612	3	AAZ53967	Aaz53967 Neisseria	c 964	11.4	81.4	804	12	ACH90938	Ach90938 Human gen
891	11.4	81.4	612	12	ADQ36932	Adq36932 Cell prol	c 965	11.4	81.4	807	4	ABL24401	AbL24401 Drosophill
892	11.4	81.4	612	12	ADQ36932	Adq36932 Cell stre	c 966	11.4	81.4	807	11	ACT33497	Act33497 Rice abio
893	11.4	81.4	613	13	ADK33151	Adk33151 Plant ful	c 967	11.4	81.4	814	6	ABK64931	Abk64931 Rice rtdo
894	11.4	81.4	618	10	ABQ80467	Abq80467 Rat subtl	c 968	11.4	81.4	814	6	ABK64931	Abk64931 Rice rtdo

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C 969 11.4 81.4 816 4 AAD03962 Aad03962 Human act
C 970 11.4 81.4 816 6 ABS73266 Abs73266 DNA encod
C 971 11.4 81.4 816 12 ADP28828 Adp28828 Human sec
C 972 11.4 81.4 816 13 ADQ83359 Adq83359 Human tum
C 973 11.4 81.4 816 13 ACN39435 Acn39435 Tumour-as
C 974 11.4 81.4 816 2 AAT33174 Aat33174 Mutated O
C 975 11.4 81.4 821 10 ADB52632 Adb52632 Primary r
C 976 11.4 81.4 821 11 ADW21810 Adw21810 Rat hepat
C 977 11.4 81.4 825 10 ABZ28826 Abz28826 N. gonorr
C 978 11.4 81.4 828 3 AAZ53604 Aaz53604 Neisseria
C 979 11.4 81.4 830 10 ADH28934 Adh28934 Human chr
C 980 11.4 81.4 833 12 ADG63275 Adg63275 Transcript
C 981 11.4 81.4 839 13 ADX12269 Adx12269 Plant full
C 982 11.4 81.4 841 13 ADX49038 Adx49038 Plant full
C 983 11.4 81.4 843 13 ADX48835 Adx48835 Plant full
C 984 11.4 81.4 843 4 ABL21765 Abl21765 Drosophila
C 985 11.4 81.4 847 11 ADM44906 Adm44906 Insect re
C 986 11.4 81.4 849 11 ABD02753 Abd02753 Pseudomon
C 987 11.4 81.4 854 3 AAA64412 Aaa64412 DNA encod
C 988 11.4 81.4 861 11 ACH94679 Ach94679 Klebsiell
C 989 11.4 81.4 861 12 ADC35784 Adc35784 Novel mou
C 990 11.4 81.4 867 14 ACL66762 Acl66762 M. xanthu
C 991 11.4 81.4 871 6 ABO16669 Abq16669 Oligonuc
C 992 11.4 81.4 876 12 ACR57509 Acr57509 B. coli be
C 993 11.4 81.4 876 12 ADG62867 Adg62867 Apo-B RNA
C 994 11.4 81.4 879 2 AAQ71632 Aaq71632 Apo-B RNA
C 995 11.4 81.4 879 11 ABD14987 Abd14987 Pseudomon
C 996 11.4 81.4 885 3 AAZ55541 Aaz55541 Feline CD
C 997 11.4 81.4 885 3 AAZ55540 Aaz55540 Feline CD
C 998 11.4 81.4 885 10 ADC75660 Aac75660 DNA homol
C 999 11.4 81.4 886 2 AAQ82741 Aaq82741 Chicken t
1000 11.4 81.4 886 2 AAQ82741 Aaq82741 Chicken t

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## ALIGNMENTS

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RESULT 1
ID ADW79935 standard; RNA; 14 BP.
XX
AC ADW79935;
XX
DT 21-APR-2005 (first entry)
XX
DE Bacterial immunomodulatory Cpg oligoribonucleotide, SEQ ID NO:2.
XX
KW Immune modulation; immune stimulation; bacterial infection; infection;
KW endotoxin shock; antibacterial; antimicrobial; immunomodulator;
KW immunostimulant; adjuvant; ss.
XX
OS Bacteria.
XX
FH Key Location/Qualifiers
FT misc_feature 1..2
FT misc_feature /*tag= a
FT misc_feature /note= "Cpg dinucleotide"
FT misc_feature 13..14
FT misc_feature /*tag= b
FT misc_feature /note= "Cpg dinucleotide"
XX
XX US2005032731-A1.
XX
XX 10-FEB-2005.
XX
XX 15-MAR-2004; 2004US-00800926.
XX
XX 11-MAY-1993; 93US-00059745.
XX 20-JAN-1995; 95US-00376175.
XX 18-AUG-1995; 95US-00517016.
XX 29-OCT-1996; 96US-00739264.
XX 17-NOV-1998; 98US-00193653.
XX 18-JUN-2001; 2001US-00883550.

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XX (MARS/) MARSHALL W. E.
XX Marshall WE;
XX WPI, 2005-161694/17.
XX
XX Composition for modulating and/or stimulating immune system of animal
XX useful for withstanding microbial infections and lethality of endotoxin
XX shock, comprises low molecular weight oligoribonucleotide from bacteria.
XX
XX Claim 5; SEQ ID NO 2; 17pp; English.
XX
XX The invention relates to a composition for modulating and/or stimulating
XX the immune system of an animal, comprising bacterial oligoribonucleotides
XX (ORN) with a molecular weight of less than 10 kD. The bacterial ORNs are
XX preferably ADW79934-ADW79936, contain Cpg motifs and are resistant to
XX RNase. Bacteria produce RNase-resistant Cpg ORNs in response to stresses
XX such as a change in environment, including the neutral pH they encounter
XX when they colonize animals. The immune systems of animals have co-evolved
XX to recognize such Cpg ORNs as being derived from bacteria, and has
XX adapted a non-toxic alerting response to their release from bacteria. The
XX invention also relates to a method for the preparation of the bacterial
XX ORNs by subjecting bacteria to one or more periods of stress, separating
XX the ORNs and media from the bacteria, and filtering the separated product
XX to remove substances with a molecular weight of more than 10 kD; and a
XX method of using the filtrate to modulate/stimulate the immune system of
XX an animal to withstand microbial infection. The composition and methods
XX of the invention are useful for modulating and/or stimulating the immune
XX system of animals (including humans, poultry and livestock), particularly
XX to withstand microbial infections or the onset of endotoxin shock. The
XX compositions may be administered orally (e.g., as a food supplement) or
XX parentally, and may also be administered as an adjuvant for oral or
XX parenteral vaccines. The compositions may additionally be used topically
XX to protect against ear, nose and vaginal infections. They may further be
XX used to extend the viability of monocytes, thereby improving their
XX ability to mature into macrophages to fight infection, and may be used to
XX downregulate the cytotoxicity of macrophages to prevent them from
XX destroying normal T-cells in people with HIV infections. The composition
XX of the invention contains ORNs released by either harmless or pathogenic
XX bacteria, but is free from bacterial cells. Unlike Cpg
XX oligodeoxyribonucleotides (ODNs), the bacterial Cpg ORNs and compositions
XX containing them are non-toxic. The present sequence represents a
XX specifically claimed bacterial Cpg oligoribonucleotide present in
XX compositions of the invention.
XX
XX Sequence 14 BP; 3 A; 5 C; 3 G; 0 T; 3 U; 0 Other;
XX
XX Query Match 100.0%; Score 14; DB 14; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 4e+02;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CGUACUGCAACUG 14
XX Db 1 CGUACUGCAACUG 14
XX
XX RESULT 2
XX ADS60734
XX ID ADS60734 standard; cDNA; 1786 BP.
XX
XX AC ADS60734;
XX
XX DT 02-DEC-2004 (first entry)
XX
XX DE Bacterial polynucleotide #12721.
XX
XX Recombinant DNA construct; transformed plant; improved plant property;
XX cold tolerance; heat tolerance; drought tolerance; herbicide; omosis;
XX pathogen tolerance; pest tolerance; plant disease resistance;
XX cell cycle pathway modification; plant growth regulator;
XX homologous recombination; seed oil yield; protein yield; carbohydrate;
XX nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

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KM Bacterial polynucleotide; gene; ss.  
OS Bacteria.  
XX US2003233675-A1.  
XX 18-DEC-2003.  
XX 20-FEB-2003; 2003US-00369493.  
XX 21-FEB-2002; 2002US-0360039P.  
XX (CAOY/) CAO Y.  
XX (HINK/) HINKLE G J.  
XX (SLAT/) SLATER S C.  
XX (CHEN/) CHEN X.  
XX (GOLD/) GOLDMAN B S.  
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.  
XX  
XX The invention relates to a recombinant DNA construct comprising a  
XX promoter functional in a plant cell, where the promoter is positioned to  
XX provide for expression of a polynucleotide encoding a polypeptide from a  
XX microbial source. The invention also relates to a transformed plant  
XX comprising the recombinant DNA construct and a method of producing a  
XX transformed plant having an improved property. The plant is a crop plant  
XX such as maize or soybean. The method of producing a transformed plant  
XX having an improved property comprises transforming a plant with the  
XX recombinant DNA construct and growing the transformed plant, where the  
XX polynucleotide or polypeptide is useful for improving plant properties.  
XX The recombinant DNA construct is useful for producing plants with  
XX improved plant properties, e.g. improved cold, heat or drought tolerance,  
XX tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
XX increased resistance to plant disease, better growth rate by modification  
XX of the cell cycle pathway with plant growth regulators, increased rate of  
XX homologous recombination, modified seed oil or protein yield and/or  
XX content, improved yield by modification of carbohydrate, nitrogen or  
XX phosphorus use and/or uptake, by modification of photosynthesis or by  
XX providing improved plant growth and development under at least one stress  
XX condition. This sequence represents a bacterial polynucleotide used in  
XX the scope of the invention. Note: The sequence data for this patent did  
XX not form part of the printed specification but was obtained in electronic  
XX format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
XX  
SQ Sequence 1786 BP; 374 A; 597 C; 455 G; 360 T; 0 U; 0 Other;  
QY Query Match 100.0%; Score 14; DB 13; Length 1786;  
Db Best Local Similarity 78.6%; Pred. No. 5.5e+02;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
1 CGUACUGCAACUCG 14  
128 CGTACTGCAACTCG 141  
RESULT 3  
ID ADS49626 standard; cDNA; 1981 BP.  
XX  
XX ADS49626;  
XX 02-DEC-2004 (first entry)  
XX Bacterial polynucleotide #4369.  
XX

XX  
XX Recombinant DNA construct; transformed plant; improved plant property;  
XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
XX pathogen tolerance; pest tolerance; plant disease resistance;  
XX cell cycle pathway modification; plant growth regulator;  
XX homologous recombination; seed oil yield; protein yield; carbohydrate;  
XX nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
XX bacterial polynucleotide; gene; ss.  
XX Bacteria.  
XX US2003233675-A1.  
XX 18-DEC-2003.  
XX 20-FEB-2003; 2003US-00369493.  
XX 21-FEB-2002; 2002US-0360039P.  
XX (CAOY/) CAO Y.  
XX (HINK/) HINKLE G J.  
XX (SLAT/) SLATER S C.  
XX (CHEN/) CHEN X.  
XX (GOLD/) GOLDMAN B S.  
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.  
XX  
XX New recombinant DNA construct comprising a promoter positioned to provide  
XX for expression of a polynucleotide encoding a polypeptide from a  
XX microbial source, useful for producing plants with improved properties.  
XX  
XX Claim 1; SEQ ID NO 28056; 122bp; English.  
XX  
XX The invention relates to a recombinant DNA construct comprising a  
XX promoter functional in a plant cell, where the promoter is positioned to  
XX provide for expression of a polynucleotide encoding a polypeptide from a  
XX microbial source. The invention also relates to a transformed plant  
XX comprising the recombinant DNA construct and a method of producing a  
XX transformed plant having an improved property. The plant is a crop plant  
XX such as maize or soybean. The method of producing a transformed plant  
XX having an improved property comprises transforming a plant with the  
XX recombinant DNA construct and growing the transformed plant, where the  
XX polynucleotide or polypeptide is useful for improving plant properties.  
XX The recombinant DNA construct is useful for producing plants with  
XX improved plant properties, e.g. improved cold, heat or drought tolerance,  
XX tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
XX increased resistance to plant disease, better growth rate by modification  
XX of the cell cycle pathway with plant growth regulators, increased rate of  
XX homologous recombination, modified seed oil or protein yield and/or  
XX content, improved yield by modification of carbohydrate, nitrogen or  
XX phosphorus use and/or uptake, by modification of photosynthesis or by  
XX providing improved plant growth and development under at least one stress  
XX condition. This sequence represents a bacterial polynucleotide used in  
XX the scope of the invention. Note: The sequence data for this patent did  
XX not form part of the printed specification but was obtained in electronic  
XX format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
XX  
SQ Sequence 1981 BP; 448 A; 584 C; 648 G; 301 T; 0 U; 0 Other;  
QY Query Match 100.0%; Score 14; DB 13; Length 1981;  
Db Best Local Similarity 78.6%; Pred. No. 5.5e+02;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
1 CGUACUGCAACUCG 14  
1510 CGTACTGCAACTCG 1497  
RESULT 4  
ID ACA25094/c





CC production. This sequence represents a bacterial polynucleotide used in  
 CC the scope of the invention. Note: The sequence data for this patent did  
 CC not form part of the printed specification but was obtained in electronic  
 CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

XX Sequence 2080 BP; 474 A; 610 C; 680 G; 316 T; 0 U; 0 Other;

Query Match 100.0%; Score 14; DB 13; Length 2080;

Best Local Similarity 78.6%; Pred. No. 5.6e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUCG 14

Db 1510 CGTACTGCAACTCG 1497

RESULT 6  
 ACA45239/c  
 ID ACA45239 standard; DNA; 2460 BP.

XX AC ACA45239;

XX DT 19-JUN-2003 (first entry)

XX DE Prokaryotic essential gene #26896.

XX KW Antisense; ds; prokaryotic essential gene; cell proliferation;  
 XX drug design; gene.

XX OS Pseudomonas syringae.

XX PN NO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002MO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948933.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (BLIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
 XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
 XX WPI; 2003-029926/02.

XX DR P-PSDB; ABU41369.

XX PT New antisense nucleic acids, useful for identifying proteins or screening  
 XX for homologous nucleic acids required for cellular proliferation to  
 XX isolate candidate molecules for rational drug discovery programs.

XX PS Claim 14; SEQ ID NO 33109; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of  
 CC the 613 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target  
 CC prokaryotic essential genes. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)

XX SQ Sequence 2460 BP; 556 A; 704 C; 776 G; 424 T; 0 U; 0 Other;

Query Match 100.0%; Score 14; DB 8; Length 2460;

Best Local Similarity 78.6%; Pred. No. 5.6e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUCG 14

Db 1408 CGTACTGCAACTCG 1395

RESULT 7  
 ADU44189  
 ID ADU44189 standard; DNA; 21 BP.

XX AC ADU44189;

XX DT 27-JAN-2005 (first entry)

XX DE Knock-down target sequence #9368.

XX KW ds; RNA production; protein production; drug development;  
 XX knock-down target.

XX OS Unidentified.

XX PN MO2004094636-A1.

XX PD 04-NOV-2004.

XX PF 24-APR-2003; 2003MO-EP004362.

XX PR 24-APR-2003; 2003MO-EP004362.

XX PA (GALA-) GALAPAGOS GENOMICS NV.

XX PI (VSCB/) VAN DER SCHUREN J.

XX PI Arts GJF, Lambrecht MJY, Djokic K, Clasen RJ, Mestic B;  
 XX Griffioen S, Bergs CTL;

XX DR WPI; 2004-775940/76.

XX PT New knockdown sequences, useful in lowering the amount of RNA and/or  
 XX protein production in cells used in drug development process.

XX PS Claim 11; SEQ ID NO 9430; 402pp; English.

XX The invention relates to a polynucleotide comprising an RNA sequence. The  
 CC polynucleotide, vector, libraries, and method are useful in lowering the  
 CC amount of RNA and/or protein production in cells used in drug development  
 CC process. The present sequence represents a knock-down target sequence.

XX SQ Sequence 21 BP; 6 A; 8 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 92.9%; Score 13; DB 13; Length 21;

Best Local Similarity 76.9%; Pred. No. 1.5e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13  
 ||:|||||:  
 Db 2 GCTACTGCAACTC 14

RESULT 8  
 ABRN51005  
 ID ABRN51005 standard; DNA; 65 BP.

AC ABRN51005;

XX 15-JUL-2002 (first entry)

DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:23753.

XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
 KW splice variant; transcriptome; oligonucleotide library; ss.

OS Mus musculus.

PN M0200210449-A2.

PD 07-FEB-2002.

PF 20-JUL-2001; 2001WO-1B001903.

XX 28-JUL-2000; 2000US-0221607P.

PR 02-MAY-2001; 2001US-0287724P.

XX (COMP-) COMPUGEN INC.

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

DR WPI; 2002-257383/30.

PT New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNA transcribed from a transcription unit of a  
 PT genome, useful for detecting tissue-, pathology-, and developmental-  
 PT specific genes.

XX Example 1; SEQ ID NO 23753; 47bp; English.

CC The present invention describes oligonucleotide libraries for detecting  
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
 CC )transcriptome comprises messenger RNAs transcribed from multiple  
 CC transcription units that populate a genome. The library comprises several  
 CC oligonucleotides, each capable of hybridizing selectively to a set of  
 CC messenger RNAs transcribed from a given transcription unit of the genome,  
 CC which encodes one or more messenger RNA splice variants. The  
 CC oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterizing the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcriptomes. The libraries may also be used as specialized mini  
 CC libraries to detect transcripts of a sub-transcriptome under a particular  
 CC biological or pathological state, and so allowing the detection of tissue  
 CC - and pathology-specific genes such as those genes only expressed in  
 CC specific tissue under a specific pathological condition; to detect  
 CC developmental specific genes; and to detect RNA transcripts and splice  
 CC variants of a transcriptome of a patient suffering from a particular  
 CC disorder. ABRN27253 to ABRN59589 represent oligonucleotide sequences from  
 CC rats, humans and mice, which are used in the exemplification of the  
 CC present invention. N.B. The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 65 BP; 17 A; 23 C; 10 G; 15 T; 0 U; 0 Other;

Query Match 92.9%; Score 13; DB 6; Length 65;  
 Best Local Similarity 76.9%; Pred. No. 1.7e+03;  
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCAACUCG 14  
 ||:|||||:  
 Db 31 GCTACTGCAACTCG 43

RESULT 9  
 ACD68769/c  
 ID ACD68769 standard; DNA; 100 BP.

AC ACD68769;

XX 18-SEP-2003 (first entry)

DE E. coli K12 MG1655 biochip probe SEQ ID 39.

XX Biochip; gene expression; gut; diagnostic; detection; probe; ss.

XX Escherichia coli.

PN EP1260592-A1.

PD 27-NOV-2002.

PF 17-MAY-2001; 2001EP-0012179.

XX 17-MAY-2001; 2001EP-0012179.

XX (MMGB-) MMGB-BIOTECH AG.

PI Dommer H, Dreischer B, Huber A, Weber J;

DR WPI; 2003-241155/24.

PT Biochip containing probes complementary with open reading frames in  
 PT Escherichia coli K12, useful for detecting gene expression and expression  
 PT patterns.

XX Claim 3; Page 17; 2004pp; German.

CC This invention describes a novel biochip comprising probe spots, each  
 CC containing many identical probes. The probes are nucleotide sequences of  
 CC 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at  
 CC least one includes a segment of at least 20 bases identical with, or  
 CC complementary to, a segment of an open reading frame (orf) of Escherichia  
 CC coli K12. The biochip is used for specific detection of gene expression  
 CC in K12 and for determining the gene expression pattern, e.g. for  
 CC diagnostic determination of which E. coli strains are present in the gut,  
 CC and to determine the effects of e.g. growth media on gene expression. The  
 CC biochip provides as comprehensive as possible detection of the K12  
 CC genome, with simultaneous analysis of many different genes with a single  
 CC device, and comparison of gene expression between K12 and its mutants or  
 CC other E. coli strains in a single experiment. Apart from qualitative and  
 CC quantitative information about gene expression, it also allows  
 CC measurements of population densities for the various strains. The use of  
 CC synthetic oligonucleotides for preparation of probes allows free  
 CC variation in probe length and ensures high purity (and thus selectivity,  
 CC reactivity and reproducibility); also synthetic probes are generally  
 CC shorter than probes prepared by polymerase chain reaction. ACD68731 to  
 CC ACD81540 represent oligonucleotide probes used with the biochip described  
 CC in the invention

XX Sequence 100 BP; 29 A; 28 C; 29 G; 14 T; 0 U; 0 Other;

Query Match 92.9%; Score 13; DB 8; Length 100;  
 Best Local Similarity 76.9%; Pred. No. 1.7e+03;  
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCAACUCG 14  
 ||:|||||:  
 Db 14 GCTACTGCAACTCG 2

RESULT 10

ACD68770/c  
 ID ACD68770 standard; DNA, 100 BP.  
 AC ACD68770;  
 DT 18-SEP-2003 (first entry)  
 DE B. coli K12 MG1655 biochip probe SEQ ID 40.  
 KM Biochip; gene expression; gut; diagnostic; detection; probe; ss.  
 XX Escherichia coli.  
 OS  
 PN EPI260592-A1.  
 XX  
 PD 27-NOV-2002.  
 PF 17-MAY-2001; 2001EP-00112179.  
 PR 17-MAY-2001; 2001EP-00112179.  
 XX (MWGB-) MWGB-BIOTECH AG.  
 PA  
 PI Donner H, Drescher B, Huber A, Weber J;  
 XX WPI; 2003-241155/24.  
 DR  
 XX  
 PT Biochip containing probes complementary with open reading frames in  
 PT Escherichia coli K12, useful for detecting gene expression and expression  
 XX patterns.  
 PS Claim 3; Page 17; 2004pp; German.  
 XX  
 CC This invention describes a novel biochip comprising probe spots, each  
 CC containing many identical probes. The probes are nucleotide sequences of  
 CC 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at  
 CC least one includes a segment of at least 20 bases identical with, or  
 CC complementary to, a segment of an open reading frame (orf) of Escherichia  
 CC coli K12. The biochip is used for specific detection of gene expression  
 CC in K12 and for determining the gene expression pattern, e.g. for  
 CC diagnostic determination of which B. coli strains are present in the gut,  
 CC and to determine the effects of e.g. growth media on gene expression. The  
 CC biochip provides as comprehensive as possible detection of the K12  
 CC genome, with simultaneous analysis of many different genes with a single  
 CC device, and comparison of gene expression between K12 and its mutants or  
 CC other B. coli strains in a single experiment. Apart from qualitative and  
 CC quantitative information about gene expression, it also allows  
 CC measurements of population densities for the various strains. The use of  
 CC synthetic oligonucleotides for preparation of probes allows free  
 CC variation in probe length and ensures high purity (and thus selectivity,  
 CC reactivity and reproducibility); also synthetic probes are generally  
 CC shorter than probes prepared by polymerase chain reaction. ACD68731 to  
 CC ACD81540 represent oligonucleotide probes used with the biochip described  
 CC in the invention  
 XX  
 SQ Sequence 100 BP; 29 A; 23 C; 34 G; 14 T; 0 U; 0 Other;  
 QY  
 DB 2 GUACUGCAACUCG 14  
 52 GTAGCTGCACTCG 40

XX  
 DE Formate dehydrogenase nucleotide sequence.  
 KM Formate dehydrogenase; Hyphomicrobium; ds.  
 XX  
 OS Hyphomicrobium sp.  
 PN JP2000245471-A.  
 XX  
 PD 12-SEP-2000.  
 PF 01-MAR-1999; 99JP-00052548.  
 PR 01-MAR-1999; 99JP-00052548.  
 XX  
 PA (NIRA) UNITIKA LTD.  
 XX  
 DR WPI; 2000-622119/60.  
 DR P-PSDB; AAY85650.  
 XX  
 PT New Hyphomicrobium sp. formate dehydrogenase gene for producing formate  
 PT dehydrogenase of high specific activity, high temperature stability and  
 XX high pH stability.  
 PS Claim 2; Page 5-6; 9pp; Japanese.  
 XX  
 CC This invention relates to a gene encoding a formate dehydrogenase from  
 CC Hyphomicrobium sp. A transformant containing the new gene is used for the  
 CC preparation of formate dehydrogenase of high specific activity, low  
 CC Michaelis constant (Km) value against formic acid and NAD<sup>+</sup>, high  
 CC temperature stability and high pH stability. The present sequence  
 CC represents the gene of the invention  
 XX  
 SQ Sequence 1197 BP; 290 A; 350 C; 323 G; 234 T; 0 U; 0 Other;  
 QY  
 DB 1 CGUACUGCAACUC 13  
 431 CGTAGCTGCACTC 443

RESULT 12  
 ID ADS51056 standard; cDNA, 1306 BP.  
 XX  
 AC ADS51056;  
 XX  
 DT 02-DEC-2004 (first entry)  
 DE Bacterial polynucleotide #5799.  
 XX  
 KM Recombinant DNA construct; transformed plant; improved plant property;  
 KM cold tolerance; heat tolerance; drought tolerance; herbicide resistance;  
 KM pathogen tolerance; pest tolerance; plant disease resistance;  
 KM cell cycle pathway modification; plant growth regulator;  
 KM homologous recombination; seed oil yield; protein yield; carbohydrate;  
 KM nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
 KM bacterial polynucleotide; gene; ss.  
 XX  
 OS Bacteria.  
 XX  
 PN US2003233675-A1.  
 XX  
 PD 18-DEC-2003.  
 PF 20-FEB-2003; 2003US-00369493.  
 PR 21-FEB-2002; 2002US-0360039P.  
 XX  
 PA (CAOY/) CAO Y.





CC invention. Human secreted proteins have activities based on the tissues  
CC and cells the genes are expressed in. Examples of activities include:  
CC cytotoxic; antineoplastic; antiarthritic; dermatological; cardiant;  
CC antiinflammatory; gastrointestinal; and anti-ulcer. The polynucleotides  
CC and polypeptides can be used in the prevention, treatment and diagnosis  
CC of diseases associated with inappropriate polypeptide expression.  
CC Disorders that may be treated or prevented include solid tumours,  
CC rheumatoid arthritis, psoriasis, diabetic retinopathy, myocardial  
CC angiogenesis, Crohn's disease and ulcers. The polynucleotides and their  
CC complementary sequences may also be used as DNA probes in diagnostic  
CC assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate  
CC the presence of similar nucleic acid sequences in samples, and therefore  
CC which patients may be in need of restorative therapy. The polypeptides  
CC may also be used as antigens in the production of antibodies against the  
CC polypeptide and in assays to identify modulators (agonists and  
CC antagonists) of polypeptide expression and activity. The anti-polypeptide  
CC antibodies and antagonists may also be used to down regulate expression  
CC and activity. AAF3028 to AAF3036 and AAB64665 represent sequences used  
CC in the exemplification of the present invention

XX SQ Sequence 1488 BP; 496 A; 290 C; 253 G; 449 T; 0 U; 0 Other;

Query Match 92.9%; Score 13; DB 4; Length 1488;  
Best Local Similarity 76.9%; Pred. No. 2.1e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAACGCAACG 13  
DB 658 GGAACGCAACG 670

RESULT 17  
AAS52489/c  
ID AAS52489 standard; DNA; 1647 BP.

XX AAS52489;

XX 13-FEB-2002 (first entry)

XX E. coli DNA for cellular proliferation protein #211.

XX Antisense; ds; prokaryotic cellular proliferation gene; antibiotic;  
KM antibacterial; drug design.

XX Escherichia coli.

XX MO200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009180.

XX 21-MAR-2000; 2000US-0191078P.

XX 23-MAY-2000; 2000US-0206848P.

XX 26-MAY-2000; 2000US-0207727P.

XX 23-OCT-2000; 2000US-0242578P.

XX 27-NOV-2000; 2000US-0253625P.

XX 22-DEC-2000; 2000US-0257931P.

XX 16-FEB-2001; 2001US-0269308P.

XX (ELIT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlsen KU, Zykkind JW, Wall D, Trawick JD, Carr GJ;  
PI Yamamoto RT, Xu HH;

XX WPI; 2001-611495/70.

XX P-PSDB; AAU34630.

XX New polynucleotides for the identification and development of  
PT antibiotics, comprise sequences of antisense nucleic acids.

XX Claim 27; SEQ ID NO 6126; 511bp; English.

CC The invention relates to antisense inhibitors of genes essential to  
CC prokaryotic cellular proliferation, their use in identifying the genes,  
CC their use in the discovery of novel antibiotics, the essential genes  
CC themselves and the encoded proteins. The prokaryotes used are Escherichia  
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,  
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also  
CC useful for the identification of potential new targets for antibiotic  
CC development. The antisense nucleic acids can also be used to identify  
CC proteins used in proliferation, to express these proteins, and to obtain  
CC antibodies capable of binding to the expressed proteins. The proteins can  
CC be used to screen compounds in rational drug discovery programmes. The  
CC antisense nucleic acid sequence is also useful to screen for homologous  
CC nucleic acids which are required for cell proliferation in a wide variety  
CC of organisms. The present sequence encodes an essential prokaryotic  
CC cellular proliferation protein. Note: The sequence data for this patent  
CC did not form part of the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 1647 BP; 400 A; 402 C; 488 G; 357 T; 0 U; 0 Other;

Query Match 92.9%; Score 13; DB 4; Length 1647;  
Best Local Similarity 76.9%; Pred. No. 2.1e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAACGCAACG 14  
DB 1533 GGAACGCAACG 1521

RESULT 18  
ACA32562/c  
ID ACA32562 standard; DNA; 1647 BP.

XX ACA32562;

XX 19-JUN-2003 (first entry)

XX Prokaryotic essential gene #14219.

XX Antisense; ds; prokaryotic essential gene; cell proliferation;  
KM drug design; gene.

XX Escherichia coli.

XX MO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342823P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KU, Zykkind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX P-PSDB; ABU28692.

XX New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.

XX Claim 14; SEQ ID NO 20432; 1766bp; English.

XX The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression





CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
 CC coding sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 1732 BP; 422 A; 452 C; 438 G; 420 T; 0 U; 0 Other;

Query Match 92.9%; Score 13; DB 5; Length 1732;  
 Best Local Similarity 76.9%; Pred. No. 2.1e+03;  
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCAACUCG 14  
 ||:|||||:  
 Db 1683 GRACTGCAACTCG 1671

RESULT 21  
 AAS90081/c  
 ID AAS90081 standard; cDNA; 1919 BP.

XX AC AAS90081;  
 XX DT 13-FEB-2002 (first entry)  
 XX DE DNA encoding novel human diagnostic protein #25885.  
 XX KM Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 XX food supplement; medical imaging; diagnostic; genetic disorder; ss.  
 XX OS Homo sapiens.  
 XX PN MO200175067-A2.  
 XX PD 11-OCT-2001.  
 XX PF 30-MAR-2001; 2001WO-US008631.  
 XX PR 31-MAR-2000; 2000US-00540217.  
 XX PR 23-AUG-2000; 2000US-00649167.  
 XX PA (HYS- ) HYSSEQ INC.  
 XX PI Drmanac RT, Liu C, Tang YT;  
 XX DR WPI; 2001-639362/73.  
 XX DR P-PSDB; ABG25894.  
 XX PT New isolated polynucleotide and encoded polypeptides, useful in  
 XX PT diagnostics, forensics, gene mapping, identification of mutations  
 XX PT responsible for genetic disorders or other traits and to assess  
 XX PT biodiversity.  
 XX PS Claim 1; SEQ ID NO 25885; 103bp; English.

XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used

CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
 CC coding sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 1919 BP; 469 A; 514 C; 488 G; 448 T; 0 U; 0 Other;

Query Match 92.9%; Score 13; DB 5; Length 1919;  
 Best Local Similarity 76.9%; Pred. No. 2.1e+03;  
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCAACUCG 14  
 ||:|||||:  
 Db 1683 GRACTGCAACTCG 1671

RESULT 22  
 AAI14703  
 ID AAI14703 standard; DNA; 1945 BP.

XX AC AAI14703;  
 XX DT 12-OCT-2001 (first entry)  
 XX DE Probe #4636 for gene expression analysis in human cervical cell sample.  
 XX KM Probe; human; microarray; gene expression; cervical epithelial cell;  
 XX cervical cancer; ss.  
 XX OS Homo sapiens.  
 XX PN MO200157278-A2.  
 XX PD 09-AUG-2001.  
 XX PF 30-JAN-2001; 2001WO-US000670.  
 XX PR 04-FEB-2000; 2000US-0180312P.  
 XX PR 26-MAY-2000; 2000US-0207456P.  
 XX PR 30-JUN-2000; 2000US-00608408.  
 XX PR 03-AUG-2000; 2000US-00632366.  
 XX PR 21-SEP-2000; 2000US-0234687P.  
 XX PR 27-SEP-2000; 2000US-0236359P.  
 XX PR 04-OCT-2000; 2000GB-00024263.  
 XX PA (MOLF-) MOLECULAR DYNAMICS INC.  
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX DR WPI; 2001-488901/53.  
 XX PT Human genome-derived single exon nucleic acid probes useful for analyzing  
 XX PT gene expression in human cervical epithelial cells.  
 XX PS Claim 25; SEQ ID NO 4636; 487bp; English.

XX CC The present invention relates to human single exon nucleic acid probes  
 CC (SENPs). The present sequence is one such probe. The SENPs are derived  
 CC from human Hela cells. The SENPs can be used to produce a single exon  
 CC microarray, which can be used for measuring human gene expression in a

CC sample derived from human cervical epithelial cells. By measuring gene  
CC expression, the probes are therefore useful in grading and/or staging of  
CC diseases of the cervix, notably cervical cancer. Note: The sequence data  
CC for this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 1945 BP; 453 A; 617 C; 484 G; 391 T; 0 U; 0 Other;

SO Query Match 92.9%; Score 13; DB 4; Length 1945;

Best Local Similarity 76.9%; Pred. No. 2.1e+03;

Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 263 GUNACGCACTCG 275

RESULT 23

ABAS6435 standard; DNA, 1945 BP.

XX ABAS6435;

XX 01-FEB-2002 (first entry)

XX Human foetal liver single exon nucleic acid probe #4740.

XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

XX Homo sapiens.

XX WO200157277-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000669.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human fetal liver.

XX Claim 1; SEQ ID NO 4740; 639pp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring

XX human gene expression in a sample derived from human foetal liver. The

XX single exon nucleic acid probes may be used for predicting, measuring and

XX displaying gene expression in samples derived from human fetal liver. The

XX present sequence is a single exon nucleic acid probe of the invention.

XX Note: The sequence data for this patent did not form part of the printed

XX specification, but was obtained in electronic format directly from WIPO

Db 263 GUNACGCACTCG 275

RESULT 24

AAI36072 standard; DNA, 1945 BP.

XX AAI36072;

XX 17-OCT-2001 (first entry)

XX Probe #4758 used to measure gene expression in human placenta sample.

XX Probe; microarray; human; placenta; antenatal diagnosis;

XX genetic disorder; ss.

XX Homo sapiens.

XX WO200157272-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000663.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-48897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human placenta.

XX Claim 25; SEQ ID NO 4758; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SRNP).

XX The present sequence is one such probe. The probes are useful for

XX producing a microarray for predicting, measuring and displaying gene

XX expression in samples derived from human placenta. The probes are useful

XX for antenatal diagnosis of human genetic disorders

XX Sequence 1945 BP; 453 A; 617 C; 484 G; 391 T; 0 U; 0 Other;

SO Query Match 92.9%; Score 13; DB 4; Length 1945;

Best Local Similarity 76.9%; Pred. No. 2.1e+03;

Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 263 GUNACGCACTCG 275

RESULT 25

ABAA5908 standard; DNA, 1945 BP.

XX ABAA5908;

XX 01-FEB-2002 (first entry)

XX Human breast cell single exon nucleic acid probe #4603.

XX Human; microarray; single exon probe; gene expression; breast; disease;

XX cancer; ss.

XX	Homo sapiens.
OS	
XX	WO200157271-A2.
PN	
XX	09-AUG-2001.
XX	
PF	30-JAN-2001; 2001WO-US000662.
XX	
PR	04-FEB-2000; 2000US-0180312P.
PR	26-MAY-2000; 2000US-0207456P.
PR	30-JUN-2000; 2000US-00608408.
PR	03-AUG-2000; 2000US-00632366.
PR	21-SEP-2000; 2000US-0234687P.
PR	27-SEP-2000; 2000US-0236359P.
PR	04-OCT-2000; 2000GB-00024263.
XX	
PA	(MOLB-) MOLECULAR DYNAMICS INC.
XX	
P1	Penn SG, Hanzel DK, Chen W, Rank DR;
XX	
DR	WPI; 2001-496933/54.
XX	
PT	New spatially-addressable set of single exon nucleic acid probes, useful
PT	for measuring gene expression in sample derived from human breast,
PT	comprises number of single exon nucleic acid probes.
XX	
PS	Claim 1; SEQ ID NO 4603; 327pp + Sequence Listing; English.
XX	
CC	The invention relates to a spatially-addressable set of single exon
CC	nucleic acid probes for measuring gene expression in a sample derived
CC	from human breast and BT 474 cells. The method involves contacting the
CC	probes with a collection of detectably labelled nucleic acids derived
CC	from mRNA of human breast, and then measuring the label bound to each
CC	probe of the microarray. The probes are useful for verifying the
CC	expression of regions of genomic DNA predicted to encode proteins. They
CC	are useful for gene discovery, and for determining predisposition and/or
CC	prognosing breast disease. Gene expression analysis is useful for
CC	assessing the toxicity of chemical agents on cells. The microarray of
CC	this invention presents a far greater diversity of probes for measuring
CC	gene expression, with far less bias than expressed sequence tag
CC	microarrays. The method is suitable for rapid production of functional
CC	information from genomic sequence. The present sequence is a single exon
CC	nucleic acid probe of the invention. Note: The sequence data for this
CC	patent did not form part of the printed specification, but was obtained
CC	in electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	
SO	Sequence 1945 BP; 453 A; 617 C; 484 G; 391 T; 0 U; 0 Other;
Query Match	92.9%; Score 13; DB 4; Length 1945;
Best Local Similarity	76.9%; Pred. No. 2.1e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;	
0y	2 GUACUGCAACUCG 14
Db	263 GTACTGCACCTCG 275
RESULT 26	
ABA26067	
ID	ABA26067 standard; DNA; 1945 BP.
XX	
AC	ABA26067;
XX	
DT	23-JAN-2002 (first entry)
DE	Probe #4533 for gene expression analysis in human heart cell sample.
XX	
XX	Human; gene expression; heart; microarray; vascular system; probe;
KM	cardiovascular disease; hypertension; cardiac arrhythmia;
XX	congenital disease; ss.
XX	

OS	Homo sapiens.
XX	
PN	MO200157274-A2.
PD	
XX	
XX	09-AUG-2001.
PF	
XX	30-JAN-2001; 2001WO-US000666.
XX	
PR	04-FEB-2000; 2000US-0180312P.
PR	26-MAY-2000; 2000US-0207456P.
PR	30-JUN-2000; 2000US-00608408.
PR	03-AUG-2000; 2000US-00632366.
PR	21-SEP-2000; 2000US-0234687P.
PR	27-SEP-2000; 2000US-0236359P.
PR	04-OCT-2000; 2000GB-00024263.
XX	
PA	(MOLE-) MOLECULAR DYNAMICS INC.
PI	
XX	Penn SG, Hanzel DK, Chen W, Rank DR,
XX	
DR	WPI; 2001-488899/53.
XX	
XX	Single exon nucleic acid probes for analyzing gene expression in human
PT	hearts.
XX	
PS	Claim 1; SEQ ID NO 4533; 530pp; English.
XX	
CC	The present invention relates to single exon nucleic acid probes for
CC	measuring human gene expression in a sample derived from human heart. The
CC	present sequence is one such probe. The probes may be used for
CC	predicting, measuring and displaying gene expression in samples derived
CC	from the human heart via microarrays. By measuring gene expression, the
CC	probes are useful for predicting, diagnosing, grading, staging,
CC	monitoring and prognosing diseases of the human heart and vascular system
CC	e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC	congenital heart disease. Note: The sequence data for this patent did not
CC	form part of the printed specification, but was obtained in electronic
CC	format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 1945 BP; 453 A; 617 C; 484 G; 391 T; 0 U; 0 Other;
XX	
Query Match	92.9%; Score 13; DB 4; Length 1945;
Best Local Similarity	76.9%; Pred. No. 2.1e+03;
Matches 10; Conservative	3; Mismatches 0; Indels 0; Gaps 0;
OY	2 GUACGCAACUCG 14
	:     :
Db	263 GTACTGCACCTCG 275
RESULT 27	
ID	AAK30108 standard; DNA; 1945 BP.
XX	
AC	AAK30108;
XX	
DT	06-NOV-2001 (first entry)
XX	
DE	Human bone marrow expressed single exon probe SEQ ID NO: 4665.
XX	
KW	Human; bone marrow expressed exon; gene expression analysis; probe;
XX	microarray; cancer; leukemia; lymphoma; myeloma; ss.
OS	Homo sapiens.
PN	WO200157276-A2.
PD	
XX	
XX	09-AUG-2001.
PF	
XX	30-JAN-2001; 2001WO-US000668.
XX	
PR	04-FEB-2000; 2000US-0180312P.
PR	26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-488900/53.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for analyzing  
XX gene expression in human bone marrow.  
XX  
PS Example 4; SEQ ID NO 4665; 658bp + Sequence Listing; English.  
XX  
CC The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC bone marrow. They can be used to measure gene expression in bone marrow  
CC samples, which may enable the improved diagnosis and treatment of cancers  
CC such as lymphoma, leukaemia and myeloma. The present sequence is one of  
CC the probes of the invention  
XX  
SQ Sequence 1945 BP; 453 A; 617 C; 484 G; 391 T; 0 U; 0 Other;  
XX  
Query Match 92.9%; Score 13; DB 4; Length 1945;  
Best Local Similarity 76.9%; Pred. No. 2.1e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
XX  
OY 2 GUACUGCACTCG 14  
DB 263 GTRCTGCACTCG 275  
XX  
RESULT 28  
AAK04600  
ID AAK04600 standard; DNA; 1945 BP.  
XX  
AC AAK04600;  
XX  
DT 05-NOV-2001 (first entry)  
XX  
DE Human brain expressed single exon probe SEQ ID NO: 4591.  
XX  
KW Human; brain expressed exon; gene expression analysis; probe; microarray;  
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;  
KM ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200157275-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000667.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-483446/52.  
XX  
PT Single exon nucleic acid probes for analyzing gene expression in human  
PT brains.

XX  
PS Example 4; SEQ ID NO 4591; 650bp + Sequence Listing; English.  
XX  
CC The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC brain. They can be used to measure gene expression in brain cell samples,  
CC which may enable the diagnosis and improved treatment of nervous system  
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
CC epilepsy and cancers. The present sequence is one of the probes of the  
CC invention  
XX  
SQ Sequence 1945 BP; 453 A; 617 C; 484 G; 391 T; 0 U; 0 Other;  
XX  
Query Match 92.9%; Score 13; DB 4; Length 1945;  
Best Local Similarity 76.9%; Pred. No. 2.1e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
XX  
OY 2 GUACUGCACTCG 14  
DB 263 GTRCTGCACTCG 275  
XX  
RESULT 29  
ABS29757  
ID ABS29757 standard; DNA; 1945 BP.  
XX  
AC ABS29757;  
XX  
DT 25-FEB-2003 (first entry)  
XX  
DE Human liver single exon probe, SEQ ID NO 4747.  
XX  
KW Human; single exon nucleic acid probe; liver; cirrhosis;  
KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;  
KW coronary heart disease; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200157273-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000664.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-488998/53.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human adult liver.  
XX  
PS Claim 1; SEQ ID NO 4747; 658bp; English.  
XX  
CC The invention relates to a single exon nucleic acid probe (SENP) (I) for  
CC measuring human gene expression in a sample derived from human adult  
CC liver, comprising one of 13109 defined nucleotide sequences given in the  
CC specification (or complements/ fragments). The probe hybridises at high  
CC stringency to a nucleic acid molecule expressed in the human adult liver.  
CC (I) may be used for predicting, measuring and displaying gene expression  
CC in samples derived from human adult liver. The genes identified may be  
CC involved in genetic liver diseases such as cirrhosis,  
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is  
CC associated with coronary heart disease. ABS25011-ABS51005 represent human

CC liver single exon nucleic acid probes of the invention. Note: The  
 CC sequence information for this patent does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX  
 SQ Sequence 1945 BP; 453 A; 617 C; 484 G; 391 T; 0 U; 0 Other;

Query Match 92.9%; Score 13; DB 4; Length 1945;  
 Best Local Similarity 76.9%; Pred. No. 2.1e+03;  
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GUACUGCAACUG 14  
 Db 263 GTACTGCAACTCG 275

RESULT 30  
 ID AA104509 standard; DNA; 1945 BP.

XX AA104509;

DT 09-OCT-2001 (first entry)

XX Probe #4500 used to measure gene expression in human breast sample.

XX Probe; human; breast disease; breast cancer; development disorder; ss;  
 KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.

XX Homo sapiens.

XX WO200157270-A2.

XX 09-AUG-2001.

XX 29-JAN-2001; 2001WO-US000661.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLR-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-476286/51.

XX Novel single exon nucleic acid probe used to measuring gene expression in  
 PT a human breast.

XX Claim 25; SEQ ID NO 4500; 322pp; English.

XX The present invention relates to novel single exon nucleic acid probes.

XX The present sequence is one such probe. The probes are useful for

XX measuring human gene expression in a human breast sample, where the probe

XX hybridises at high stringency to a nucleic acid expressed in the human

XX breast. The probes are useful for predicting, diagnosing, grading,

XX staging, monitoring and prognosing diseases of the human breast,

XX particularly those diseases with polygenic aetiology. The diseases

XX include: breast cancer, disorders of development, inflammatory diseases

XX of the breast, fibrocystic changes, proliferative breast disease and non-

XX carcinoma tumours. Note: The sequence data for this patent did not form

XX part of the printed specification, but was obtained in electronic format

XX directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 1945 BP; 453 A; 617 C; 484 G; 391 T; 0 U; 0 Other;

XX Query Match 92.9%; Score 13; DB 5; Length 1945;

XX Best Local Similarity 76.9%; Pred. No. 2.1e+03;

Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 GUACUGCAACUG 14  
 Db 263 GTACTGCAACTCG 275

RESULT 31  
 ID ABS04688 standard; DNA; 1945 BP.

XX ABS04688;

XX 19-AUG-2002 (first entry)

XX Human genome-derived single exon probe from lung SEQ ID No 4679.

XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;

XX chronic obstructive pulmonary disease; interstitial lung disease;

XX familial idiopathic pulmonary fibrosis; neurofibromatosis;

XX tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;

XX Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemorrhage;

XX pulmonary alveolar proteinosis; lymphangioleiomyomatosis; Karsenger syndrome;

XX primary ciliary dyskinesia; pulmonary hypertension;

XX hyaline membrane disease.

XX Homo sapiens.

XX WO200186003-A2.

XX 15-NOV-2001.

XX 30-JAN-2001; 2001WO-US000665.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLR-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2002-114183/15.

XX Spatially-addressable set of single exon nucleic acid probes, used to

XX measure gene expression in human lung samples.

XX Claim 1; SEQ ID NO 4679; 634pp; English.

XX The invention relates to a spatially-addressable set of single exon

XX nucleic acid probes for measuring gene expression in a sample derived

XX from human lung comprising single exon nucleic acid probes having one of

XX 12614 nucleic acid sequences mentioned in the specification, or their

XX complements or the 12387 open reading frames derived from the 12614

XX probes. Also included are a microarray comprising the novel set of probes

XX; the novel set of probes which hybridise at high stringency to a nucleic

XX acid expressed in the human lung; measuring gene expression in a sample

XX derived from human lung, comprising (a) contacting the array with a

XX collection of detectably labeled nucleic acids derived from human lung

XX mRNA, and (b) measuring the label detectably bound to each probe of the

XX array; identifying exons in a eukaryotic genome, comprising (a)

XX algorithmically predicting at least one exon from genomic sequences of

XX the eukaryote; and (b) detecting specific hybridisation of detectably

XX labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,

XX having a fragment identical to the predicted exon, the probe is included

XX in the above mentioned microarray; assigning exons to a single gene,

XX comprising (a) identifying exons from genomic sequence by the method

XX above and (b) measuring the expression of each of the exons in several

CC	tissues and/or cell types using hybridization to a single exon
CC	microarrays having a probe with the exon, where a common pattern of
CC	expression of the exons in the tissues and/or cell types indicates that
CC	the exons should be assigned to a single gene; a peptide comprising one
CC	of 12011 sequences, mentioned in the specification, or encoded by the
CC	probes/open reading frames (ORF). The probes are used for gene expression
CC	analysis, and for identifying exons in a gene, particularly using human
CC	lung derived mRNA and for the study of lung diseases such as asthma, lung
CC	cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC	disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC	tubercous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC	Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC	histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC	Karsenger syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC	dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC	present sequence is a single exon probe of the invention. Note: The
CC	sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences
CC	
XX	
SO	Sequence 1945 BP; 453 A; 617 C; 484 G; 391 T; 0 U; 0 Other;
QY	
2	GUACUGCAACUCG 14
Db	263 GTACTGCAACTCG 275
AC	ACC61225 standard; DNA; 2000 BP.
AC	ACC61225;
DT	20-JUN-2003 (first entry)
XX	
DE	Gene sequence #SEQ ID 1232.
XX	
KM	Multi-protein complex; eukaryote; drug target; diagnosis; gene; ds.
OS	Saccharomyces cerevisiae.
PN	EP1258494-A1.
PD	20-NOV-2002.
PF	20-DEC-2001; 2001EP-00130253.
XX	
PR	15-MAY-2001; 2001EP-00111774.
XX	
PA	(CELL-) CELLZONE AG.
PI	Baer A, Gavin A, Grandi P, Krause R, Krause UD, Kuester BD;
PI	Marzloch M, Schultz J, Superti-Furga GD;
XX	
DR	WPI: 2003-250078/25.
XX	P-PSDB; ABR53183.
PT	New isolated protein complexes useful for diagnosing a disease or
PT	disorder, or as a target for an active agent of a pharmaceutical,
PT	preferably a drug target in the treatment or prevention of disease or
PT	disorder.
XX	
PS	Disclosure; SEQ ID NO 1232; 17bp + Sequence Listing; English.
XX	
CC	The invention relates to multi-protein complexes from eukaryotes. Proteins
CC	of the invention and DNA sequences encoding them are given in records
CC	ABR532568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are
CC	obtainable by using a protein as a bait and isolating the set of proteins
CC	which is attached thereto from cells. Such protein complexes may comprise

CC up to 30 distinct proteins. Protein complexes of the invention are useful  
CC for diagnosing a disease or disorder, or as a target for an active agent  
CC of a pharmaceutical, preferably a drug target in the treatment or  
CC prevention of a disease or disorder. Note: The sequence data for this  
CC patent is not represented in the printed specification, but is based on  
CC sequence information supplied by the European Patent Office. The complete  
CC document is available on CD-ROM

XX Sequence 2000 BP; 681 A; 345 C; 390 G; 584 T; 0 U; 0 Other;  
SQ

Query Match 92.9%; Score 13; DB 10; Length 2000;  
Best Local Similarity 76.9%; Pred. No. 2.1e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0

OY 2 GUACUGCACTCG 14  
| : | : | : | : | : |  
Db 1296 GTACTGCAACTCG 1284

RESULT 33  
ADK63219/C  
ID ADK63219 standard; DNA; 2000 BP.  
XX  
XX ADK63219;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
XX Disease treating protein complex-derived gene #735.  
DE  
XX  
XX protein complex; drug target; diagnosis; gene; ds.  
KM  
XX  
OS unidentified.  
XS  
XX  
XX EPI338608-A2.  
PN  
XX  
PD 27-AUG-2003.  
XX  
XX  
XX 20-DEC-2002; 2002EP-00102902.  
PF  
XX  
XX 20-DEC-2001; 2001EP-00130253.  
PR  
XX  
XX (CELL-) CELLZOME AG.  
PA  
XX  
XX Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J,  
P1 Marzioch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;  
P1 Michon A, Lautwein C, Rick J;  
XX WPI; 2003-638460/61.  
DR P-PSDB; ADK63218.

New proteins and protein complexes from eukaryotes, useful as targets in  
PT drug screening, or in diagnosing or screening for the presence of a  
PT disease or disorder, or a predisposition for developing a disease or  
PT disorder in a subject.

Disclousre; SEQ ID NO 1470; 13pp; English.

The invention relates to novel protein complexes comprising a first and a  
XX second protein, or its derivative, fragment, homologue or variant. The  
XX proteins are selected from given protein complexes, which are not defined  
XX in the specification. The variants are encoded by nucleic acids that  
XX hybridize to the nucleic acids encoding the proteins under low stringency  
XX conditions. The protein complexes are useful as targets for an active  
XX agent of a pharmaceutical. These protein complexes are particularly  
XX useful as drugs targets for the treatment or preventing of a disease or  
XX disorder. The complexes and methods above are useful in diagnosing or  
XX screening for the presence of a disease or disorder or a predisposition  
XX for developing a disease or disorder in a subject. These are also useful  
XX in screening for a drug for treatment or prevention of a disease or  
XX disorder. The molecule that modulates the amount, activity or protein  
XX components of the complex is useful for the manufacture of a medicament  
XX for the treatment or prevention of a disease or disorder. This sequence  
XX corresponds to a gene of the invention. (Note: the sequence data for this



CC patent did not form part of the printed specification but was obtained  
 CC from the EPO in electronic format).

XX Sequence 2000 BP; 681 A; 345 C; 390 G; 584 T; 0 U; 0 Other;

XX Query Match 92.9%; Score 13; DB 10; Length 2000;

XX Best Local Similarity 76.9%; Pred. No. 2.1e+03;

XX Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

XX 2 GUACUGCAACUG 14

XX 1296 GTACTGCACTCG 1284

XX RESULT 34

XX AAS88191/c

XX ID AAS88191 standard; CDNA; 2133 BP.

XX AAS88191;

XX 13-FRB-2002 (first entry)

XX DNA encoding novel human diagnostic protein #23995.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

XX 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX P-PSDB; ABG24004.

XX Claim 1; SEQ ID NO 23995; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)

XX sequences. (I) is useful as hybridisation probes, polymerase chain

XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

XX and in recombinant production of (II). The polynucleotides are also used

XX in diagnostics as expressed sequence tags for identifying expressed

XX genes. (I) is useful in gene therapy techniques to restore normal

XX activity of (II) or to treat disease states involving (II). (II) is

XX useful for generating antibodies against it, detecting or quantitating a

XX polypeptide in tissue, as molecular weight markers and as a food

XX supplement. (II) and its binding partners are useful in medical imaging

XX of sites expressing (II). (I) and (II) are useful for treating disorders

XX involving aberrant protein expression or biological activity. The

XX polypeptide and polynucleotide sequences have applications in

XX Sequence 2133 BP; 518 A; 542 C; 579 G; 494 T; 0 U; 0 Other;

XX Query Match 92.9%; Score 13; DB 5; Length 2133;

XX Best Local Similarity 76.9%; Pred. No. 2.1e+03;

XX Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

XX 2 GUACUGCAACUG 14

XX 2019 GTACTGCACTCG 2007

XX RESULT 35

XX AAT93775

XX ID AAT93775 standard; DNA; 2963 BP.

XX AAT93775;

XX 29-JUN-1998 (first entry)

XX PSD-93 coding sequence.

XX PSD-93; nNOS; neuronal nitric oxide synthase; Alzheimer's disease;

XX diagnosis; muscular dystrophy; skeletal muscle; Huntington's disease;

XX Duchenne muscular dystrophy; Becker muscular dystrophy; dystrophin;

XX sarcolemma; PDZ domain; neurodegenerative disease; gene therapy;

XX amyotrophic lateral sclerosis; ds.

XX Rattus sp.

XX Key Location/Qualifiers

XX CDS 1..42

XX /tag= a

XX /note= "PSD-93 partial sequence (see AAW34659) "

XX CDS 43..150

XX /tag= b

XX /note= "PSD-93 partial sequence (see AAW34660) "

XX CDS 151..195

XX /tag= C

XX /note= "PSD-93 partial sequence (see AAW34661) "

XX CDS 196..2844

XX /tag= d

XX /transl\_except= (pos: 2137..2139, aa: Phe)

XX /note= "PSD-93 partial sequence (see AAW34662) "

XX CDS 2845..2961

XX /tag= e

XX /note= "PSD-93 partial sequence (see AAW34663), no stop

XX codon given"

XX WO9733173-A1.

XX 12-SEP-1997.

XX 06-MAR-1997; 97WO-US003897.

XX 08-MAR-1996; 96US-00613114.

XX (REGC ) UNIT CALIPORNIA.

XX Bredt DS, Brennan JB, Chao DS;

XX WPI; 1997-47055/43.

XX P-PSDB; AAW34659, AAW34660, AAW34661, AAW34662, AAW34663.

XX Diagnosing muscular dystrophy by detecting absence or decrease of

XX neuronal nitric oxide synthase (nNOS) in skeletal muscle sarcolemma -

XX using new nNOS binding post-synaptic density proteins, PSD-93 and PSD-95;

XX also used for the diagnosis, prophylaxis and treatment of stroke and

XX other neurodegenerative diseases.

XX Claim 17; Page 72-73; 124pp; English.

XX This sequence encodes the post synaptic density protein-93 (PSD-93). PSD-

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XX

93 can be used in the method by detecting the absence or a decrease of neuronal dystrophy (MD) in a mammal by detecting absence or a decrease of neuronal nitric oxide synthase (nNOS) in a skeletal muscle sample. Patients with Duchenne or Becker MD lack normal levels of nNOS in skeletal muscle, in addition to lack of functional dystrophin. nNOS is normally targeted to the sarcolemma by associating to dystrophin (via the N-terminal PDZ domain (66 aa motif bearing homology to a heterogeneous family of signaling enzymes localized at cell-cell junctions) of nNOS, interacting specifically with the PDZ domain of the alpha 1-syntrophin component). The binding proteins PSD-93 and -95 also have a PDZ domain and interact with nNOS, mediating binding of nNOS to the NMDA receptor located at synapses. The PSD proteins are involved in the development and progression of stroke and some neurodegenerative diseases (e.g., Huntington's and Alzheimer's diseases and amyotrophic lateral sclerosis), so inhibiting them (or their binding) can be used to treat etc. Such diseases (associated with overactivation of NMDA receptors by excessive levels of nNOS. This method allows early diagnosis of MD. MD can now be treated by gene therapy, using only the fragment of dystrophin involved in formation of the nNOS/sarcolemma/dystrophin complex, rather than the complete dystrophin gene which is too large to manipulate

Sequence 2963 BP; 897 A; 641 C; 696 G; 729 T; 0 U; 0 Other;

Query Match 92.9%; Score 13; DB 2; Length 2963;  
Best Local Similarity 76.9%; Pred. No. 2.2e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

2 GUACUGCAACUCG 14  
|||:|||||:  
1430 GTACTGCACACTCG 1442

RESULT 36  
AAS30082/C  
ID AAS30082 standard; cDNA; 3222 BP.  
XX  
AAS30082;  
XX  
DT 13-FEB-2002 (first entry)  
XX  
DB DNA encoding novel human diagnostic protein #25886.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW Food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US008631.  
XX  
PR 31-MAR-2000; 2000US-00540217.  
PR 23-AUG-2000; 2000US-00649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Dermanac RT, Liu C, Tang YT;  
XX  
DR WPI; 2001-639362/73.  
DR P-PSDB; ABG25895.  
XX  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX  
XX  
XX Claim 1; SEQ ID NO 25886; 103bp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridization probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

CC	and in recombinant production of (II). The polynucleotides are also used
CC	in diagnostics as expressed sequence tags for identifying expressed
CC	genes. (I) is useful in gene therapy techniques to restore normal
CC	activity of (II) or to treat disease states involving (II). (II) is
CC	useful for generating antibodies against it, detecting or quantitating a
CC	polypeptide in tissue, as molecular weight markers and as a food
CC	supplement. (II) and its binding partners are useful in medical imaging
CC	of sites expressing (II). (I) and (II) are useful for treating disorders
CC	Involving aberrant protein expression or biological activity. The
CC	polypeptide and polynucleotide sequences have applications in
CC	diagnostics, forensics, gene mapping, identification of mutations
CC	responsible for genetic disorders or other traits to assess biodiversity
CC	and to produce other types of data and products dependent on DNA and
CC	amino acid sequences. AAS61197-AAS94564 represent novel human diagnostic
CC	coding sequences of the invention. Note: The sequence data for this
CC	patent did not appear in the printed specification, but was obtained in
CC	electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
SQ	Sequence 3222 BP; 727 A; 880 C; 863 G; 752 T; 0 U; 0 Other;
Query Match	92.9%; Score 13; DB 5; Length 3222;
Best Local Similarity	76.9%; Pred. No. 2.2e+03;
Matches	10; Conservative 3; Mismatches 0; Indels 0; Gaps 0.
OY	2 GUACUGCACTCG 14    ::   ::
Db	2019 GTACTGCACTCG 2007
RESULT 37	
ID	ADRs4732/c
ID	ADRs4732 standard; DNA; 3443 BP.
XX	
AC	ADRs4732;
DT	04-NOV-2004 (first entry)
DE	Aspergillus fumigatus essential gene genomic sequence #543.
KW	Fungicide; Aspergillus fumigatus infection; Farmer's lung disease; drug screening; ds.
OS	Aspergillus fumigatus.
PX	
PN	WO2004067709-A2.
PD	12-AUG-2004.
PP	16-JAN-2004; 2004WO-US001099.
PR	17-JAN-2003; 2003US-0441281P.
PR	13-JUN-2003; 2003US-0478196P.
PA	(ELIT-) ELITRA PHARM INC. (ELIT-) ELITRA PHARM LTD.
PI	Jiang B, Hu W, Lemieux S, Roemer T;
DR	WPI; 2004-594200/57.
DR	P-PSDB; ADR86493.
PT	New purified or isolated Aspergillus fumigatus nucleic acid molecule
PT	encoding a gene product, useful for diagnosing and/or treating invasive
PT	fungal infections, such as Farmer's lung disease.
BS	Claim 3; SEQ ID NO 543; 164pp; English.
CC	The present invention relates to Aspergillus fumigatus genes that are
CC	essential and are potential targets for drug screening. The methods and
CC	compositions of the present invention are useful for diagnosing and/or
CC	treating invasive Aspergillus fumigatus infection, including the allergic
CC	forms of the disease, such as Farmer's lung disease. They can also be

CC used in various drug discovery purposes, such as expression of the  
 CC recombinant protein, hybridization assay and construction of nucleic acid  
 CC arrays. The present sequence represents an *Aspergillus fumigatus*  
 CC essential gene full length genomic sequence, used during diagnosis and  
 CC drug development in the invention. These genes share a high degree of  
 CC sequence conservation with known essential genes of candida albicans. The  
 CC sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format from WIPO.

XX Sequence 3443 BP; 823 A; 843 C; 807 G; 970 T; 0 U; 0 Other;

Query Match 92.9%; Score 13; DB 13; Length 3443;  
 Best Local Similarity 76.9%; Pred. No. 2.2e+03;

Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCAACUC 14  
 ||:|||||:  
 DB 1057 GTAGTGCACCTCG 1045

RESULT 38  
 AAX20500/c  
 ID AAX20500 standard; DNA; 14063 BP.

XX AAX20500;

XX 05-MAY-1999 (first entry)

XX Polynucleotide sequence from the genome of *Treponema pallidum*.

XX *Treponema pallidum* infection; syphilis; *Borrelia infection*; animal;  
 KM enzyme production; ds.

XX *Treponema pallidum*.

XX MO865034-A2.

XX 30-DEC-1998.

XX 23-JUN-1998; 98WO-US013041.

XX 24-JUN-1997; 97US-0050667P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Fraser CM;

XX WPI; 1999-081273/07.

XX New isolated *Treponema pallidum* nucleic acids - used to develop products  
 PT for the detection, diagnosis, characterisation, prevention and therapy of  
 PT *T. pallidum* infections, particularly syphilis.

XX Claim 1; Page 178-186; 1150pp; English.

XX AAX20500-21243 represent polynucleotide sequences from the genome of  
 CC *Treponema pallidum*. The sequences can be used for detection, diagnosis,  
 CC characterisation, prevention and therapy for *T. pallidum* infections,  
 CC particularly syphilis. They can also be used for detecting diseases,  
 CC related to *Borrelia* infections in animals, and for the production of  
 CC biosynthetic products such as enzymes

XX Sequence 14063 BP; 3225 A; 4086 C; 3507 G; 3225 T; 0 U; 20 Other;

Query Match 92.9%; Score 13; DB 2; Length 14063;  
 Best Local Similarity 76.9%; Pred. No. 2.4e+03;

Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13  
 ||:|||||:  
 DB 5719 GGTACTGCACCTC 5707

RESULT 39  
 AD213310/c  
 ID AD213310 standard; DNA; 83493 BP.

XX AD213310;

XX 16-JUN-2005 (first entry)

XX Murine cancer-associated genomic DNA #71.

XX Diagnosis; DNA microarray; microarray; bclchip; cancer; neoplasm;

XX Cytochrome; gene; ds.

XX Mus sp.

XX MO2005031001-A2.

XX 23-SEP-2004; 2004WO-US031617.

XX 23-SEP-2003; 2003US-00669920.

XX (CHIR) CHIRON CORP.

XX Morris DW, Malandro MS;

XX WPI; 2005-273395/28.

XX Nucleic acid array useful for detecting cancer associated nucleic acid,  
 PT comprises two or more nucleic acid probes.

XX Disclosure; SEQ ID NO 830; 198pp; English.

XX The invention relates to a nucleic acid array for detecting a cancer  
 CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.  
 CC The invention also relates to a peptide array comprising two or more  
 CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound  
 CC that binds to a polypeptide, an isolated antibody or its fragment which  
 CC binds to a polypeptide, which is prepared by immunizing a host animal  
 CC with a composition comprising the polypeptide or its antigen binding  
 CC fragment and collecting cells from the host expressing antibodies against  
 CC the antigen or its antigen binding fragment, a composition comprising the  
 CC antibody and a carrier, a method of screening for anticancer activity, a  
 CC method of detecting a CA nucleic acid, a method of diagnosing cancer, a  
 CC method of treating cancer and a method of inhibiting expression of a CA  
 CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA  
 CC nucleic acids. The antibody is useful for detecting the presence or  
 CC absence of cancer cells in an individual which involves contacting cells  
 CC from the individual with the antibody and detecting a complex of a CA  
 CC protein from the cancer cells and the antibody, where the detection of  
 CC the complex correlates with the presence of cancer cells in the  
 CC individual. The composition is useful for inhibiting growth of cancer  
 CC cells in an individual or for delivering a therapeutic agent to cancer  
 CC cells in an individual. The invention is also useful for diagnosing  
 CC cancer, for treating cancer and for inhibiting expression of a CA gene in  
 CC a cell. This sequence represents murine cancer-associated genomic DNA of  
 CC the invention.

XX Sequence 83493 BP; 22528 A; 17868 C; 19019 G; 24033 T; 0 U; 45 Other;

Query Match 92.9%; Score 13; DB 14; Length 83493;  
 Best Local Similarity 76.9%; Pred. No. 2.6e+03;

Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13  
 ||:|||||:  
 DB 36317 GGTACTGCACCTC 36305

RESULT 40  
 AB067196\_6/c  
 Continuation (7 of 7) of AB067196 from base 600001 (Listeria innocua contig DNA sequence

WP Sequence split into 7 fragments LOCUS AB067196 Accession Ab067196  
WP Fragment Name Begin End  
WP AB067196\_0 1 110000  
WP AB067196\_1 100001 210000  
WP AB067196\_2 200001 310000  
WP AB067196\_3 300001 410000  
WP AB067196\_4 400001 510000  
WP AB067196\_5 500001 610000  
WP AB067196\_6 600001 684707

Query Match 92.9%; Score 13; DB 6; Length 84707;  
Best Local Similarity 76.9%; Pred. No. 2.7e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUCGCACTC 13  
DB 46081 CGTACTGCACTC 46069

## RESULT 41

AB069245\_26  
Continuation (27 of 31) of AB069245 from base 2600001 (Listeria innocua DNA sequence #68)

WP Sequence split into 31 fragments LOCUS AB069245 Accession Ab069245  
WP Fragment Name Begin End  
WP AB069245\_00 1 110000  
WP AB069245\_01 100001 210000  
WP AB069245\_02 200001 310000  
WP AB069245\_03 300001 410000  
WP AB069245\_04 400001 510000  
WP AB069245\_05 500001 610000  
WP AB069245\_06 600001 710000  
WP AB069245\_07 700001 810000  
WP AB069245\_08 800001 910000  
WP AB069245\_09 900001 1010000  
WP AB069245\_10 1000001 1110000  
WP AB069245\_11 1100001 1210000  
WP AB069245\_12 1200001 1310000  
WP AB069245\_13 1300001 1410000  
WP AB069245\_14 1400001 1510000  
WP AB069245\_15 1500001 1610000  
WP AB069245\_16 1600001 1710000  
WP AB069245\_17 1700001 1810000  
WP AB069245\_18 1800001 1910000  
WP AB069245\_19 1900001 2010000  
WP AB069245\_20 2000001 2110000  
WP AB069245\_21 2100001 2210000  
WP AB069245\_22 2200001 2310000  
WP AB069245\_23 2300001 2410000  
WP AB069245\_24 2400001 2510000  
WP AB069245\_25 2500001 2610000  
WP AB069245\_26 2600001 2710000  
WP AB069245\_27 2700001 2810000  
WP AB069245\_28 2800001 2910000  
WP AB069245\_29 2900001 3010000  
WP AB069245\_30 3000001 3011208

Query Match 92.9%; Score 13; DB 6; Length 110000;  
Best Local Similarity 76.9%; Pred. No. 2.7e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUCGCACTC 13  
DB 34732 CGTACTGCACTC 34744

## RESULT 42

AB039175\_12/c  
Continuation (13 of 35) of AB039175 from base 1200001 (L. pneumophila DNA SEQ ID NO 3507)

WP Sequence split into 35 fragments LOCUS AB039175 Accession Ab039175  
WP Fragment Name Begin End  
WP AB039175\_00 1 110000  
WP AB039175\_01 100001 210000  
WP AB039175\_02 200001 310000

WP AB039175\_03 300001 410000  
WP AB039175\_04 400001 510000  
WP AB039175\_05 500001 610000  
WP AB039175\_06 600001 710000  
WP AB039175\_07 700001 810000  
WP AB039175\_08 800001 910000  
WP AB039175\_09 900001 1010000  
WP AB039175\_10 1000001 1110000  
WP AB039175\_11 1100001 1210000  
WP AB039175\_12 1200001 1310000  
WP AB039175\_13 1300001 1410000  
WP AB039175\_14 1400001 1510000  
WP AB039175\_15 1500001 1610000  
WP AB039175\_16 1600001 1710000  
WP AB039175\_17 1700001 1810000  
WP AB039175\_18 1800001 1910000  
WP AB039175\_19 1900001 2010000  
WP AB039175\_20 2000001 2110000  
WP AB039175\_21 2100001 2210000  
WP AB039175\_22 2200001 2310000  
WP AB039175\_23 2300001 2410000  
WP AB039175\_24 2400001 2510000  
WP AB039175\_25 2500001 2610000  
WP AB039175\_26 2600001 2710000  
WP AB039175\_27 2700001 2810000  
WP AB039175\_28 2800001 2910000  
WP AB039175\_29 2900001 3010000  
WP AB039175\_30 3000001 3110000  
WP AB039175\_31 3100001 3210000  
WP AB039175\_32 3200001 3310000  
WP AB039175\_33 3300001 3410000  
WP AB039175\_34 3400001 3503610

Query Match 92.9%; Score 13; DB 14; Length 110000;  
Best Local Similarity 76.9%; Pred. No. 2.7e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUCGCACTC 13  
DB 88966 CGTACTGCACTC 88954

## RESULT 43

AB042401\_12/c  
Continuation (13 of 34) of AB042401 from base 1200001 (L. pneumophila DNA SEQ ID NO 6733).

WP Sequence split into 34 fragments LOCUS AB042401 Accession Ab042401  
WP Fragment Name Begin End  
WP AB042401\_00 1 110000  
WP AB042401\_01 100001 210000  
WP AB042401\_02 200001 310000  
WP AB042401\_03 300001 410000  
WP AB042401\_04 400001 510000  
WP AB042401\_05 500001 610000  
WP AB042401\_06 600001 710000  
WP AB042401\_07 700001 810000  
WP AB042401\_08 800001 910000  
WP AB042401\_09 900001 1010000  
WP AB042401\_10 1000001 1110000  
WP AB042401\_11 1100001 1210000  
WP AB042401\_12 1200001 1310000  
WP AB042401\_13 1300001 1410000  
WP AB042401\_14 1400001 1510000  
WP AB042401\_15 1500001 1610000  
WP AB042401\_16 1600001 1710000  
WP AB042401\_17 1700001 1810000  
WP AB042401\_18 1800001 1910000  
WP AB042401\_19 1900001 2010000  
WP AB042401\_20 2000001 2110000  
WP AB042401\_21 2100001 2210000  
WP AB042401\_22 2200001 2310000  
WP AB042401\_23 2300001 2410000  
WP AB042401\_24 2400001 2510000  
WP AB042401\_25 2500001 2610000

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WP AEB42401_26 260001 2710000
WP AEB42401_27 270001 2810000
WP AEB42401_28 280001 2910000
WP AEB42401_29 290001 3010000
WP AEB42401_30 300001 3110000
WP AEB42401_31 310001 3210000
WP AEB42401_32 320001 3310000
WP AEB42401_33 330001 345687

Query Match 92.9%; Score 13; DB 14; Length 110000;
Best Local Similarity 76.9%; Pred. No. 2.7e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUC 13
Db 98980 CGTACTGCAACTC 98968

RESULT 44
AEB42736_6/c
Continuation (7 of 8) of AEB42736 from base 600001 (L. pneumophila DNA SEQ ID NO 7068.)
WP Sequence split into 8 fragments LOCUS AEB42736 Accession Aeb42736
WP Fragment Name Begin End
WP AEB42736_0 1 110000
WP AEB42736_1 10001 21000
WP AEB42736_2 20001 31000
WP AEB42736_3 30001 41000
WP AEB42736_4 40001 51000
WP AEB42736_5 50001 61000
WP AEB42736_6 60001 71000
WP AEB42736_7 70001 740626

Query Match 92.9%; Score 13; DB 14; Length 110000;
Best Local Similarity 76.9%; Pred. No. 2.7e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUC 13
Db 60645 CGTACTGCAACTC 60633

RESULT 45
AEB35722/c
ID AEB35722 standard; DNA; 184368 BP.
XX
XX AEB35722;
AC
XX 08-SEP-2005 (first entry)
DT
XX L. pneumophila DNA SEQ ID NO 54.
DE
XX detection; infection; Antibacterial; Vaccine; ds; gene.
KM
XX Legionella pneumophila.
OS
XX WO2005049642-A2.
XX
XX 02-JUN-2005.
PD
XX
XX 23-SEP-2004; 2004MO-IB003578.
PR
XX
XX 21-NOV-2003; 2003FR-00013687.
XX
XX (INSP ) INST PASTEUR.
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UTLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Buchrieser C, Tichit M, Etienne J, Ma L, Cazale C, Glaser P;
PI Ruanlok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;
XX Jarraud S;
XX WPI; 2005-388305/40.
DR

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XX New genome of Legionella pneumophila Paris strain and derived
PT polypeptides, useful for detection or identification of the strain and
PT for treatment and prevention of infections.
XX
XX Claim 1; SEQ ID NO 54; 660bp; English.
PS
XX
XX The invention relates to an isolated or purified nucleotide sequences (I)
CC from Legionella pneumophila Paris strain. (I), and their related
CC sequences or fragments, are useful as primers and probes for detection
CC and amplification, including differentiation between the Paris and
CC Philadelphia strains of Legionella pneumophila and to prepare recombinant
CC (hybrid) polypeptides (II). (II) are also useful for preparation of
CC specific antibodies (Ab), also used for detection/identification of
CC Legionella, and some (II), specifically those involved in synthesis of
CC surface proteins, are targets for identification of inhibitors. (II), or
CC vectors that contain (I), are useful as vaccines and immunogenic
CC compositions, for treatment and prevention of infections by L.
CC pneumophila. The present sequence represents a L. pneumophila DNA.
XX
XX Sequence 184368 BP; 57341 A; 33604 C; 36303 G; 57120 T; 0 U; 0 Other;
SQ

Query Match 92.9%; Score 13; DB 14; Length 184368;
Best Local Similarity 76.9%; Pred. No. 2.7e+03;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACUGCAACUC 13
Db 119323 CGTACTGCAACTC 119311

RESULT 46
AEB39170
ID AEB39170 standard; DNA; 207461 BP.
XX
XX AEB39170;
AC
XX 08-SEP-2005 (first entry)
DT
XX L. pneumophila DNA SEQ ID NO 3502.
DE
XX detection; infection; Antibacterial; Vaccine; ds; gene.
KM
XX Legionella pneumophila.
OS
XX WO2005049642-A2.
XX
XX 02-JUN-2005.
PD
XX
XX 23-SEP-2004; 2004MO-IB003578.
PR
XX
XX 21-NOV-2003; 2003FR-00013687.
XX
XX (INSP ) INST PASTEUR.
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UTLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Buchrieser C, Tichit M, Etienne J, Ma L, Cazale C, Glaser P;
PI Ruanlok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;
XX Jarraud S;
XX WPI; 2005-388305/40.
DR
XX
XX New genome of Legionella pneumophila Paris strain and derived
PT polypeptides, useful for detection or identification of the strain and
PT for treatment and prevention of infections.
XX
XX Example 9; SEQ ID NO 3502; 660bp; English.
XX
XX The invention relates to an isolated or purified nucleotide sequences (I)
CC from Legionella pneumophila Paris strain. (I), and their related
CC sequences or fragments, are useful as primers and probes for detection
CC

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CC and amplification, including differentiation between the Paris and  
CC Philadelphia strains of Legionella pneumophila and to prepare recombinant  
CC (hybrid) polypeptides (II). (II) are also useful for preparation of  
CC specific antibodies (Ab), also used for detection/identification of  
CC Legionella, and some (I), specifically those involved in synthesis of  
CC surface proteins, are targets for identification of inhibitors. (II), or  
CC vectors that contain (I) are useful as vaccines and immunogenic  
CC compositions, for treatment and prevention of infections by L.  
CC pneumophila. The present sequence represents a L. pneumophila DNA.  
XX  
SQ Sequence 207461 BP; 66316 A; 40889 C; 36511 G; 63745 T; 0 U; 0 Other;  
Query Match 92.9%; Score 13; DB 14; Length 207461;  
Best Local Similarity 76.9%; Pred. No. 2.7e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGUACUGCAACUC 13  
DB 80862 CGTACTGCAATC 80874  
RESULT 47  
ADS37261  
ID ADS37261 standard; DNA; 201 BP.  
AC  
XX ADS37261;  
XX  
DT 16-DEC-2004 (first entry)  
DE Human autoimmune disease-related SNP context sequence - SEQ ID 2475.  
XX  
XX  
KW single nucleotide polymorphism detection; SNP detection;  
KW rheumatoid arthritis; type 1 diabetes; multiple sclerosis;  
KW systemic lupus erythematosus; inflammatory bowel disease; psoriasis;  
KW thyroiditis; celiac disease; pernicious anaemia; asthma; vitiligo;  
KW glomerulonephritis; Grave's disease; myocarditis; Sjogren's disease;  
KW primary systemic vasculitis; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO2004083403-A2.  
XX  
PD 30-SEP-2004.  
XX  
PF 18-MAR-2004; 2004WO-US008461.  
XX  
PR 18-MAR-2003; 2003US-0455444P.  
PR 25-APR-2003; 2003US-0465241P.  
PA (APPL-) APPLERA CORP.  
PI Cargill M, Begovich AB, Alexander HC;  
XX  
XX WPI; 2004-728480/71.  
DR  
XX  
XX  
PT New isolated nucleic acid molecule comprises at least 8 contiguous  
PT nucleotides where one of the nucleotides is a single nucleotide  
PT polymorphism (SNP), useful for diagnosing or treating autoimmune  
PT diseases, e.g. rheumatoid arthritis.  
XX  
XX  
PS Claim 16; SEQ ID NO 2475; 123pp; English.  
XX  
XX The invention comprises amino acid and coding sequences containing  
CC genetic polymorphisms associated with an altered risk of developing an  
CC autoimmune disease (e.g. rheumatoid arthritis). The invention further  
CC comprises a method of identifying an individual that has an altered risk  
CC of developing an autoimmune disease, comprising detecting a single  
CC nucleotide polymorphism (SNP) in a nucleic acid of the invention. The DNA  
CC and protein sequences of the invention are useful for diagnosing and  
CC treating autoimmune diseases, such as: rheumatoid arthritis, type 1  
CC diabetes, multiple sclerosis, systemic lupus erythematosus, inflammatory  
CC bowel diseases, psoriasis, thyroiditis, celiac disease, pernicious  
CC anaemia, asthma, vitiligo, glomerulonephritis, Grave's disease,  
CC aneemia, asthma, vitiligo, glomerulonephritis, Grave's disease,

CC myocarditis, Sjogren's disease, or primary systemic vasculitis. The  
CC present DNA sequence represents a human autoimmune disease-related  
CC genetic-based SNP context sequence of the invention. NOTE: The present  
CC sequence is not shown in the specification, but has been retrieved from  
CC the WIPO website.  
XX  
SQ Sequence 201 BP; 59 A; 35 C; 45 G; 61 T; 0 U; 1 Other;  
Query Match 90.0%; Score 12.6; DB 13; Length 201;  
Best Local Similarity 76.9%; Pred. No. 3.1e+03;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGUACUGCAACUC 13  
DB 99 CGTACTGCAATC 111  
RESULT 48  
ADS40621/C  
ID ADS40621 standard; DNA; 201 BP.  
AC  
XX ADS40621;  
XX  
DT 16-DEC-2004 (first entry)  
DE Human autoimmune disease-related SNP context sequence - SEQ ID 5835.  
XX  
XX  
KW single nucleotide polymorphism detection; SNP detection;  
KW rheumatoid arthritis; type 1 diabetes; multiple sclerosis;  
KW systemic lupus erythematosus; inflammatory bowel disease; psoriasis;  
KW thyroiditis; celiac disease; pernicious anaemia; asthma; vitiligo;  
KW glomerulonephritis; Grave's disease; myocarditis; Sjogren's disease;  
KW primary systemic vasculitis; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO2004083403-A2.  
XX  
PD 30-SEP-2004.  
XX  
PF 18-MAR-2004; 2004WO-US008461.  
XX  
PR 18-MAR-2003; 2003US-0455444P.  
PR 25-APR-2003; 2003US-0465241P.  
PA (APPL-) APPLERA CORP.  
PI Cargill M, Begovich AB, Alexander HC;  
XX  
XX WPI; 2004-728480/71.  
DR  
XX  
XX  
PT New isolated nucleic acid molecule comprises at least 8 contiguous  
PT nucleotides where one of the nucleotides is a single nucleotide  
PT polymorphism (SNP), useful for diagnosing or treating autoimmune  
PT diseases, e.g. rheumatoid arthritis.  
XX  
XX  
PS Claim 16; SEQ ID NO 5835; 123pp; English.  
XX  
XX The invention comprises amino acid and coding sequences containing  
CC genetic polymorphisms associated with an altered risk of developing an  
CC autoimmune disease (e.g. rheumatoid arthritis). The invention further  
CC comprises a method of identifying an individual that has an altered risk  
CC of developing an autoimmune disease, comprising detecting a single  
CC nucleotide polymorphism (SNP) in a nucleic acid of the invention. The DNA  
CC and protein sequences of the invention are useful for diagnosing and  
CC treating autoimmune diseases, such as: rheumatoid arthritis, type 1  
CC diabetes, multiple sclerosis, systemic lupus erythematosus, inflammatory  
CC bowel diseases, psoriasis, thyroiditis, celiac disease, pernicious  
CC anaemia, asthma, vitiligo, glomerulonephritis, Grave's disease,  
CC myocarditis, Sjogren's disease, or primary systemic vasculitis. The  
CC present DNA sequence represents a human autoimmune disease-related  
CC genetic-based SNP context sequence of the invention. NOTE: The present  
CC sequence is not shown in the specification, but has been retrieved from

CC the WIPO website.  
 XX Sequence 201 BP; 61 A; 45 C; 35 G; 59 T; 0 U; 1 Other;  
 SQ Query Match 90.0%; Score 12.6; DB 13; Length 201;  
 Best Local Similarity 76.9%; Pred. No. 3.1e+03;  
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13  
 ||:|||||:  
 DB 103 CGVACTGCAACTC 91

RESULT 49  
 AAA28522/c  
 ID AAA28522 standard; CDNA; 2290 BP.  
 XX  
 AC AAA28522;  
 XX  
 DT 29-AUG-2000 (first entry)  
 XX  
 DE Human opioid growth factor receptor cDNA of spliced form A.  
 XX  
 KM OGR; opioid growth factor receptor; growth inhibitor; proliferative;  
 KM cytoabatic; vulnerary. gene therapy; antagonist; chromosome 20q13.3; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 34..2007  
 FT /\*tag= a  
 XX  
 PN WO200026340-A2.  
 PD 11-MAY-2000.  
 XX  
 PF 02-NOV-1999; 99MO-US025802.  
 XX  
 PR 03-NOV-1998; 98US-0106879P.  
 PA (PENN-) PENN STATE RES FOUND.  
 XX  
 PI Zagon IS, McLaughlin PJ, Verderame MF;  
 XX  
 DR WPI; 2000-365594/31.  
 XX  
 PT New cDNA encoding rat and human opioid growth factor receptors which  
 PT modulate cell growth, useful for treating cancer.  
 XX  
 PS Claim 1; Page 77-78; 91pp; English.  
 XX  
 CC Primers generated from rat opioid growth factor receptor (OGFR) cDNA were  
 CC used to clone a fragment of the human OGFR cDNA. The complete sequence of  
 CC human OGFR was assembled with a combination of 3' and 5' RACE. 5' RACE  
 CC consistently yielded a single species of cDNA, while the 3' RACE revealed  
 CC extensive alternative splicing. The alternate splice forms were missing  
 CC the imperfect repeats or differed in the number of imperfect repeats. The  
 CC human OGFR gene chromosomal location was determined by FISH as 20q13.3.  
 CC expression vector are useful for detecting expression or levels of an  
 CC OGFR in a tissue. OGFR nucleic acids can be used to inhibit growth of  
 CC cells in vitro. The antisense sequences and antibodies can be used to  
 CC promote growth of cells in vitro. Cell growth can be promoted by  
 CC interfering with the OGFR ligand-receptor system, especially where a  
 CC subject suffers from a tissue wound. Treating cancer comprises enhancing  
 CC the function of the OGFR ligand-receptor system in cancerous cells of a  
 CC patient or administering the OGFR nucleic acid to the patient

SQ Sequence 2290 BP; 470 A; 713 C; 807 G; 297 T; 0 U; 3 Other;  
 Query Match 90.0%; Score 12.6; DB 3; Length 2290;  
 Best Local Similarity 69.2%; Pred. No. 3.6e+03;  
 Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13  
 ||:|||||:  
 DB 1969 CGTMTGCAACTC 1957

RESULT 50  
 ADS36480/c  
 ID ADS36480 standard; DNA; 29871 BP.  
 XX  
 AC ADS36480;  
 XX  
 DT 16-DEC-2004 (first entry)  
 XX  
 DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1694.  
 XX  
 KM single nucleotide polymorphism detection; SNP detection;  
 KM rheumatoid arthritis; type 1 diabetes; multiple sclerosis;  
 KM systemic lupus erythematosus; inflammatory bowel disease; psoriasis;  
 KM chryoiditis; celiac disease; pernicious anaemia; asthma; vitiligo;  
 KM glomerulonephritis; Grave's disease; myocarditis; Sjogren's disease;  
 KM primary systemic vasculitis; de.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004083403-A2.  
 PD 30-SEP-2004.  
 XX  
 PF 18-MAR-2004; 2004MO-US008461.  
 XX  
 PR 18-MAR-2003; 2003US-045544P.  
 PR 25-APR-2003; 2003US-0465241P.  
 PA (APPL-) APPLERA CORP.  
 XX  
 PI Cargill M, Begovitch AB, Alexander HC;  
 XX  
 DR WPI; 2004-728480/71.  
 XX  
 PT New isolated nucleic acid molecule comprises at least 8 contiguous  
 PT nucleotides where one of the nucleotides is a single nucleotide  
 PT polymorphism (SNP), useful for diagnosing or treating autoimmune  
 PT diseases, e.g. rheumatoid arthritis.  
 XX  
 PS Claim 16; SEQ ID NO 1694; 123pp; English.  
 XX  
 CC The invention comprises amino acid and coding sequences containing  
 CC genetic polymorphisms associated with an altered risk of developing an  
 CC autoimmune disease (e.g. rheumatoid arthritis). The invention further  
 CC comprises a method of identifying an individual that has an altered risk  
 CC of developing an autoimmune disease, comprising detecting a single  
 CC nucleotide polymorphism (SNP) in a nucleic acid of the invention. The DNA  
 CC and protein sequences of the invention are useful for diagnosing and  
 CC treating autoimmune diseases, such as: rheumatoid arthritis, type 1  
 CC diabetes, multiple sclerosis, systemic lupus erythematosus, inflammatory  
 CC bowel diseases, psoriasis, thyroiditis, celiac disease, pernicious  
 CC anaemia, asthma, vitiligo, glomerulonephritis, Grave's disease,  
 CC myocarditis, Sjogren's disease, or primary systemic vasculitis. The  
 CC present nucleic acid represents a human autoimmune disease-related  
 CC genomic DNA sequence of the invention. NOTE: The present sequence is not  
 CC shown in the specification, but has been retrieved from the WIPO website.  
 XX

SQ Sequence 29871 BP; 8723 A; 7387 C; 6374 G; 7338 T; 0 U; 49 Other;  
 Query Match 90.0%; Score 12.6; DB 13; Length 29871;  
 Best Local Similarity 76.9%; Pred. No. 4.2e+03;  
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13  
 ||:|||||:  
 DB 14198 CGVACTGCAACTC 14186



Thu Mar 23 15:50:24 2006

Search completed: March 18, 2006, 18:54:38  
Job time : 344.346 secs

us-10-800-926-2.rng

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OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 18:35:00 ; Search time 711.308 Seconds  
(without alignments)  
1118.796 Million cell updates/sec

Title: US-10-800-926-2

Perfect score: 14

Sequence: 1 cguacugcaacug 14

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 1000 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_scs:\*  
11: gb\_sy:\*  
12: gb\_un:\*  
13: gb\_vl:\*  
14: gb\_hcgs:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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C 2	14	100.0	10151 15	AF484941
C 3	14	100.0	11318 1	AE012045
C 4	14	100.0	14169 1	AE009858
C 5	14	100.0	96360 8	AP003867
C 6	14	100.0	99251 14	AL592045
C 7	14	100.0	101249 15	AP003884
C 8	14	100.0	110000 1	AE016853
C 9	14	100.0	110000 14	CP000058
C 10	14	100.0	110000 14	CR954209
C 11	14	100.0	110000 15	LMPLCR18_00
C 12	14	100.0	110000 15	AP008214
C 13	14	100.0	110000 15	AP008215
C 14	14	100.0	110000 15	CR382131_08
C 15	14	100.0	110000 15	CR382131_09
C 16	14	100.0	133106 15	AP004759
C 17	14	100.0	140409 14	AC044825
C 18	14	100.0	148848 15	AP005426

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36	13	92.9	615	1 AY136528
37	13	92.9	620	10 BV502883
38	13	92.9	693	10 BV507671
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91	13	92.9	39502	3 AY534910

AP005429	Oryza sat
BX088687	zebrafish
AC108605	Rattus no
AC103229	Rattus no
BX640547	zebrafish
AC021883	Homo sapi
BX294153	Periplaneta
COS54118	Sequence
AX988576	Sequence
AX988577	Sequence
AF069774	Mus muscu
AF069774	Mus muscu
L10992	Trypanosoma
AF232912	Macaca mu
AY011660	Ateles fu
L38870	Macaca mul
L38869	Macaca mul
AK111239	Oryza sat
AY136528	Acidovor
BV507671	gff62a12
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BV530657	G591P6179
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D64054	Myxine gluc
BV550217	S215P6032
E38273	Formate deh
AJ344089	Klebsiell
AJ08467	Enterobac
AY985960	Unculture
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AY013692	Unculture
AR405992	Sequence
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AX830750	Sequence
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AY133724	Arabidops
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AF388675	Mus muscu
AB051073	Hypomelicr
M34638	S.cerevisia
U53368	Rattus norv
U49049	Rattus norv
AC019684	Drosophill
AY920799	Aequorea
M34474	S.cerevisia
AJ415676	Nicotiana
AB001200	Treponeema
AB011567	Lepidoptir
AF197465	Pseudomon
AB084950	Nicotiana
AJ786382	Streptomy
D90850	E.coli geno
AL158136	Human DNA
L09634	Caenorhabdi
AC084551	Caenorhab
U00008	centilome_4
AY534910	Unculture

92	92	40198	15	YSCLE084	U19729 Saccharomyc	165	13	92.9	160950	14	AC163250	AC163250 Loxodonta	
93	13	42734	2	CEBY3	Z96047 Caenorhabdi	166	13	92.9	164301	14	AC018671	AC018671 Homo sapi	
94	13	43586	14	OSTIG0036	AL732335 Oryza sat	167	13	92.9	164925	18	AC098966	AC098966 Homo sapi	
95	13	58623	14	AC101064	AC101064 Mus muscu	168	13	92.9	164996	14	AC087372	AC087372 Homo sapi	
96	13	63105	14	AC120027	AC120027 Homo sapi	169	13	92.9	166117	14	CR855265	CR855265 Dario rer	
97	13	63643	14	AC090923	AC090923 Homo sapi	170	13	92.9	167511	14	AC162049	AC162049 Bos tauru	
98	13	66145	15	H0609A12	AL512544 Oryza sat	171	13	92.9	167812	14	AC125875	AC125875 Rattus no	
99	13	66506	14	AC120028	AC120028 Homo sapi	172	13	92.9	167851	8	AC118660	AC118660 Homo sapi	
100	13	68272	14	AC090171	AC090171 Homo sapi	173	13	92.9	168196	14	AC145953	AC145953 Pan trogl	
101	13	84707	6	AX417037	AX417037 Sequence	174	13	92.9	168297	9	AC116801	AC116801 Mus muscu	
102	13	88538	14	AC164461	AC164461 Bos tauru	175	13	92.9	168662	14	AC022241	AC022241 Homo sapi	
103	13	89855	14	AC074220	AC074220 Mus muscu	176	13	92.9	168909	8	AC010165	AC010165 Homo sapi	
104	13	98630	15	AC006535	AC006535 Genomic s	177	13	92.9	169453	8	AC096558	AC096558 Homo sapi	
105	13	101104	1	CP000089_44	Contiuation (45 o	178	13	92.9	170260	5	BX908763	BX908763 Zebrafish	
106	13	103273	8	AC139932	AC139932 Homo sapi	179	13	92.9	171072	8	CNS057E6	AL558335 Human chr	
107	13	104321	15	AP006142	AP006142 Lotus cor	180	13	92.9	171973	14	AC013571	AC013571 Homo sapi	
108	13	104712	8	AL390786	AL390786 Human DNA	181	13	92.9	172127	14	AC013572	AC013572 Homo sapi	
109	13	107489	8	AL137804	AL137804 Human DNA	182	13	92.9	173384	8	PTR448G23	PTR448G23 Pan trogl	
110	13	107819	15	CNS08C8U	AL731880 Oryza sat	183	13	92.9	175916	14	AC007747	AC007747 Homo sapi	
111	13	109022	15	AP004926	AP004926 Lotus cor	184	13	92.9	175916	14	CR85031	CR85031 Dario rer	
112	13	92.9	110000	1	AE005174_30	Contiuation (31 o	185	13	92.9	182172	15	CNS07YPC	AL713343 Oryza sat
113	13	92.9	110000	1	AE005174_31	Contiuation (32 o	186	13	92.9	183224	14	AC166615	AC166615 Oryctolag
114	13	92.9	110000	1	AE005674_23	Contiuation (24 o	187	13	92.9	184518	8	AC099524	AC099524 Homo sapi
115	13	92.9	110000	1	CR628336_12	Contiuation (13 o	188	13	92.9	184558	14	AC020570	AC020570 Homo sapi
116	13	92.9	110000	1	CR628337_12	Contiuation (13 o	189	13	92.9	185444	14	AC158419	AC158419 Homo sapi
117	13	92.9	110000	1	U00096_22	Contiuation (23 o	190	13	92.9	187787	9	AC121802	AC121802 Mus muscu
118	13	92.9	110000	1	U00096_23	Contiuation (24 o	191	13	92.9	188131	14	AC161201	AC161201 Mus muscu
119	13	92.9	110000	1	AE017354_12	Contiuation (13 o	192	13	92.9	188743	14	AC069135	AC069135 Homo sapi
120	13	92.9	110000	1	AP006716_04	Contiuation (5 o	193	13	92.9	189722	14	AC164403	AC164403 Homo sapi
121	13	92.9	110000	1	AP008231_20	Contiuation (21 o	194	13	92.9	192065	14	AC148556	AC148556 Papio anu
122	13	92.9	110000	1	BA000007_30	Contiuation (31 o	195	13	92.9	192617	14	AC123751	AC123751 Mus muscu
123	13	92.9	110000	1	BA000030_32	Contiuation (33 o	196	13	92.9	193101	14	AC009561	AC009561 Homo sapi
124	13	92.9	110000	1	BA000030_59	Contiuation (60 o	197	13	92.9	193579	9	AC130675	AC130675 Mus muscu
125	13	92.9	110000	1	CP000075_08	Contiuation (9 o	198	13	92.9	193900	14	AC165972	AC165972 Mus muscu
126	13	92.9	110000	14	AC020850_2	Contiuation (3 o	199	13	92.9	194550	14	AC148837	AC148837 Homo sapi
127	13	92.9	110000	14	CR954199_02	Contiuation (3 o	200	13	92.9	194551	14	AC092291	AC092291 Homo sapi
128	13	92.9	110000	14	CR954201_03	Contiuation (4 o	201	13	92.9	196164	5	BX119916	BX119916 Zebrafish
129	13	92.9	110000	14	CT005261_1	Contiuation (11 o	202	13	92.9	199047	9	AC103574	AC103574 Rattus no
130	13	92.9	110000	14	CT005267_10	Contiuation (12 o	203	13	92.9	207476	14	AC157524	AC157524 Mus muscu
131	13	92.9	110000	14	CT005267_11	Contiuation (12 o	204	13	92.9	208695	9	AL671478	AL671478 Mouse DNA
132	13	92.9	110000	14	LMFLCR32_04	Contiuation (5 o	205	13	92.9	209121	5	CR589950	CR589950 Zebrafish
133	13	92.9	110000	15	AP008218_158	Contiuation (159	206	13	92.9	209162	5	CR589950	CR589950 Zebrafish
134	13	92.9	110000	15	AP008218_158	Contiuation (210	207	13	92.9	209567	9	AC158236	AC158236 Mus muscu
135	13	92.9	110000	15	AB017347_06	Contiuation (7 of	208	13	92.9	212870	14	AC156189	AC156189 Bos tauru
136	13	92.9	110000	15	AP008207_212	Contiuation (213	209	13	92.9	212936	14	AC020970	AC020970 Mus muscu
137	13	92.9	110000	15	AP008207_213	Contiuation (214	210	13	92.9	215999	9	AC102792	AC102792 Mus muscu
138	13	92.9	110000	15	AP008210_330	Contiuation (331	211	13	92.9	217642	14	AC115542	AC115542 Rattus no
139	13	92.9	110000	15	AP008211_016	Contiuation (17 o	212	13	92.9	219491	14	AC092256	AC092256 Mus muscu
140	13	92.9	113312	15	CNS08C83	Contiuation (17 o	213	13	92.9	220503	14	AC163192	AC163192 Bos tauru
141	13	92.9	114057	2	AC091527	AC091527 Tryptanoso	214	13	92.9	220503	14	AC163192	AC163192 Bos tauru
142	13	92.9	116115	2	AC091527	AC091527 Tryptanoso	215	13	92.9	220503	14	AC163192	AC163192 Bos tauru
143	13	92.9	118650	14	AC153108	AC153108 Loxodonta	216	13	92.9	225793	14	AC156131	AC156131 Bos tauru
144	13	92.9	124175	14	AC163103	AC163103 Mus muscu	217	13	92.9	227676	9	AC109506	AC109506 Mus muscu
145	13	92.9	124350	14	AC129011	AC129011 Leishmani	218	13	92.9	227676	9	AC109506	AC109506 Mus muscu
146	13	92.9	125238	8	AC008842	AC008842 Homo sapi	219	13	92.9	229463	14	AC150456	AC150456 Mus muscu
147	13	92.9	131867	2	AY449460	AY449460 Oikopleur	220	13	92.9	231840	5	AL954746	AL954746 Zebrafish
148	13	92.9	131891	8	AC008131	AC008131 Homo sapi	221	13	92.9	234660	14	AC134709	AC134709 Bos tauru
149	13	92.9	132678	1	AY596294	AY596294 Haliotacul	222	13	92.9	234696	14	AC160179	AC160179 Bos tauru
150	13	92.9	134290	2	AC159439	AC159439 Tryptanoso	223	13	92.9	236599	14	AC095895	AC095895 Rattus no
151	13	92.9	134580	8	AC002526	AC002526 Human PAC	224	13	92.9	237041	14	AC164273	AC164273 Bos tauru
152	13	92.9	135578	8	AF064861	AF064861 Homo sapi	225	13	92.9	238060	9	AC148336	AC148336 Mus muscu
153	13	92.9	140626	15	OS0N00057	OS0N00057 Oryza sat	226	13	92.9	240475	14	AC099247	AC099247 Rattus no
154	13	92.9	141424	14	AC162149	AC162149 Dasypus n	227	13	92.9	243051	9	AC126217	AC126217 Rattus no
155	13	92.9	142350	5	BX664625	BX664625 Zebrafish	228	13	92.9	243468	14	AC103320	AC103320 Rattus no
156	13	92.9	145796	15	AC130598	AC130598 Oryza sat	229	13	92.9	244407	14	AC133427	AC133427 Rattus no
157	13	92.9	147817	15	AP003267	AP003267 Oryza sat	230	13	92.9	250323	14	AC119713	AC119713 Rattus no
158	13	92.9	152714	8	BS000156	BS000156 Pan trogl	231	13	92.9	255705	14	AC097750	AC097750 Rattus no
159	13	92.9	153617	8	AC012306	AC012306 Homo sapi	232	13	92.9	256019	8	AC016525	AC016525 Homo sapi
160	13	92.9	154066	8	HS24018	AL021808 Pan trogl	233	13	92.9	256719	9	AC154873	AC154873 Mus muscu
161	13	92.9	154375	14	AC145837	AC145837 Human DNA	234	13	92.9	258622	14	AC020877	AC020877 Mus muscu
162	13	92.9	157395	8	CNS07E8	AL512359 Human chr	235	13	92.9	258938	14	AC099416	AC099416 Mus muscu
163	13	92.9	158710	9	AC126539	AC126539 Mus muscu	236	13	92.9	271275	14	AC135198	AC135198 Rattus no
164	13	92.9	159767	14	AC023529	AC023529 Homo sapi	237	13	92.9	295689	14	AB016985	AB016985 Shigella

238	13	92.9	301130	1	AB016763	AE016763	Becherich	311	12.4	88.6	782	2	AY13559	AY13559	Drosophila
C 239	13	92.9	301332	1	AB017012	AB017012	Bacillus	312	12.4	88.6	785	10	BV663682	BV663682	Arabidopsis
240	13	92.9	302101	1	AB016784	AB016784	Pseudomon	C 313	12.4	88.6	788	2	AF187078	AF187078	Aedes aeg
241	13	92.9	305050	1	AL596173	AL596173	Listeria	C 314	12.4	88.6	788	2	AF266757	AF266757	Aedes aeg
242	13	92.9	309502	14	AL512434	AL512434	Bos taurus	C 315	12.4	88.6	798	6	BD125095	BD125095	Primer fo
243	13	92.9	309626	8	AY332722	AY332722	Homo sapi	C 316	12.4	88.6	798	6	BD127034	BD127034	Primer fo
C 244	13	92.9	340000	8	HS21C079	AL163272	Homo sapi	C 317	12.4	88.6	798	6	CQ780386	CQ780386	Sequence
C 245	13	92.9	345630	14	AC098829	AC098829	Rattus no	C 318	12.4	88.6	798	6	CQ782325	CQ782325	Sequence
C 246	13	92.9	346027	14	AC128885	AC128885	Rattus no	C 319	12.4	88.6	812	10	BV545689	BV545689	gm197f05
C 247	13	92.9	348313	1	CR378666	CR378666	Photobact	C 320	12.4	88.6	828	15	AF321883	AF321883	Neutropor
C 248	13	92.9	349697	1	BX842649	BX842649	Bellovib	C 321	12.4	88.6	831	1	ECORRFX	ECORRFX	E. coli rbo
C 249	13	92.9	349980	6	AX417038	AX417038	Sequence	C 322	12.4	88.6	838	1	AF632066	AF632066	Sequence
C 250	13	92.9	349980	6	AX417038	AX417038	Sequence	C 323	12.4	88.6	841	10	BV523655	BV523655	Sequence
251	12.6	90.0	201	6	CQ927442	CQ927442	Sequence	C 324	12.4	88.6	852	2	AY198134	AY198134	Aedes aeg
C 252	12.6	90.0	201	6	CQ927442	CQ927442	Sequence	C 325	12.4	88.6	862	2	MOSTRIP	MOSTRIP	Sequence
C 253	12.6	90.0	29871	6	CQ926631	CQ926631	Sequence	C 326	12.4	88.6	867	6	AR624404	AR624404	Sequence
254	12.6	90.0	321019	6	CQ926631	CQ926631	Sequence	C 327	12.4	88.6	883	8	HSN331221	HSN331221	Sequence
C 255	12.4	88.6	100	6	AX988725	AX988725	Sequence	C 328	12.4	88.6	889	6	AX144281	AX144281	Sequence
C 256	12.4	88.6	100	6	AX988725	AX988725	Sequence	C 329	12.4	88.6	899	6	BD125006	BD125006	Primer fo
257	12.4	88.6	100	6	AX988725	AX988725	Sequence	C 330	12.4	88.6	906	6	BD126264	BD126264	Primer fo
258	12.4	88.6	100	6	AX988725	AX988725	Sequence	C 331	12.4	88.6	906	6	BD126965	BD126965	Primer fo
259	12.4	88.6	128	6	BD131217	BD131217	Cytotoxic	C 332	12.4	88.6	906	6	CQ780297	CQ780297	Sequence
260	12.4	88.6	128	6	AX003031	AX003031	Sequence	C 333	12.4	88.6	906	6	CQ781555	CQ781555	Sequence
261	12.4	88.6	140	6	AR522163	AR522163	Sequence	C 334	12.4	88.6	906	6	CQ782256	CQ782256	Sequence
C 262	12.4	88.6	283	6	CQ436183	CQ436183	Sequence	C 335	12.4	88.6	906	6	CQ782256	CQ782256	Sequence
263	12.4	88.6	287	15	AY022329	AY022329	Oryza sat	C 336	12.4	88.6	915	10	BV545222	BV545222	Sequence
C 264	12.4	88.6	333	6	BD026046	BD026046	Sequence	C 337	12.4	88.6	925	1	AJ783702	AJ783702	Sequence
C 265	12.4	88.6	333	6	AX886436	AX886436	Sequence	C 338	12.4	88.6	960	6	CQ582132	CQ582132	Sequence
C 266	12.4	88.6	346	1	FS251394	AJ251394	Frankia s	C 339	12.4	88.6	969	6	CQ735117	CQ735117	Sequence
267	12.4	88.6	349	6	AR102510	AR102510	Sequence	C 340	12.4	88.6	1005	6	AR625940	AR625940	Sequence
C 268	12.4	88.6	355	9	MMR45PR	X06186	Moule rDNA	C 341	12.4	88.6	1007	6	AR618675	AR618675	Sequence
C 269	12.4	88.6	359	10	BV005953	BV005953	ORF 377 S	C 342	12.4	88.6	1017	6	AR347554	AR347554	Sequence
270	12.4	88.6	366	6	E14891	E14891	Partial seq	C 343	12.4	88.6	1026	15	DD017765	DD017765	Sequence
C 271	12.4	88.6	399	6	BD108597	BD108597	EST and e	C 344	12.4	88.6	1028	6	CQ608220	CQ608220	Sequence
C 272	12.4	88.6	399	6	AR413044	AR413044	Sequence	C 345	12.4	88.6	1032	6	AX535312	AX535312	Sequence
C 273	12.4	88.6	399	6	AX969878	AX969878	Sequence	C 346	12.4	88.6	1103	6	AX574002	AX574002	Sequence
C 274	12.4	88.6	401	1	AB054942	AB054942	Pseudobac	C 347	12.4	88.6	1104	6	AR386154	AR386154	Sequence
275	12.4	88.6	421	11	AR452983	AR452983	Synthetic	C 348	12.4	88.6	1126	15	OSRDC22	OSRDC22	Sequence
C 276	12.4	88.6	438	1	LGA187925	AJ387925	Lactococc	C 349	12.4	88.6	1144	6	AX770122	AX770122	Sequence
C 277	12.4	88.6	438	6	AX354209	AX354209	Sequence	C 350	12.4	88.6	1163	15	AF289119	AF289119	Sequence
C 278	12.4	88.6	449	1	AY702514	AY702514	Mannheimi	C 351	12.4	88.6	1185	15	AF289117	AF289117	Muscari a
C 279	12.4	88.6	480	2	AU028367	U28367	Aedes aegy	C 352	12.4	88.6	1194	15	BT019033	BT019033	Zea mays
280	12.4	88.6	480	5	AF139089	AF139089	Gymnotus	C 353	12.4	88.6	1195	6	AX772832	AX772832	Sequence
281	12.4	88.6	516	1	AY613943	AY613943	Xanthomon	C 354	12.4	88.6	1195	15	AK101344	AK101344	Oryza sat
C 282	12.4	88.6	535	6	BD124944	BD124944	Primer fo	C 355	12.4	88.6	1196	8	HSN33584	HSN33584	Sequence
C 283	12.4	88.6	535	6	BD126975	BD126975	Primer fo	C 356	12.4	88.6	1202	2	TCMJ5422	TCMJ5422	Sequence
C 284	12.4	88.6	535	6	CQ780235	CQ780235	Sequence	C 357	12.4	88.6	1205	15	ZEU90266	ZEU90266	Sequence
C 285	12.4	88.6	535	6	CQ782266	CQ782266	Sequence	C 358	12.4	88.6	1206	6	BD172008	BD172008	Mutant of
C 286	12.4	88.6	555	6	BD133927	BD133927	Novel met	C 359	12.4	88.6	1206	6	CQ800935	CQ800935	Sequence
C 287	12.4	88.6	558	6	E03074	E03074	DNA sequenc	C 360	12.4	88.6	1206	6	E14890	E14890	Mycobacteri
C 288	12.4	88.6	558	6	E54935	E54935	Vibrio para	C 361	12.4	88.6	1206	6	AR615673	AR615673	Sequence
C 289	12.4	88.6	567	15	AY586280	AY586280	Phycophth	C 362	12.4	88.6	1206	6	AX452067	AX452067	Sequence
C 290	12.4	88.6	572	6	RATRDNA1S	M26165	Rattus nov	C 363	12.4	88.6	1230	2	ASU18347	ASU18347	Sequence
C 291	12.4	88.6	597	6	AR500487	AR500487	Sequence	C 364	12.4	88.6	1238	2	AY071660	AY071660	Drosophila
C 292	12.4	88.6	597	6	AR515769	AR515769	Sequence	C 365	12.4	88.6	1246	2	TCMJ5421	TCMJ5421	Sequence
C 293	12.4	88.6	625	9	RATTIMPIX	L29512	Rat metallo	C 366	12.4	88.6	1248	15	AK061308	AK061308	Oryza sat
C 294	12.4	88.6	627	10	AF287295	AF287295	Drosophila	C 367	12.4	88.6	1256	15	AK106002	AK106002	Oryza sat
C 295	12.4	88.6	630	11	AY657581	AY657581	Synthetic	C 368	12.4	88.6	1257	15	AF425715	AF425715	Laguncula
C 296	12.4	88.6	645	6	CQ590925	CQ590925	Sequence	C 369	12.4	88.6	1257	15	AF425716	AF425716	Sequence
C 297	12.4	88.6	646	1	AY328003S07	AY328003	Symbiont	C 370	12.4	88.6	1259	15	AK070917	AK070917	Oryza sat
C 298	12.4	88.6	648	6	BD126283	BD126283	Primer fo	C 371	12.4	88.6	1259	15	CPY16901	CPY16901	Limonium
C 299	12.4	88.6	648	6	CQ781574	CQ781574	Sequence	C 372	12.4	88.6	1271	2	AY069282	AY069282	Drosophila
300	12.4	88.6	664	10	BV566985	BV566985	tpa62b04	C 373	12.4	88.6	1275	1	AB106890	AB106890	Thiodacil
301	12.4	88.6	701	10	BV241019	BV241019	S234P6324	C 374	12.4	88.6	1279	15	GSP312254	GSP312254	Sequence
C 302	12.4	88.6	715	1	AB064319	AB064319	Vibrio pa	C 375	12.4	88.6	1284	15	BT006584	BT006584	Arabidops
C 303	12.4	88.6	717	10	BV289200	BV289200	S232P6254	C 376	12.4	88.6	1284	15	AF507911	AF507911	Sequence
304	12.4	88.6	737	6	AR506567	AR506567	Sequence	C 377	12.4	88.6	1287	6	AX961341	AX961341	Sequence
C 305	12.4	88.6	743	6	BD124964	BD124964	Primer fo	C 378	12.4	88.6	1287	6	AX961341	AX961341	Sequence
C 306	12.4	88.6	743	6	BD126374	BD126374	Primer fo	C 379	12.4	88.6	1292	15	AAAN312252	AAAN312252	Sequence
C 307	12.4	88.6	743	6	CQ780255	CQ780255	Sequence	C 380	12.4	88.6	1292	15	AAAN402918	AAAN402918	Sequence
C 308	12.4	88.6	743	6	CQ781665	CQ781665	Sequence	C 381	12.4	88.6	1293	15	LTE286365	LTE286365	Sequence
C 309	12.4	88.6	757	8	HSN333315	AJ333315	Homo sapi	C 382	12.4	88.6	1302	6	CQ964339	CQ964339	Sequence
C 310	12.4	88.6	759	10	BV552387	BV552387	S221P6090	C 383	12.4	88.6	1304	15	LMA286364	LMA286364	Limonium

384	12.4	88.6	1318	15	CPY16900	Y16900 Limonium s1	457	12.4	88.6	2370	6	AR384634	AR384634 Sequence
385	12.4	88.6	1319	15	DAF312253	AJ1223 Dyerophyt	c 458	12.4	88.6	2404	5	AF098788	AF098788 Gallus ga
386	12.4	88.6	1320	15	LGU286358	AJ286358 Limoniaet	c 459	12.4	88.6	2406	5	AX770134	AX770134 Sequence
387	12.4	88.6	1322	15	CPY16903	Y16903 Limonium de	460	12.4	88.6	2409	6	BD273957	BD273957 Sequence
388	12.4	88.6	1332	15	CPY16907	Y16907 Psylliosetac	461	12.4	88.6	2409	6	AX005499	AX005499 Sequence
389	12.4	88.6	1334	15	CME286561	AJ286331 Ceratolim	462	12.4	88.6	2416	6	CS071123	CS071123 Sequence
390	12.4	88.6	1335	15	AF206789	AF206789 Limonium	c 463	12.4	88.6	2431	6	CQ719959	CQ719959 Sequence
391	12.4	88.6	1339	15	CPY16904	Y16904 Limonium vu	c 464	12.4	88.6	2451	6	BD273958	BD273958 Sequence
392	12.4	88.6	1331	15	LAX286362	Y16906 Plumbago ca	465	12.4	88.6	2451	6	AX005501	AX005501 Sequence
393	12.4	88.6	1331	15	CPY16906	Y16908 Armeria apl	c 466	12.4	88.6	2465	1	SAU439341	SAU439341 Sequence
394	12.4	88.6	1331	15	CPY16908	Y16909 Dictyolimon	c 467	12.4	88.6	2485	15	Y1250339	Y1250339 Sequence
395	12.4	88.6	1331	15	CPY16909	AJ286350 Ceratolim	c 468	12.4	88.6	2495	6	AR338781	AR338781 Sequence
396	12.4	88.6	1340	15	CME286360	AJ301572 Unculture	c 469	12.4	88.6	2520	6	BD127364	BD127364 Primer fo
c 397	12.4	88.6	1341	3	UBA301572	AJ301572 Limonium	c 470	12.4	88.6	2520	6	CQ782887	CQ782887 Sequence
398	12.4	88.6	1342	15	LDU286363	AJ286363 Limonium	c 471	12.4	88.6	2520	8	AK074923	AK074923 Homo sapi
399	12.4	88.6	1345	15	CF3286357	AJ286333 Ceratolim	c 472	12.4	88.6	2543	6	BD127330	BD127330 Primer fo
400	12.4	88.6	1358	1	HVO238879	AJ238879 Haloferax	c 473	12.4	88.6	2543	6	CQ782820	CQ782820 Sequence
401	12.4	88.6	1359	6	AR387715	AR387715 Sequence	c 474	12.4	88.6	2543	8	AK074858	AK074858 Homo sapi
402	12.4	88.6	1360	15	S1F286359	AJ286359 Saharant	c 475	12.4	88.6	2547	6	BD127344	BD127344 Primer fo
403	12.4	88.6	1362	1	AY654839	AY654839 Mucis bac	c 476	12.4	88.6	2547	6	CQ782847	CQ782847 Sequence
404	12.4	88.6	1371	15	AK064363	AK064363 Oryza sat	c 477	12.4	88.6	2547	8	AK074880	AK074880 Homo sapi
405	12.4	88.6	1371	15	AY128246	AY128246 Malaura t	c 478	12.4	88.6	2556	6	AX416615	AX416615 Sequence
406	12.4	88.6	1398	15	AEP39277	U33268 Aesculus pa	c 479	12.4	88.6	2563	6	BD127943	BD127943 Primer fo
407	12.4	88.6	1402	15	APU39277	U33268 Dicteronia	c 480	12.4	88.6	2563	6	CQ784000	CQ784000 Sequence
408	12.4	88.6	1402	15	DSU39268	U33268 Aesculus pa	c 481	12.4	88.6	2563	8	AK075013	AK075013 Homo sapi
409	12.4	88.6	1408	15	BH1402929	AJ402929 Billa hi	c 482	12.4	88.6	2578	1	DM5A9RC	DM5A9RC
410	12.4	88.6	1427	15	AY841666	AJ402929 Billa hi	c 483	12.4	88.6	2605	2	PSEAVRC	PSEAVRC
411	12.4	88.6	1428	15	AA297639	Z97643 Acantholim	c 484	12.4	88.6	2622	6	AR387855	AR387855 Sequence
412	12.4	88.6	1428	15	AA297640	Z97643 Acantholim	c 485	12.4	88.6	2622	6	CO577722	CO577722 Sequence
413	12.4	88.6	1428	15	AA297640	Z97643 Acantholim	c 486	12.4	88.6	2645	6	AX777339	AX777339 Sequence
414	12.4	88.6	1428	15	LC297643	Z97643 Limonium ca	c 487	12.4	88.6	2645	6	AX777339	AX777339 Sequence
415	12.4	88.6	1428	15	LD297644	Z97644 Limonium de	c 488	12.4	88.6	2680	2	BT010011	BT010011 Drosophi
416	12.4	88.6	1428	15	LM297642	Z97644 Limoniaetru	c 489	12.4	88.6	2723	2	CPU21667	CPU21667 Cryptospori
417	12.4	88.6	1428	15	LR297645	Z97645 Limonium ri	c 490	12.4	88.6	2806	6	AY060857	AY060857 Drosophi
418	12.4	88.6	1428	15	LS297646	Z97646 Limonium sp	c 491	12.4	88.6	2806	6	AX770124	AX770124 Sequence
419	12.4	88.6	1428	15	MTU403017	AJ403017 Malaura t	c 492	12.4	88.6	2852	6	CO590924	CO590924 Sequence
420	12.4	88.6	1428	15	AEP39277	L13181 Acer saccha	c 493	12.4	88.6	2861	6	CO592322	CO592322 Sequence
421	12.4	88.6	1428	15	AF215532	AF215532 Grafientr	c 494	12.4	88.6	2874	6	CO586236	CO586236 Sequence
422	12.4	88.6	1428	15	AF215530	AF215530 Meriania	c 495	12.4	88.6	3007	8	HOSAL8024	HOSAL8024 Sequence
423	12.4	88.6	1429	15	AF215531	AF215531 Adelobotr	c 496	12.4	88.6	3010	8	BC015009	BC015009 Homo sapi
424	12.4	88.6	1434	15	AF046930	AF215531 Adelobotr	c 497	12.4	88.6	3033	15	AY685231	AY685231 Neurospor
425	12.4	88.6	1449	15	AJ786659	AJ786659 Limonium	c 498	12.4	88.6	3095	4	AT618974	AT618974 Bos tauru
426	12.4	88.6	1449	15	ECOTHPY	AK11000 Oryza sat	c 499	12.4	88.6	3114	2	AT609524	AT609524 Drosophi
c 427	12.4	88.6	1513	1	ECOTHPY	L03720 B. coli hea	c 500	12.4	88.6	3148	6	CQ608219	CQ608219 Sequence
428	12.4	88.6	1513	15	RXCRBCUD	M77702 Rheum x cul	c 501	12.4	88.6	3171	1	ECOTHPY	ECOTHPY
429	12.4	88.6	1557	6	CO875959	CO875959 Sequence	c 502	12.4	88.6	3219	15	AF236387	AF236387 Schizosac
430	12.4	88.6	1584	6	AX429129	AX429129 Sequence	c 503	12.4	88.6	3232	2	BT001403	BT001403 Drosophi
431	12.4	88.6	1585	6	AX063438	AK063438 Oryza sat	c 504	12.4	88.6	3237	15	AJ7861427	AJ7861427 Soridaria
432	12.4	88.6	1621	2	AF241364	AF241364 Drosophi	c 505	12.4	88.6	3244	6	CO582131	CO582131 Sequence
c 433	12.4	88.6	1709	2	BT001266	BT001266 Drosophi	c 506	12.4	88.6	3244	9	MDU03457	MDU03457 Mus muscul
c 434	12.4	88.6	1710	1	LBAPBGL	M20151 L. casei P-b	c 507	12.4	88.6	3244	9	MDU03458	MDU03458 Mus muscul
c 435	12.4	88.6	1723	2	AY118718	AY118718 Drosophi	c 508	12.4	88.6	3398	6	CO578429	CO578429 Sequence
c 436	12.4	88.6	1735	1	AF346487	AF346487 Acetobact	c 509	12.4	88.6	3472	6	CO580922	CO580922 Sequence
c 437	12.4	88.6	1735	8	AF052110	AF052110 Homo sapi	c 510	12.4	88.6	3490	6	CO584338	CO584338 Sequence
c 438	12.4	88.6	1739	1	AF031189	AF031189 Chironati	c 511	12.4	88.6	3490	15	AY945225	AY945225 Aspergill
c 439	12.4	88.6	1739	15	AK110577	AK110577 Oryza sat	c 512	12.4	88.6	3507	6	CO590031	CO590031 Sequence
c 440	12.4	88.6	1750	1	AB072394	AB072394 Mycobacte	c 513	12.4	88.6	3552	15	AK119852	AK119852 Oryza sat
c 441	12.4	88.6	1770	1	AY083508	AY083508 Rhodococc	c 514	12.4	88.6	3710	6	CO589272	CO589272 Sequence
c 442	12.4	88.6	1770	1	AX824488	AX824488 Sequence	c 515	12.4	88.6	3712	2	DMPHOS3XI	DMPHOS3XI Sequence
c 443	12.4	88.6	1779	15	YSCLTG3	D16304 Yeast LTG3	c 516	12.4	88.6	3733	6	CO580305	CO580305 Sequence
c 444	12.4	88.6	1782	6	AX659988	AX659988 Sequence	c 517	12.4	88.6	3939	6	AX179644	AX179644 Sequence
c 445	12.4	88.6	1809	15	AY570722	AY570722 Otreococc	c 518	12.4	88.6	4185	13	AY357736	AY357736 Streptoc
c 446	12.4	88.6	1880	2	CAR290962	AJ290962 Clytus ar	c 519	12.4	88.6	4185	1	STRPOB	STRPOB
c 447	12.4	88.6	1915	15	AY093149	AY093149 Arbidops	c 520	12.4	88.6	4382	2	BT021440	BT021440 Drosophi
c 448	12.4	88.6	2003	8	HIMDAPC1	M64356 Human decay	c 521	12.4	88.6	4407	2	BT003173	BT003173 Drosophi
c 449	12.4	88.6	2059	15	THINDALA	Z22594 T. narizianu	c 522	12.4	88.6	4462	1	AF126720	AF126720 Mycobacte
c 450	12.4	88.6	2075	1	ARGERMA	M1176 Arthrobacte	c 523	12.4	88.6	4525	6	BD183405	BD183405 Novel gen
c 451	12.4	88.6	2133	15	AK120817	AK120817 Oryza sat	c 524	12.4	88.6	4607	13	AY842284	AY842284 Lymantria
c 452	12.4	88.6	2263	6	AX202076	AX202076 Sequence	c 525	12.4	88.6	4729	1	AF282898	AF282898 Burkhold
c 453	12.4	88.6	2277	1	ECOSMBA	D13334 Baccherichia	c 526	12.4	88.6	4845	1	AY541701	AY541701 Ralstonia
c 454	12.4	88.6	2280	5	DRU41419	U41419 Danio rerio	c 527	12.4	88.6	4993	1	PFU04052	PFU04052 Pseudomonas
c 455	12.4	88.6	2326	15	AK121040	AK121040 Oryza sat	c 528	12.4	88.6	5000	2	AF099015	AF099015 Streptomy
c 456	12.4	88.6	2349	15	AY262750	AY262750 Kluyverom	c 529	12.4	88.6	5069	2	BT009939	BT009939 Drosophi

530	12.4	88.6	5188	6	COS68235	Sequence	C 603	12.4	88.6	17982	14	AC013097	AC013097 Drosophila
531	12.4	88.6	5217	1	AF287482	Chlorobium	604	12.4	88.6	18149	15	AY884187	AY884187 Cocciobio
532	12.4	88.6	5229	1	LCIACCT	L. casei	605	12.4	88.6	18931	1	AF501263	AF501263 Brwnia c
533	12.4	88.6	5628	1	RCAPIC02F	M64624 Rhodobacter	606	12.4	88.6	20000	15	SPBPE88B	AL691490 S.pombe c
534	12.4	88.6	5683	8	HS242780	AR619416 Homo sapi	607	12.4	88.6	20029	1	AE008874	AE008874 Salmonell
535	12.4	88.6	6203	6	AR619416	AR619416 Sequence	608	12.4	88.6	20472	7	AY746495	AY746495 Enterobac
536	12.4	88.6	6398	11	AB119528	AB119528 Food-grad	609	12.4	88.6	20644	5	CR788239	CR788239 Zebrafish
537	12.4	88.6	6600	8	AY438640	AY438640 Homo sapi	610	12.4	88.6	21918	1	AE008853	AE008853 Salmonell
538	12.4	88.6	7004	7	LHSSB	L46883 Bacterioph	611	12.4	88.6	22118	6	AY951618	AY951618 Sequence
539	12.4	88.6	7114	6	COS80304	COS80304 Sequence	612	12.4	88.6	22118	9	MM455SRNA	X82564 M.musculus
540	12.4	88.6	7353	15	CNS09540	BX072545 Oryza sat	613	12.4	88.6	23223	14	AC005975	AC005975 Drosophila
541	12.4	88.6	7363	2	AY229969	AY229969 Drosophila	614	12.4	88.6	23650	1	AE008894	AE008894 Salmonell
542	12.4	88.6	7365	6	COS87408	COS87408 Sequence	615	12.4	88.6	24000	1	AE004856	AE004856 Pseudomon
543	12.4	88.6	7601	1	AB070454	AB070454 Rhodococc	616	12.4	88.6	24105	15	AY884189	AY884189 Streptomy
544	12.4	88.6	7766	13	AB096304	AB096304 Cercopit	617	12.4	88.6	24720	14	AB632203	AB632203 Streptomy
545	12.4	88.6	7910	13	AB096301	AB096301 Cercopit	618	12.4	88.6	25656	14	AC020181	AC020181 Drosophila
546	12.4	88.6	7950	1	AF016298	AF016298 Rhodobact	619	12.4	88.6	27521	1	AB112586	AB112586 Streptomy
547	12.4	88.6	7985	13	AB096202	AB096202 Cercopit	620	12.4	88.6	27546	13	ASP437059	ASP437059 Ascovirus
548	12.4	88.6	8004	13	AB096203	AB096203 Baboon he	621	12.4	88.6	28432	6	COS76998	COS76998 Sequence
549	12.4	88.6	8544	6	COS60214	COS60214 Sequence	622	12.4	88.6	29659	5	CR354374	CR354374 Zebrafish
550	12.4	88.6	8802	6	COS90030	COS90030 Sequence	623	12.4	88.6	30000	13	BHV130XB	Z48053 Bovine herd
551	12.4	88.6	9555	13	AF458647	AF458647 Squirtrel	624	12.4	88.6	30228	14	AC020449	AC020449 Drosophila
552	12.4	88.6	10007	1	AE008951	AE008951 Agrobacte	625	12.4	88.6	31068	1	AY603426	AY603426 Pseudomon
553	12.4	88.6	10135	1	AE010419	AE010419 Methanopy	626	12.4	88.6	31129	9	AF441733	AF441733 Mus muscu
554	12.4	88.6	10138	1	AE011927	AE011927 Xanthomon	627	12.4	88.6	31505	14	AC015140	AC015140 Drosophila
555	12.4	88.6	10153	1	AE011904	AE011904 Xanthomon	628	12.4	88.6	32634	1	AF293355	AF293355 Streptomy
556	12.4	88.6	10165	1	AE002089	AE002089 Deinococc	629	12.4	88.6	32800	1	AY394844	AY394844 Pseudomon
557	12.4	88.6	10189	1	AE004715	AE004715 Pseudomon	630	12.4	88.6	33064	14	AY338477	AY338477 Streptomy
558	12.4	88.6	10315	1	AE004650	AE004650 Pseudomon	631	12.4	88.6	34100	2	DMC3981	DMC3981 Drosophila
559	12.4	88.6	10387	1	PAU19797	PAU19797 Pseudomon	632	12.4	88.6	34305	2	CEW02812	CEW02812 Caenorhab
560	12.4	88.6	10387	6	AX191733	AX191733 Sequence	633	12.4	88.6	34676	14	AC013929	AC013929 Drosophila
561	12.4	88.6	10412	1	AE012064	AE012064 Xanthomon	634	12.4	88.6	35336	1	MSGV367	MSGV367 AD000008 Mycobacte
562	12.4	88.6	10475	1	AE004937	AE004937 Pseudomon	635	12.4	88.6	35540	1	AP389112	AP389112 Rhizobium
563	12.4	88.6	10652	1	AE004194	AE004194 Vibrio ch	636	12.4	88.6	35591	15	AC151928	AC151928 Pseudomon
564	12.4	88.6	10653	1	AE004194	AE004194 Vibrio ch	637	12.4	88.6	35807	15	AC151928	AC151928 Pseudomon
565	12.4	88.6	10732	1	AE004274	AE004274 Vibrio ch	638	12.4	88.6	36804	15	CR382133	CR382133 Uncultured
566	12.4	88.6	10794	1	AE0012150	AE0012150 Xanthomon	639	12.4	88.6	37440	1	MC0B1450	MC0B1450 Mycobacte
567	12.4	88.6	10835	1	AE005749	AE005749 Caulobact	640	12.4	88.6	38065	14	AC166544	AC166544 Neisseria h
568	12.4	88.6	10916	1	AE004781	AE004781 Pseudomon	641	12.4	88.6	38620	14	MC0B2548	MC0B2548 Mycobacte
569	12.4	88.6	10968	1	AF141883	AF141883 Pseudomon	642	12.4	88.6	38916	1	CBRG01C7	CBRG01C7 Caenorhab
570	12.4	88.6	11009	1	AE007898	AE007898 Agrobacte	643	12.4	88.6	39419	2	CBRG44E09	CBRG44E09 Caenorhab
571	12.4	88.6	11108	1	AE012151	AE012151 Xanthomon	644	12.4	88.6	41984	2	AF129076	AF129076 Homo sapi
572	12.4	88.6	11141	1	AE011650	AE011650 Xanthomon	645	12.4	88.6	42051	8	CBRG44D18	CBRG44D18 Homo sapi
573	12.4	88.6	11180	1	AE004733	AE004733 Pseudomon	646	12.4	88.6	42430	2	STR5TMP1	STR5TMP1 Homo sapi
574	12.4	88.6	11196	1	AE012055	AE012055 Xanthomon	647	12.4	88.6	43339	1	AT851161	AT851161 Homo sapi
575	12.4	88.6	11204	6	AX370213	AX370213 Sequence	648	12.4	88.6	43741	8	AC018185	AC018185 Drosophila
576	12.4	88.6	11334	1	AE001186	AE001186 Treponema	649	12.4	88.6	43829	14	AX574197	AX574197 Mycobacte
577	12.4	88.6	11421	1	AE004505	AE004505 Pseudomon	650	12.4	88.6	45055	6	AC091640	AC091640 Homo sapi
578	12.4	88.6	11797	1	AE011603	AE011603 Leptospir	651	12.4	88.6	45633	14	AC013865	AC013865 Drosophila
579	12.4	88.6	12046	1	AE005017	AE005017 Halobacte	652	12.4	88.6	46607	14	AC013865	AC013865 Drosophila
580	12.4	88.6	12198	1	AE001953	AE001953 Deinococc	653	12.4	88.6	48352	2	DMH7M4	DMH7M4 AL133504 Drosophila
581	12.4	88.6	12236	1	AE012147	AE012147 Xanthomon	654	12.4	88.6	48553	3	AL451134	AL451134 Human DNA
582	12.4	88.6	12280	1	AE005787	AE005787 Caulobact	655	12.4	88.6	48827	8	AC016994	AC016994 Homo sapi
583	12.4	88.6	12970	1	SPU10405	SPU10405 Streptomy	656	12.4	88.6	49349	9	AL451134	AL451134 Human DNA
584	12.4	88.6	13345	1	AE001977	AE001977 Deinococc	657	12.4	88.6	49534	7	AF396866	AF396866 Bacteriop
585	12.4	88.6	13484	14	AC014236	AC014236 Drosophila	658	12.4	88.6	50000	6	AM335264	AM335264 Sequence
586	12.4	88.6	13579	1	AE005061	AE005061 Halobacte	659	12.4	88.6	50000	6	AM335266	AM335266 Sequence
587	12.4	88.6	13625	1	AE004363	AE004363 Vibrio ch	660	12.4	88.6	51711	1	CP000060	CP000060 Pseudomon
588	12.4	88.6	14138	1	AE004766	AE004766 Pseudomon	661	12.4	88.6	51808	5	AC104683	AC104683 Dancio rer
589	12.4	88.6	14283	6	COS77721	COS77721 Sequence	662	12.4	88.6	52250	7	AY500153	AY500153 Mycobacte
590	12.4	88.6	14988	1	AB015053	AB015053 Pseudomon	663	12.4	88.6	54841	14	AC017535	AC017535 Drosophila
591	12.4	88.6	15042	6	CQ62852	CQ62852 Sequence	664	12.4	88.6	55903	14	AC091475	AC091475 Homo sapi
592	12.4	88.6	15197	1	AC013889	AC013889 Drosophila	665	12.4	88.6	56268	14	AC091240	AC091240 Mus muscu
593	12.4	88.6	15711	6	CQ608651	CQ608651 Sequence	666	12.4	88.6	56999	14	AC008776	AC008776 Homo sapi
594	12.4	88.6	16499	6	COS89271	COS89271 Sequence	667	12.4	88.6	57789	14	AC0091570	AC0091570 Homo sapi
595	12.4	88.6	16520	1	AE001105	AE001105 Archaeogl	668	12.4	88.6	58756	14	AP006484	AP006484 Continuation (5 of
596	12.4	88.6	16704	1	AE004876	AE004876 Pseudomon	669	12.4	88.6	58866	14	AC114556	AC114556 Homo sapi
597	12.4	88.6	16941	1	AE004749	AE004749 Pseudomon	670	12.4	88.6	59237	14	AC091279	AC091279 Mus muscu
598	12.4	88.6	17183	1	AE001986	AE001986 Deinococc	671	12.4	88.6	59816	1	AP333038	AP333038 Streptomy
599	12.4	88.6	17280	14	AC017852	AC017852 Drosophila	672	12.4	88.6	60573	14	AC018267	AC018267 Drosophila
600	12.4	88.6	17425	14	RSU17129	RSU17129 Rhodococcus	673	12.4	88.6	60671	14	AC017512	AC017512 Homo sapi
601	12.4	88.6	17477	14	CR954305_8	Continuation (9 of	674	12.4	88.6	61490	14	AC025630	AC025630 Homo sapi
602	12.4	88.6	17973	1	MSM238027	MSM238027 Mycobacte	675	12.4	88.6	61796	14	AC020875	AC020875 Mus muscu



c 676	12.4	88.6	61845	1	AY623658	AY623658 Aeromicro	c 749	12.4	88.6	110000	1	CP000091_08	Continuation (9 of
c 677	12.4	88.6	63851	14	AC165666	AC165666 Bob tauu	c 750	12.4	88.6	110000	1	CP000091_09	Continuation (10 o
c 678	12.4	88.6	63933	14	AC090570	AC090570 Homo sapi	c 751	12.4	88.6	110000	1	CP000091_10	Continuation (11 o
c 679	12.4	88.6	64027	14	AC018192	AC018192 Drosophi	c 752	12.4	88.6	110000	1	CR555306_21	Continuation (12 o
c 680	12.4	88.6	64283	14	AC105693_3	Continuation (4 of	c 753	12.4	88.6	110000	1	CR555306_24	Continuation (25 o
c 681	12.4	88.6	65005	14	AC091277	AC091277 Mus muscu	c 754	12.4	88.6	110000	1	CR555306_39	Continuation (40 o
c 682	12.4	88.6	65076	15	NCB13020	AL451015 Neurospor	c 755	12.4	88.6	110000	1	CR331997_05	Continuation (6 of
c 683	12.4	88.6	65144	14	AC090665	Continuation (4 of	c 756	12.4	88.6	110000	1	CR331997_10	Continuation (11 o
c 684	12.4	88.6	65612	2	AE003597_3	Continuation (4 of	c 757	12.4	88.6	110000	1	CR331997_22	Continuation (23 o
c 685	12.4	88.6	66796	14	AC017435	AC017435 Drosophi	c 758	12.4	88.6	110000	1	U00096_07	U00096 Escherichia
c 686	12.4	88.6	67392	14	AC018284	AC018284 Drosophi	c 759	12.4	88.6	110000	1	U00096_01	Continuation (12 of
c 687	12.4	88.6	68301	14	AC131486	AC131486 Lytechinu	c 760	12.4	88.6	110000	1	AE013558_26	Continuation (27 o
c 688	12.4	88.6	68939	7	AF547430	AF547430 Mycobacte	c 761	12.4	88.6	110000	1	AE014295_15	Continuation (16 o
c 689	12.4	88.6	70843	14	AC147864	AC147864 Gopherus	c 762	12.4	88.6	110000	1	AE014295_16	Continuation (17 o
c 690	12.4	88.6	70966	14	AC079058	AC079058 Homo sapi	c 763	12.4	88.6	110000	1	AE014295_20	Continuation (21 o
c 691	12.4	88.6	71616	15	ATAC022287	AC142979 Xenopus t	c 764	12.4	88.6	110000	1	AE014295_21	Continuation (22 o
c 692	12.4	88.6	72494	14	AC144979	AC144979 Xenopus t	c 765	12.4	88.6	110000	1	AE016824_1	Continuation (12 of
c 693	12.4	88.6	72638	15	AB007645	AB007645 Arabidops	c 766	12.4	88.6	110000	1	AE016853_05	Continuation (16 of
c 694	12.4	88.6	72704	6	AR619878	AR619878 Sequence	c 767	12.4	88.6	110000	1	AE016853_06	Continuation (17 of
c 695	12.4	88.6	73778	14	AC090743	AC090743 Homo sapi	c 768	12.4	88.6	110000	1	AE016853_25	Continuation (8 of
c 696	12.4	88.6	73803	15	NCB11822	AL356834 Neurospor	c 769	12.4	88.6	110000	1	AE016853_32	Continuation (26 o
c 697	12.4	88.6	74355	1	AY120853	AY120853 Synechoco	c 770	12.4	88.6	110000	1	AE016853_34	Continuation (33 o
c 698	12.4	88.6	74502	14	AC024300	AC024300 Homo sapi	c 771	12.4	88.6	110000	1	AE016853_36	Continuation (35 o
c 699	12.4	88.6	75335	15	BX842627	BX842627 Neurospor	c 772	12.4	88.6	110000	1	AE017220_38	Continuation (47 o
c 700	12.4	88.6	76269	15	AC006436	AC006436 Drosophi	c 773	12.4	88.6	110000	1	AE017220_38	Continuation (39 o
c 701	12.4	88.6	78124	15	BX842681	BX842681 Neurospor	c 774	12.4	88.6	110000	1	AE017220_42	Continuation (43 o
c 702	12.4	88.6	78962	14	AC040956	AC040956 Mus muscu	c 775	12.4	88.6	110000	1	AE017220_43	Continuation (44 o
c 703	12.4	88.6	80646	14	AC013962	AC013962 Drosophi	c 776	12.4	88.6	110000	1	AE017340_12	Continuation (13 o
c 704	12.4	88.6	82727	1	BC082K	D26562 Escherichia	c 777	12.4	88.6	110000	1	AE017340_13	Continuation (14 o
c 705	12.4	88.6	82855	14	AC009354	AC009354 Drosophi	c 778	12.4	88.6	110000	1	AP006618_05	Continuation (6 of
c 706	12.4	88.6	83433	14	AP006501_12	Continuation (13 o	c 779	12.4	88.6	110000	1	AP006618_05	Continuation (19 o
c 707	12.4	88.6	84011	14	AP002084	AP002084 Homo sapi	c 780	12.4	88.6	110000	1	AP006618_38	Continuation (19 o
c 708	12.4	88.6	84549	14	AC006243	AC006243 Drosophi	c 781	12.4	88.6	110000	1	AP006618_35	Continuation (36 o
c 709	12.4	88.6	87283	14	AC017652	AC017652 Drosophi	c 782	12.4	88.6	110000	1	AP006618_52	Continuation (53 o
c 710	12.4	88.6	87776	14	AP007309	AP007309 Lotus cor	c 783	12.4	88.6	110000	1	AP006840_14	Continuation (15 o
c 711	12.4	88.6	88378	15	AC133002	AC133002 Oryza sat	c 784	12.4	88.6	110000	1	AP006840_15	Continuation (16 o
c 712	12.4	88.6	88621	14	AP004128	AP004128 Oryza sat	c 785	12.4	88.6	110000	1	AP006841_34	Continuation (35 o
c 713	12.4	88.6	88672	14	AC014992	AC014992 Drosophi	c 786	12.4	88.6	110000	1	AP006878_10	Continuation (11 o
c 714	12.4	88.6	89208	14	CR954208_6	Continuation (7 of	c 787	12.4	88.6	110000	1	AP006878_11	Continuation (12 o
c 715	12.4	88.6	89747	8	AL591022	AL591022 Human DNA	c 788	12.4	88.6	110000	1	AP008226_16	Continuation (17 o
c 716	12.4	88.6	90100	14	AC104180	AL591022 Human DNA	c 789	12.4	88.6	110000	1	AP008231_04	Continuation (15 of
c 717	12.4	88.6	90582	8	AL583882	AL583882 Human DNA	c 790	12.4	88.6	110000	1	AY596297_20	Continuation (5 of
c 718	12.4	88.6	91430	1	ECOR5F	D83556 Escherichia	c 791	12.4	88.6	110000	1	BA000007_00	BA000007 Escherich
c 719	12.4	88.6	91723	8	AC010903	AC010903 Homo sapi	c 792	12.4	88.6	110000	1	BA000007_01	Continuation (2 of
c 720	12.4	88.6	93932	2	AC004766	AC004766 Drosophi	c 793	12.4	88.6	110000	1	BA000022_47	Continuation (48 o
c 721	12.4	88.6	94207	14	CT009593	CT009593 Dando rer	c 794	12.4	88.6	110000	1	BA000022_30	Continuation (31 o
c 722	12.4	88.6	95637	15	BX842594	BX842594 Neurospor	c 795	12.4	88.6	110000	1	BA000030_28	Continuation (39 o
c 723	12.4	88.6	96348	14	CT005246_5	Continuation (6 of	c 796	12.4	88.6	110000	1	BA000030_33	Continuation (47 o
c 724	12.4	88.6	97538	14	AC017943	AC017943 Drosophi	c 797	12.4	88.6	110000	1	BA000030_46	Continuation (47 o
c 725	12.4	88.6	97862	5	BX936370	BX936370 Zebrafish	c 798	12.4	88.6	110000	1	BA000030_61	Continuation (62 o
c 726	12.4	88.6	98053	15	AC149809	AC149809 Medicago	c 799	12.4	88.6	110000	1	BA000030_67	Continuation (68 o
c 727	12.4	88.6	99194	15	AP003704	AP003704 Oryza sat	c 800	12.4	88.6	110000	1	BA000031_24	Continuation (125 o
c 728	12.4	88.6	101330	2	AC007177	AC007177 Drosophi	c 801	12.4	88.6	110000	1	BA000035_21	Continuation (122 o
c 729	12.4	88.6	101644	15	AC006267	AC006267 Arabidops	c 802	12.4	88.6	110000	1	BA000035_30	Continuation (131 o
c 730	12.4	88.6	103574	5	BX664706	BX664706 Zebrafish	c 803	12.4	88.6	110000	1	BA000037_16	Continuation (17 o
c 731	12.4	88.6	103664	5	BX324201	BX324201 Zebrafish	c 804	12.4	88.6	110000	1	BA000040_47	Continuation (48 o
c 732	12.4	88.6	103837	1	AE000516_43	Continuation (44 o	c 805	12.4	88.6	110000	1	BA000040_50	Continuation (51 o
c 733	12.4	88.6	105328	5	BX284679	BX284679 zebrafish	c 806	12.4	88.6	110000	1	BA000040_51	Continuation (52 o
c 734	12.4	88.6	106873	13	AB096160	AB096160 Ceropphi	c 807	12.4	88.6	110000	1	BA000040_70	Continuation (71 o
c 735	12.4	88.6	108584	1	AY466441	AY466441 Saccharop	c 808	12.4	88.6	110000	1	BA000043_09	Continuation (171 o
c 736	12.4	88.6	108688	15	AC105733	AC105733 Oryza sat	c 809	12.4	88.6	110000	1	BA000043_10	Continuation (110 o
c 737	12.4	88.6	108845	15	U66917	U66917 Pseudomonas	c 810	12.4	88.6	110000	1	BA000043_16	Continuation (117 o
c 738	12.4	88.6	109081	15	CNS07YYPH	AL713936 Oryza sat	c 811	12.4	88.6	110000	1	BA000045_30	Continuation (31 o
c 739	12.4	88.6	110000	1	AE002098_12	Continuation (13 o	c 812	12.4	88.6	110000	1	BX571965_04	Continuation (5 of
c 740	12.4	88.6	110000	1	AE002098_13	Continuation (14 o	c 813	12.4	88.6	110000	1	BX571965_07	Continuation (18 o
c 741	12.4	88.6	110000	1	AE004968_05	Continuation (6 of	c 814	12.4	88.6	110000	1	BX571965_18	Continuation (119 o
c 742	12.4	88.6	110000	1	AE004968_06	Continuation (7 of	c 815	12.4	88.6	110000	1	BX571965_19	Continuation (120 o
c 743	12.4	88.6	110000	1	AE005174_00	AE005174 Escherich	c 816	12.4	88.6	110000	1	BX571965_23	Continuation (24 o
c 744	12.4	88.6	110000	1	AE005174_01	Continuation (2 of	c 817	12.4	88.6	110000	1	BX571965_36	Continuation (37 o
c 745	12.4	88.6	110000	1	AE005674_00	AE005674 Shigella	c 818	12.4	88.6	110000	1	BX571966_04	Continuation (35 of
c 746	12.4	88.6	110000	1	AE005674_01	Continuation (2 of	c 819	12.4	88.6	110000	1	BX571966_05	Continuation (16 of
c 747	12.4	88.6	110000	1	AE006470_20	Continuation (21 o	c 820	12.4	88.6	110000	1	BX571966_11	Continuation (120 o
c 748	12.4	88.6	110000	1	CP000091_03	Continuation (4 of	c 821	12.4	88.6	110000	1	BX571966_19	Continuation (12 o

822	12.4	88.6	110000	1	BX350851_48	Continuation (49 o	895	12.4	88.6	110000	14	AP006499_11	Continuation (12 o
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## ALIGNMENTS

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RESULT 1
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ACCESSION X98924.1 GI:2244676
VERSION X98924.1
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SOURCE Spodoptera litoralis nucleopolyhedrovirus
ORGANISM Spodoptera litoralis nucleopolyhedrovirus
            Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
            Nucleopolyhedrovirus.
REFERENCE 1
AUTHORS van Strien,E.A., Faktor,O., Hu,Z.H., Zuidema,D., Goldbach,R.W. and
            Viak,J.M.
TITLE Baculoviruses contain a gene for the large subunit of
            ribonucleotide reductase
JOURNAL J. Gen. Virol. 78 (Pt 9), 2365-2377 (1997)
PUBMED 9292027
REFERENCE 2 (bases 1 to 2832)
AUTHORS Faktor,O.
TITLE Direct Submision
JOURNAL Submitted (01-JUL-1996) O. Faktor, The Hebrew University of
            Jerusalem, Department of Entomology, The Faculty of Agriculture,
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DEFINITION Fusarium oxysporum class V chitin synthase (chv) gene, complete
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ACCESSION AF484941
VERSION AF484941.1 GI:28628848
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SOURCE Fusarium oxysporum
ORGANISM Fusarium oxysporum
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REFERENCE 1 (bases 1 to 10151)
AUTHORS Madrid,M.P., Di Pietro,A. and Roncero,M.I.G.
TITLE Class V chitin synthase determines pathogenesis in the vascular
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            defense compounds
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 10151)
AUTHORS Madrid,M.P., Di Pietro,A. and Roncero,M.I.G.
TITLE Direct Submision
JOURNAL Submitted (18-FEB-2002) Departamento de Genetica, Universidad de

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Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3  
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DEFINITION the complete genome.  
ACCESSION AE012045  
VERSION AE012045.1 GI:21110361  
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SOURCE Xanthomonas axonopodis pv. citri str. 306  
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REFERENCE  
AUTHORS  
Xanthomonadaceae; Xanthomonas.  
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da Silva, A.C.R., Ferro, J.A., Reinach, F.C., Parah, C.S., Furlan, L.R.,  
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Sena, J.A.D., Silva, C., de Souza, R.F., Spinoia, L.A.F., Takita, M.A.,  
Tamura, R.B., Teixeira, E.C., Tezsa, R.I.D., Trindade dos Santos, M.,  
Truffi, D., Tsai, S.M., White, F.F., Seubal, J.C. and Kitajima, J.P.  
Direct Submission  
Submitted (28-NOV-2001) Departamento de Bioquímica, Universidade de  
Sao Paulo, Av. Prof. Lineu Prestes 748, Sao Paulo, SP 05508-900,  
Brazil

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PUBMED 11792869  
 2 (bases 1 to 14169)  
 REFERENCES  
 Authors  
 TITLE  
 JOURNAL  
 Submitted (12-DEC-2001) Microbiology and Molecular Genetics,  
 University of California, Los Angeles, 405 Hilgard Ave, Los  
 Angeles, CA 90095-1489, USA  
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Query Match 100.0%; Score 14; DB 1; Length 14169;  
Best Local Similarity 78.6%; Pred. No. 5e+03; Indels 0; Gaps 0;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUG 14  
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Db 3447 CGTACTGCAACTCG 3460

RESULT 5  
AP003867/c 96360 bp DNA linear HTG 21-MAR-2002  
LOCUS Oryza sativa (japonica cultivar-group) chromosome 8 clone  
DEFINITION OJ111 B02, \*\*\* SEQUENCING IN PROGRESS \*\*\*.  
ACCESSION AP003867  
VERSION AP003867.1 GI:14646800  
KEYWORDS HTG; HTGS PHASE2.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriatroidae; Oryzaceae; Oryza.  
1  
Sasaki, T., Matsumoto, T. and Yamamoto, K.  
Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, BAC  
clone: OJ111 B02  
Published only in Database (2001)  
2 (bases 1 to 96360)  
Sasaki, T., Matsumoto, T. and Yamamoto, K.  
Direct Submission  
Submitted (09-JUL-2001) Takuji Sasaki, National Institute of  
Agrobiological Resources, Rice Genome Research Program, Kannondai  
2-1-2, Tsukuba, Ibaraki 305-8602, Japan  
E-mail: tsasaki@agr.affrc.go.jp, URL: http://rnp.dna.affrc.go.jp/.

COMMENT  
Tel:81-298-38-7441, Fax:81-298-38-7468)  
The nucleotide sequence of this BAC clone was generated by  
combining Monardo and RGP-Japan sequencing data.  
NOTE: It currently consists of 1 contigs. Gaps between the contigs  
are represented as runs of N. The order of the pieces is believed  
to be correct as given, however the sizes of the gaps between them  
are based on estimates that have provided by the submitter. This  
sequence will be replaced by the finished sequence as soon as it is  
available and the accession number will be preserved.  
\* NOTE: This is a 'working draft' sequence.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
Location/Qualifiers  
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FEATURES  
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Query Match 100.0%; Score 14; DB 14; Length 96360;  
Best Local Similarity 78.6%; Pred. No. 4e+03; Indels 0; Gaps 0;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUG 14  
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Db 15563 CGTACTGCAACTCG 15550

RESULT 6  
AL592045 99251 bp DNA linear PRI 18-MAY-2005  
LOCUS Human DNA sequence from clone RP11-275114 on chromosome 1 Contains  
DEFINITION the ACBD3 gene for acyl-Coenzyme A binding domain containing 3, the  
gene for a novel protein, a ribosomal protein L34 (RPL34)  
pseudogene and the MIXL1 gene for Mixl homeobox-like 1 (Xenopus  
laevis), complete sequence.  
ACCESSION AL592045  
VERSION AL592045.28 GI:25136611  
KEYWORDS HTG; ACBD3; MIXL1; RPL34.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.  
1 (bases 1 to 99251)  
Bellington, A.  
Direct Submission  
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk  
Clone requests: clonerequest@sanger.ac.uk  
On Nov 19, 2002 this sequence version replaced gi:25045216.  
The following abbreviations are used to associate primary accession  
numbers given in the feature table with their source databases:  
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Mp: WORMPEP; Information  
on the WORMPEP database can be found at  
http://www.sanger.ac.uk/projects/C\_elegans/wormpep This sequence  
was generated from part of bacterial clone contigs of human  
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping  
Group. Further information can be found at  
http://www.sanger.ac.uk/HGP/Chr1  
RP11-275114 is from the library RPCI-11.1 constructed by the group  
of Piefer de Jong. For further details see  
http://www.chori.org/bacpac/home.htm  
VECTOR: pBAC3.6  
----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: vegas@sanger.ac.uk



-----  
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.  
 Location/Qualifiers

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    FVKILNRCRKLSTYTVASHKIEKEOEKREERERREERERLEQEKRRER
    EERLAREERERRLIEERLRLQEQKQALMALNSQTAVFQOYAAQPGVYEQOIL
    IROLQOHYQOYMOOLYOVLAOQOALQOQOAVVASSLPTSSKVAIVSNMSV
    NQAKTHTDSSEKSLPRAARALENGPKSLPYVAPSMTRPQIQPKKIQODAD
    SVITGRGEVTVTRVPTHESSYLFWEATNTNYDIGRVTYETWDSPTAIVSHSES
    SDDEEERENIGCEKAKKANKPLDIEIVPYRRDCEEVYAGSHQPGGVYLLKP
    DNSYSLMRSGKGVYRVYTR"
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    /db_xref="UniProt/TREMBL:Q5VT18"
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CDS complement(61040..61388)  
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 100.0%; Score 14; DB 8; Length 99251;  
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 Matches 11; Conservative 3; Mismatches 0; Gaps 0;

Qy 1 CGUACUGCAACUCG 14  
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 Db 89702 CGTACTGCAACTCG 89715

RESULT 7  
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 LOCUS Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 8,  
 DEFINITION BAC clone:OJ1136\_A10.  
 ACCSSION AP003884  
 VERSION AP003884.2 GI:22212582  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriocarideae; Oryzaceae; Oryza.  
 1  
 Sasaki, T., Matsumoto, T. and Yamamoto, K.  
 Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, BAC  
 clone:OJ1136\_A10  
 Published only in Database (2001)  
 2 (Bases 1 to 101249)  
 Sasaki, T., Matsumoto, T. and Yamamoto, K.  
 Direct Submission  
 Submitted (09-JUL-2001) Takuji Sasaki, National Institute of  
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 (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rsgp.dna.affrc.go.jp/  
 Tel:81-298-38-7441, Fax:81-298-38-7468)  
 On Aug 12, 2002 this sequence version replaced gi:14646817.  
 Genes were predicted from the integrated results of the following:  
 GENSCAN (http://CCR-081.mt.edu/GENSCAN.html), RGENESH  
 (http://www.softberry.com/), Genemark.hmm  
 (http://opal.biology.gatech.edu/Genemark/), Glimmer  
 (http://www.tigr.org/cdb/glimmer/glimr\_form.html), RiceHMM  
 (http://rsgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor  
 (http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4  
 (http://glabin.cse.psu.edu/html/docs/sim4.html), gap2  
 (http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The  
 genomic sequence was searched against NCBI NonRedundant Protein  
 database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA  
 sequence database at RGP or DDBJ. Protein homologues of the coding  
 regions were searched against NCBI NonRedundant Protein database  
 with BLASTP. ESTs represent the identified cDNA sequences using  
 BLASTN with the corresponding DDBJ accession no. and RGP clone ID.  
 Full-length cDNAs represent the identified cDNA sequences using  
 BLASTN with the corresponding DDBJ accession no.  
 A gene with identity or significant homology to a protein is  
 classified based on the protein name to indicate the homology level  
 such as same name, 'putative-' and '-like protein'. A gene without  
 significant homology to any protein but with full-length cDNA or

FEATURES  
 source  
 1. 101249  
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 probably inactive due to 5' exon missing in CDS  
 probably inactive due to including stop codon(s) in CDS  
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Continuation (9 of 64) of AE016853 from base 800001 (AE016853 *Pseudomonas syringae* pv. b

Query Match 100.0%; Score 14; DB 1; Length 110000;  
Best Local Similarity 78.6%; Pred. No. 4e+03;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACUGCACTCG 14

Db 97428 CGTACTGCACTCG 97415

RESULT 9  
CP000058\_08/c  
WPCOMMENT

Sequence split into 60 fragments LOCUS CP000058 Accession CP000058

Fragment Name	Begin	End
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CP000058_02	200001	310000
CP000058_03	300001	410000
CP000058_04	400001	510000
CP000058_05	500001	610000
CP000058_06	600001	710000
CP000058_07	700001	810000
CP000058_08	800001	910000
CP000058_09	900001	1010000
CP000058_10	1000001	1110000
CP000058_11	1100001	1210000
CP000058_12	1200001	1310000
CP000058_13	1300001	1410000
CP000058_14	1400001	1510000
CP000058_15	1500001	1610000
CP000058_16	1600001	1710000
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CP000058_18	1800001	1910000
CP000058_19	1900001	2010000
CP000058_20	2000001	2110000
CP000058_21	2100001	2210000
CP000058_22	2200001	2310000
CP000058_23	2300001	2410000
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CP000058\_49 4900001 5010000  
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CP000058\_55 5500001 5610000  
CP000058\_56 5600001 5710000  
CP000058\_57 5700001 5810000  
CP000058\_58 5800001 5910000  
CP000058\_59 5900001 5928787

Continuation (9 of 60) of CP000058 from base 800001 (CP000058 *Pseudomonas syringae* pv. p

Query Match 100.0%; Score 14; DB 1; Length 110000;  
Best Local Similarity 78.6%; Pred. No. 4e+03;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACUGCACTCG 14

Db 69525 CGTACTGCACTCG 69512

RESULT 10  
CR954209\_5/c  
WPCOMMENT

Sequence split into 7 fragments LOCUS CR954209 Accession CR954209

Fragment Name	Begin	End
CR954209_0	1	110000
CR954209_1	200001	310000
CR954209_2	300001	410000
CR954209_3	400001	510000
CR954209_4	500001	610000
CR954209_5	600001	683751

Continuation (6 of 7) of CR954209 from base 500001 (CR954209 *Ostreococcus tauri* strain 07

Query Match 100.0%; Score 14; DB 1; Length 110000;  
Best Local Similarity 78.6%; Pred. No. 4e+03;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGUACUGCACTCG 14

Db 64859 CGTACTGCACTCG 64846

RESULT 11  
LMFLCHR18\_00  
WPCOMMENT

Sequence split into 11 fragments LOCUS LMFLCHR18 Accession AL499620

Fragment Name	Begin	End
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LMFLCHR18_01	100001	210000
LMFLCHR18_02	200001	310000
LMFLCHR18_03	300001	410000
LMFLCHR18_04	400001	510000
LMFLCHR18_05	500001	610000
LMFLCHR18_06	600001	710000
LMFLCHR18_07	700001	810000
LMFLCHR18_08	800001	910000
LMFLCHR18_09	900001	1010000
LMFLCHR18_10	1000001	1091246

LOCUS LMFLCHR18 1091246 bp DNA linear HTG 16-DEC-2000

DEFINITION Leishmania major strain Friedlin chromosome 18, 19, 20, 22 clone  
Chr. 18, Chr. 19, Chr. 20, Chr. 22, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 722  
unordered pieces.

ACCESSION AL499620  
VERSION AL499620.1 GI:11877283

KEYWORDS HTG; HTGS PHASE1.  
SOURCE Leishmania major  
ORGANISM Leishmania major  
REFERENCE Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
AUTHORS 1 (bases 1 to 1091246)  
TITLE Leishmania.  
JOURNAL Murphly, L., Quail, M., Harris, D., Rajandream, M., Ivens, A. and  
Barrell, B.  
Submitted (15-DEC-2000) major Genome Sequencing Consortium, The  
Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge  
CB10 1SA, UK  
For more information about this sequence or the Leishmania Project,  
see [http://www.sanger.ac.uk/Projects/L\\_major/](http://www.sanger.ac.uk/Projects/L_major/)  
CAVEATS: 1. the sequencing is still in progress  
2. this submission represents 721 unordered contigs of size 0.5kb  
or greater, separated by blocks of N  
3. it is derived from whole chromosome shotgun plus cosmid and/or  
PAC skims  
4. the data are EXTREMELY preliminary  
5. the sequence may contain E. coli, sequencing/cloning vector, or  
be cross-contaminated with other Leishmania chromosomes IMPORTANT:  
This sequence is unfinished and does not necessarily represent the  
correct sequence. Work on the sequence is in progress and the  
release of these data is based on the understanding that the  
sequence will change as work continues.  
THE ORDER OF CONTIGS IS NOT KNOWN.  
THESE DATA ARE PRELIMINARY ONLY, and annotation will follow  
shortly.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 722 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1  
844: contig of 844 bp in length  
845  
944: gap of 100 bp  
945  
1437: contig of 493 bp in length  
1438  
1537: gap of 100 bp  
1538  
2130: contig of 593 bp in length  
2131  
2230: gap of 100 bp in length  
2231  
2756: contig of 526 bp in length  
2757  
2856: gap of 100 bp  
2857  
3395: contig of 539 bp in length  
3396  
3495: gap of 100 bp  
3496  
4076: contig of 581 bp in length  
4077  
4176: gap of 100 bp  
4177  
4743: contig of 567 bp in length  
4744  
4843: gap of 100 bp  
4844  
5371: contig of 528 bp in length  
5372  
5471: gap of 100 bp  
5472  
6050: contig of 579 bp in length  
6051  
6150: gap of 100 bp  
6151  
6686: contig of 536 bp in length  
6687  
6786: gap of 100 bp  
6787  
7314: contig of 528 bp in length  
7315  
7414: gap of 100 bp  
7415  
8143: contig of 729 bp in length  
8144  
8243: gap of 100 bp  
8244  
8825: contig of 582 bp in length  
8826  
8925: gap of 100 bp  
8926  
9508: contig of 583 bp in length  
9509  
9608: gap of 100 bp  
9609  
10117: contig of 509 bp in length  
10118  
10217: gap of 100 bp  
10218  
10784: contig of 567 bp in length  
10785  
10884: gap of 100 bp  
10885  
11476: contig of 592 bp in length  
11477  
11576: gap of 100 bp  
11577  
12074: contig of 498 bp in length

12075  
12175  
12713: contig of 539 bp in length  
12714  
12813: gap of 100 bp  
12814  
13346: contig of 533 bp in length  
13347  
13446: gap of 100 bp  
13447  
13984: contig of 538 bp in length  
13985  
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14085  
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15275  
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15859  
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16512  
16611: gap of 100 bp  
16612  
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17165  
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18225  
18324: gap of 100 bp  
18325  
18915: contig of 591 bp in length  
18916  
19015: gap of 100 bp  
19016  
19573: contig of 558 bp in length  
19574  
19673: gap of 100 bp  
19674  
20185: contig of 512 bp in length  
20186  
20285: gap of 100 bp  
20286  
20876: contig of 591 bp in length  
20877  
20976: gap of 100 bp  
20977  
21549: contig of 573 bp in length  
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21649: gap of 100 bp  
21650  
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22280: gap of 100 bp  
22281  
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22851  
22950: gap of 100 bp  
22951  
23529: contig of 579 bp in length  
23530  
23629: gap of 100 bp  
23629  
24147: contig of 518 bp in length  
24148  
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24248  
24794: contig of 547 bp in length  
24795  
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24895  
25413: contig of 519 bp in length  
25414  
25513: gap of 100 bp  
25514  
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26091  
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29121  
29813: contig of 693 bp in length  
29814  
29913: gap of 100 bp  
29914  
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30452  
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31117  
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31217  
31870: contig of 654 bp in length  
31871  
31970: gap of 100 bp  
31971  
32527: contig of 557 bp in length  
32528  
32627: gap of 100 bp  
32627  
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33181  
33280: gap of 100 bp  
33281  
33800: contig of 620 bp in length  
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34000: gap of 100 bp  
34001  
34564: contig of 564 bp in length  
34565  
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34665  
35218: contig of 554 bp in length  
35219  
35318: gap of 100 bp  
35319  
35882: contig of 564 bp in length  
35883  
35982: gap of 100 bp  
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36579: contig of 597 bp in length  
36580  
36679: gap of 100 bp  
36680  
37589: contig of 910 bp in length  
37590  
37689: gap of 100 bp

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* 37690 38264: contig of 575 bp in length
* 38265 38364: gap of 100 bp
* 38365 38899: contig of 535 bp in length
* 38900 38999: gap of 100 bp
* 39000 39559: contig of 560 bp in length
* 39560 39659: gap of 100 bp
* 39660 40416: contig of 757 bp in length
* 40417 40516: gap of 100 bp
* 40517 41084: contig of 568 bp in length
* 41085 41185 42202: contig of 1018 bp in length
* 42203 42303 42832: contig of 530 bp in length
* 42833 42932: gap of 100 bp
* 42933 43927: contig of 995 bp in length
* 43928 44027: gap of 100 bp
* 44028 44822: contig of 795 bp in length
* 44823 44922: gap of 100 bp
* 44923 45474: contig of 552 bp in length
* 45475 45574: gap of 100 bp
* 45575 46218: contig of 644 bp in length
* 46219 46318: gap of 100 bp
* 46319 47064: contig of 746 bp in length
* 47065 47164: gap of 100 bp
* 47165 47708: contig of 544 bp in length
* 47709 47809 48532: contig of 724 bp in length
* 48533 49129: contig of 497 bp in length
* 49130 49228: gap of 100 bp
* 49230 49787: contig of 558 bp in length
* 49788 49887: gap of 100 bp
* 49888 50455: contig of 568 bp in length
* 50456 50555: gap of 100 bp
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Query Match 100.0%; Score 14; DB 14; Length 110000;  
Best Local Similarity 78.6%; Pred. No. 4e+03; 0; Indels 0; Gaps 0;  
Matches 11; Conservative 3; Mismatches 0;

QY 1 CGUACUCGACATCG 14  
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Db 16121 CCGACTCGACATCG 16134

RESULT 12  
AP008214.143/c  
WPCOMMENT

Sequence split into 285 fragments LOCUS AP008214 Accession AP008214

Fragment Name	Begin	End
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AP008214_004	400001	510000
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AP008214_008	800001	910000
AP008214_009	900001	1010000
AP008214_010	1000001	1110000
AP008214_011	1100001	1210000
AP008214_012	1200001	1310000
AP008214_013	1300001	1410000
AP008214_014	1400001	1510000
AP008214_015	1500001	1610000
AP008214_016	1600001	1710000
AP008214_017	1700001	1810000
AP008214_018	1800001	1910000
AP008214_019	1900001	2010000
AP008214_020	2000001	2110000
AP008214_021	2100001	2210000
AP008214_022	2200001	2310000
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AP008214_025	2500001	2610000
AP008214_026	2600001	2710000
AP008214_027	2700001	2810000
AP008214_028	2800001	2910000
AP008214_029	2900001	3010000
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AP008214\_142 14200001 14310000  
AP008214\_143 14300001 14410000  
AP008214\_144 14400001 14510000  
AP008214\_145 14500001 14610000  
AP008214\_146 14600001 14710000  
AP008214\_147 14700001 14810000  
AP008214\_148 14800001 14910000  
AP008214\_149 14900001 15010000  
AP008214\_150 15000001 15110000  
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AP008214\_153 15300001 15410000  
AP008214\_154 15400001 15510000  
AP008214\_155 15500001 15610000  
AP008214\_156 15600001 15710000  
AP008214\_157 15700001 15810000  
AP008214\_158 15800001 15910000  
AP008214\_159 15900001 16010000  
AP008214\_160 16000001 16110000  
AP008214\_161 16100001 16210000  
AP008214\_162 16200001 16310000  
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AP008214\_165 16500001 16610000  
AP008214\_166 16600001 16710000  
AP008214\_167 16700001 16810000  
AP008214\_168 16800001 16910000  
AP008214\_169 16900001 17010000

AP008214\_170 17000001 17110000  
AP008214\_171 17100001 17210000  
AP008214\_172 17200001 17310000  
AP008214\_173 17300001 17410000  
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AP008214\_185 18500001 18610000  
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AP008214\_191 19100001 19210000  
AP008214\_192 19200001 19310000  
AP008214\_193 19300001 19410000  
AP008214\_194 19400001 19510000  
AP008214\_195 19500001 19610000  
AP008214\_196 19600001 19710000

Query Match 100.0%; Score 14; DB 15; Length 110000;  
Best Local Similarity 78.6%; Pred. No. 4e+03; 0; Indels 0; Gaps 0;  
Matches 11; Conservative 3; Mismatches 0; Gaps 0;

QY 1 CCGACTGCACTCG 14  
DB 62186 CCGACTGCACTCG 62173

RESULT 13  
AP008215\_150  
WPCOMMENT

Sequence split into 227 fragments LOCUS AP008215 Accession AP008215  
Fragment Name Begin End  
AP008215\_000 1 110000  
AP008215\_001 100001 210000  
AP008215\_002 200001 310000  
AP008215\_003 300001 410000  
AP008215\_004 400001 510000  
AP008215\_005 500001 610000  
AP008215\_006 600001 710000  
AP008215\_007 700001 810000  
AP008215\_008 800001 910000  
AP008215\_009 900001 1010000  
AP008215\_010 1000001 1110000  
AP008215\_011 1100001 1210000  
AP008215\_012 1200001 1310000  
AP008215\_013 1300001 1410000  
AP008215\_014 1400001 1510000  
AP008215\_015 1500001 1610000  
AP008215\_016 1600001 1710000  
AP008215\_017 1700001 1810000  
AP008215\_018 1800001 1910000  
AP008215\_019 1900001 2010000  
AP008215\_020 2000001 2110000  
AP008215\_021 2100001 2210000  
AP008215\_022 2200001 2310000  
AP008215\_023 2300001 2410000  
AP008215\_024 2400001 2510000  
AP008215\_025 2500001 2610000  
AP008215\_026 2600001 2710000  
AP008215\_027 2700001 2810000  
AP008215\_028 2800001 2910000  
AP008215\_029 2900001 3010000  
AP008215\_030 3000001 3110000



AP008215\_031 3100001 3210000  
AP008215\_032 3200001 3310000  
AP008215\_033 3300001 3410000  
AP008215\_034 3400001 3510000  
AP008215\_035 3500001 3610000  
AP008215\_036 3600001 3710000  
AP008215\_037 3700001 3810000  
AP008215\_038 3800001 3910000  
AP008215\_039 3900001 4010000  
AP008215\_040 4000001 4100000  
AP008215\_041 4100001 4210000  
AP008215\_042 4200001 4310000  
AP008215\_043 4300001 4410000  
AP008215\_044 4400001 4510000  
AP008215\_045 4500001 4610000  
AP008215\_046 4600001 4710000  
AP008215\_047 4700001 4810000  
AP008215\_048 4800001 4910000  
AP008215\_049 4900001 5010000  
AP008215\_050 5000001 5110000  
AP008215\_051 5100001 5210000  
AP008215\_052 5200001 5310000  
AP008215\_053 5300001 5410000  
AP008215\_054 5400001 5510000  
AP008215\_055 5500001 5610000  
AP008215\_056 5600001 5710000  
AP008215\_057 5700001 5810000  
AP008215\_058 5800001 5910000  
AP008215\_059 5900001 6010000  
AP008215\_060 6000001 6110000  
AP008215\_061 6100001 6210000  
AP008215\_062 6200001 6310000  
AP008215\_063 6300001 6410000  
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AP008215\_086 8600001 8710000  
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AP008215\_088 8800001 8910000  
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AP008215\_099 9900001 10010000  
AP008215\_100 10000001 10110000  
AP008215\_101 10100001 10210000  
AP008215\_102 10200001 10310000  
AP008215\_103 10300001 10410000

AP008215\_104 10400001 10510000  
AP008215\_105 10500001 10610000  
AP008215\_106 10600001 10710000  
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AP008215\_130 13000001 13110000  
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AP008215\_191 19100001 19210000  
AP008215\_192 19200001 19310000  
AP008215\_193 19300001 19410000  
AP008215\_194 19400001 19510000  
AP008215\_195 19500001 19610000  
AP008215\_196 19600001 19710000

Query Match 100.0%; Score 14; DB 15; Length 110000;  
Best Local Similarity 78.6%; Pred. No. 4e+03;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACGCACTCG 14  
DB 27463 CGTACTGCACTCG 27476

RESULT 14  
CR382131\_08  
WPCOMMENT

Sequence split into 43 fragments LOCUS CR382131 Accession CR382131

Fragment Name	Begin	End
CR382131_00	1	110000
CR382131_01	100001	210000
CR382131_02	200001	310000
CR382131_03	300001	410000
CR382131_04	400001	510000
CR382131_05	500001	610000
CR382131_06	600001	710000
CR382131_07	700001	810000
CR382131_08	800001	910000
CR382131_09	900001	1010000
CR382131_10	1000001	1110000
CR382131_11	1100001	1210000
CR382131_12	1200001	1310000
CR382131_13	1300001	1410000
CR382131_14	1400001	1510000
CR382131_15	1500001	1610000
CR382131_16	1600001	1710000
CR382131_17	1700001	1810000
CR382131_18	1800001	1910000
CR382131_19	1900001	2010000
CR382131_20	2000001	2110000
CR382131_21	2100001	2210000
CR382131_22	2200001	2310000
CR382131_23	2300001	2410000
CR382131_24	2400001	2510000
CR382131_25	2500001	2610000
CR382131_26	2600001	2710000
CR382131_27	2700001	2810000
CR382131_28	2800001	2910000
CR382131_29	2900001	3010000
CR382131_30	3000001	3110000
CR382131_31	3100001	3210000
CR382131_32	3200001	3310000
CR382131_33	3300001	3410000
CR382131_34	3400001	3510000
CR382131_35	3500001	3610000
CR382131_36	3600001	3710000
CR382131_37	3700001	3810000

CR382131\_38 3800001 3910000  
CR382131\_39 3900001 4010000  
CR382131\_40 4000001 4110000  
CR382131\_41 4100001 4210000  
CR382131\_42 4200001 4224103

Continuation (9 of 43) of CR382131 from base 800001 (CR382131 Yarrowia lipolytica chromosome)

Query Match 100.0%; Score 14; DB 15; Length 110000;  
Best Local Similarity 78.6%; Pred. No. 4e+03;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACGCACTCG 14  
DB 106773 CGTACTGCACTCG 106786

RESULT 15  
CR382131\_09  
WPCOMMENT

Sequence split into 43 fragments LOCUS CR382131 Accession CR382131

Fragment Name	Begin	End
CR382131_00	1	110000
CR382131_01	100001	210000
CR382131_02	200001	310000
CR382131_03	300001	410000
CR382131_04	400001	510000
CR382131_05	500001	610000
CR382131_06	600001	710000
CR382131_07	700001	810000
CR382131_08	800001	910000
CR382131_09	900001	1010000
CR382131_10	1000001	1110000
CR382131_11	1100001	1210000
CR382131_12	1200001	1310000
CR382131_13	1300001	1410000
CR382131_14	1400001	1510000
CR382131_15	1500001	1610000
CR382131_16	1600001	1710000
CR382131_17	1700001	1810000
CR382131_18	1800001	1910000
CR382131_19	1900001	2010000
CR382131_20	2000001	2110000
CR382131_21	2100001	2210000
CR382131_22	2200001	2310000
CR382131_23	2300001	2410000
CR382131_24	2400001	2510000
CR382131_25	2500001	2610000
CR382131_26	2600001	2710000
CR382131_27	2700001	2810000
CR382131_28	2800001	2910000
CR382131_29	2900001	3010000
CR382131_30	3000001	3110000
CR382131_31	3100001	3210000
CR382131_32	3200001	3310000
CR382131_33	3300001	3410000
CR382131_34	3400001	3510000
CR382131_35	3500001	3610000
CR382131_36	3600001	3710000
CR382131_37	3700001	3810000
CR382131_38	3800001	3910000
CR382131_39	3900001	4010000
CR382131_40	4000001	4110000
CR382131_41	4100001	4210000
CR382131_42	4200001	4224103

Continuation (10 of 43) of CR382131 from base 900001 (CR382131 Yarrowia lipolytica chromosome)

Query Match 100.0%; Score 14; DB 15; Length 110000;  
Best Local Similarity 78.6%; Pred. No. 4e+03;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACGCACTCG 14  
DB 6773 CGTACTGCACTCG 6786

RESULT 16  
AP004759/c  
LOCUS  
DEFINITION  
Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 8,  
PAC clone: P0670E08.  
ACCESSION  
AP004759 GI:38637192  
VERSION  
AP004759.3  
KEYWORDS  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriophytaceae; Oryzaceae; Oryza.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, PAC  
clone: P0670E08  
Published Only in Database (2002)  
2 (bases 1 to 133106)  
Sasaki, T., Matsumoto, T. and Yamamoto, K.  
Direct Submission  
Submitted (13-FEB-2002) Takuji Sasaki, National Institute of  
Agrobiological Sciences, Rice Genome Research Program, Kannondai  
2-1-2, Tsukuba, Ibaraki 305-8602, Japan  
(E-mail:tsasaki@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/  
Tel:81-298-38-7441, Fax:81-298-38-7468)  
On Dec 2, 2003 this sequence version replaced gi:34328000.  
Genes were predicted from the integrated results of the following:  
GENSCAN (http://CCR-081.mt.edu/GENSCAN.html), GENESH  
(http://www.softberry.com/), GeneMark.hmm  
(http://opal.biology.gatech.edu/GeneMark/), RICEHMM  
(http://www.tigr.org/cdb/glimmer/glmr\_form.html), RICEHMM  
(http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor  
(http://bioinformatics.isate.edu/cgi-bin/sp.cgi), sim4  
(http://glodn.cse.psu.edu/html/docs/sim4.html), gap2  
(http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The  
genomic sequence was searched against NCBI NonRedundant Protein  
database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA  
sequence database at RGP or DBJ. Protein homologues of the coding  
regions were searched against NCBI NonRedundant Protein database  
with BLASTP. ESTs represent the identified cDNA sequences using  
BLASTN with the corresponding DBJ accession no. and RGP clone ID.  
Full-length cDNAs represent the identified cDNA sequences using  
BLASTN with the corresponding DBJ accession no.  
A gene with identity or significant homology to a protein is  
classified based on the protein name to indicate the homology level  
such as same name, 'putative-' and '-like protein'. A gene without  
significant homology to any protein but with full-length cDNA or  
EST homology (covering almost the entire length of partial  
sequence) is classified as an 'unknown' protein. A gene predicted  
by two or more gene prediction programs is classified as a  
'hypothetical' protein according to IRGSP standard. A gene  
predicted by a single gene prediction program is also classified as  
a probable 'hypothetical' protein and is included as a  
miscellaneous feature of the sequence.  
The orientation of the sequence is from 5' to 3' of the PAC clone.  
This sequence of P0670E08 clone has an overlap with OJ1136.A10  
(DBJ: AB003884) clone at 5' end and with OSNBA0049101 (DBJ:  
AB005490) at 3' end. Detailed information on overlap and assembly  
quality together with annotation of this entry is available at  
http://rgp.dna.affrc.go.jp/Genomeseq.html.  
Location/Qualifiers  
1. 133106  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="genomic DNA"  
/cultivar="Nipponbare"  
/db\_xref="taxon:39947"  
/chromosome="8"  
/clone="P0670E08"  
complement(4155..4698)  
/gene="P0670E08.1"

mRNA  
complement(join(4155..4598,4651..>4698))  
/gene="P0670E08.1"  
/note="start and end point are not identified"  
CDS  
complement(join(4155..4598,4651..4698))  
/gene="P0670E08.1"  
/note="predicted by GENESH etc."  
/codon\_start=1  
/product="hypothetical protein"  
/protein\_id="BAD03444.1"  
/db\_xref="GI:38637193"  
/translation="MARVAARWIMVAMMMHADKAGNSGDLARQKRGVGGGRMG  
EARNRRKAEIANGGRRPACVNGIGGRASALALATIGRGRCGVCGR  
WGRHEKRWATTIGAQKRGTRDPSGGGRGASBGTAATGAGNGQDGRPIWR  
NRW"  
complement(9606..14057)  
/gene="P0670E08.2-1"  
complement(9606..14057)  
/gene="P0670E08.2-1"  
/note="contains full-length cDNA(s) : AK120635  
non-coding transcript  
probably inactive due to including stop codon(s) in CDS"  
complement(11850..13978)  
/gene="P0670E08.2-2"  
complement(11850..>13978)  
/gene="P0670E08.2-2"  
/note="supported by full-length cDNA(s) : AK108041"  
complement(11850..13978)  
/gene="P0670E08.2-2"  
/note="contains full-length cDNA(s) : AK108041  
non-coding transcript  
probably inactive due to including stop codon(s) in CDS"  
join(15133..15163,15236..15327,16054..16091,16202..16322)  
/gene="P0670E08.3"  
join(15133..15163,15236..15327,16054..16091,16202..16322)  
/gene="P0670E08.3"  
/note="hypothetical ORF  
predicted by GeneMark.hmm  
this category is not included in IRGSP standard"  
join(16924..18185,18279..20151)  
/gene="P0670E08.4"  
join(16924..18185,18279..20151)  
/gene="P0670E08.4"  
/note="typs type transposon-like"  
complement(20190..20643)  
/gene="P0670E08.5"  
complement(20190..>20643)  
/gene="P0670E08.5"  
/note="supported by full-length cDNA(s) : AK062314"  
complement(20190..20643)  
/gene="P0670E08.5"  
/note="contains full-length cDNA(s) : AK062314  
non-coding transcript  
probably inactive due to including stop codon(s) in CDS"  
complement(join(20758..22908,23398..24423))  
/gene="P0670E08.6"  
complement(join(20758..22908,23398..24423))  
/gene="P0670E08.6"  
/note="gyrpy-type retrotransposon-like"  
complement(24490..26260)  
/gene="P0670E08.7"  
complement(24490..26260)  
/gene="P0670E08.7"  
complement(24490..26260)  
/note="probably inactive due to 5' exon missing in CDS  
pseudogene, GAG-POL precursor"  
pseudo  
complement(join(28590..28904,29841..29882))  
/gene="P0670E08.8"  
complement(join(28590..28904,29841..29882))  
/gene="P0670E08.8"  
/note="hypothetical ORF  
predicted by GENSCAN  
this category is not included in IRGSP standard"  
34966..40113

gene

mRNA  
 /gene="P0670E08.9"  
 join(34966, .35130,35266, .35300,35395, .35436,35536, .35629,  
 35759, .35955,37221, .37465,37583, .37940,38024, .38599,  
 39455, .40113)  
 /note="supported by full-length cDNA (s): AK073839"  
 join(35022, .35130,35266, .35300,35395, .35436,35536, .35629,  
 35759, .35955,37221, .37465,37583, .37940,38024, .38599,  
 39455, .39730)  
 /gene="P0670E08.9"  
 /note="contains EST(s): AU065171 (B60238)  
 contains full-length cDNA(s): AK073839"  
 /codon\_start=1  
 /product="putative glycosyltransferase"  
 /protein\_id="BAD03445.1"  
 /db\_xref="GI:38637194"  
 /translation="MWRRRRSVLLLLALTVLSPLVLTTRLSAALNQRRLDGE  
 IVQGRVASKALNPLETVSGSLKEPVIGSESEBSASSTEPSOTTEFLRKAGE  
 HKNRVSEATADARSDDDLBOVTSKQEDDGLATVSDQOQITTSQOORSESA  
 SLEENVPBOTSMENSLKNGKDALDTRIRNLDILIKAVLIGGAIKAPQYLKDL  
 RQRIREVQKYLGDASDPLPKRANRKYTLLEOTLKGLMDDCSVYKRAMLHS  
 ABEQLAHKKQVFLTQLAKTLPKGLHCLPLANBYFLDPSHQFPNKKELDLPK  
 LHYALFSDNLLAAVNVSTVLANGPHHVEHLYDRLNAPMKRMWLSNPGKAT  
 IEVNIEEFMTLNASYSPVKQLESQSMIDYERTRANSDSLKRNPKYLSLNL  
 RFLPIEYINLHKIVFLDDVYIKDLTSLMSIDMKGYIGVETGSGSPHPRDLYN  
 FSNPVYKVPDPHACGMARFPLAEKRRQNTIETIYNSKQKNDRLIMKGLTTP  
 GLTFPNKTLPLKRSNHLVJGLGNPHVSSRDLERAAVHYNGNKKWELIGLPKFNRY  
 WSAVLDYDQPLFLEKINP"  
 complement(41205, .43610)  
 /gene="P0670E08.10"  
 complement(join(41205, .41836,41910, .42428,42525, .42701,  
 42896, .43036,43133, .43610))  
 /note="supported by full-length cDNA (s): AK069803"  
 complement(join(41618, .41836,41910, .42428,42525, .42701,  
 42896, .43036,43133, .43300))  
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 /note="contains EST(s): AU172574 (E2606), AU172573 (E2606)  
 contains full-length cDNA(s): AK069803"  
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 /protein\_id="BAD03446.1"  
 /db\_xref="GI:38637195"  
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 OGTLKATDLKRRGNDVBERGVNHLIVSGNGAPDQGAASWPNKCPPIRDCKVL  
 PISVLVNNKNNVNVVNSKFFPMALLQSGAKISGVKISAPSSPTDGIHIER  
 SNGVSIADTTIATDDCISIGQGNNDIVARVHCGHGSGVSLRGVYGEQVYTHI  
 VDMTHGTMMNGVIRKTMENSPKNSAAHMLPENLYMNVONPILIDQKCYPPNCEH  
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 VRKIVGFONPKPCP"  
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 QY 1 CGUACUGCAACUGC 14  
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 Db 6469 CGTACTGCACTCG 6456  
 RESULT 17  
 AC044825 140409 bp DNA linear HTG 27-JUL-2000  
 LOCUS  
 DEFINITION Homo sapiens chromosome 1 clone RP11-275114 map 1, WORKING DRAFT  
 SEQUENCE, 39 unordered pieces.

AC044825  
 AC044825.2 GI:9502452  
 HTG: HTGS\_PHASE1; HTGS\_DRAFT.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Abrahams, H., Allen, N.,  
 Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,  
 Boguski, M.S., Bouckge, B., Brown, A., Burkett, G.,  
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 Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kam, L., Karas, A.,  
 Klein, J., Labèque, K., Lamazares, R., Landers, T., Lehotzky, J.,  
 Levine, R., Liew, G., Liu, G., Locke, K., MacDonald, P., Margulis, N.,  
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 Stange, S., Thomas, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
 Testa, S., Theodore, J., Tirrell, A., Travers, M., Trigg, J.,  
 Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,  
 Young, G., Zaitoun, J., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (12-APR-2000) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Jul 27, 2000 this sequence version replaced gi:7543788.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: MIBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submission@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: L8011  
 Center clone name: 275.1.14  
 ----- Summary Statistics  
 Sequencing vector: M13; W77815; 99% of reads  
 Sequencing vector: Plasmid; n/a; 4-0.1% of reads  
 1.00182149362477Chemistry: Dye-terminator Big Dye; 100% of  
 reads  
 ----- Assembly program: Phrap; version 0.960721  
 Consensus quality: 120391 bases at least Q40  
 Consensus quality: 129577 bases at least Q30  
 Consensus quality: 133768 bases at least Q20  
 Insert size: 160000; agarose-fp  
 Insert size: 136609; sum-of-coverage  
 Quality coverage: 3.1 in Q20 bases; agarose-fp  
 Quality cov.  
 NOTE: This is a 'working draft' sequence. It currently  
 consists of 39 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 This record will be updated with the finished sequence  
 as soon as it is available and the accession number will  
 be preserved.  
 1 1156: contig of 1156 bp in length  
 1157 1256: gap of 100 bp  
 1257 1265: contig of 1009 bp in length

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* 2266 2365: gap of 100 bp
* 2366 3576: contig of 1211 bp in length
* 3577 4845: contig of 1169 bp in length
* 4846 7367: contig of 2422 bp in length
* 7368 8595: contig of 1128 bp in length
* 8596 10409: contig of 1714 bp in length
* 10410 10509: gap of 100 bp
* 10510 11838: contig of 1329 bp in length
* 11839 11938: gap of 100 bp
* 11939 13792: contig of 1854 bp in length
* 13793 13892: gap of 100 bp
* 13893 15478: contig of 1586 bp in length
* 15479 15578: gap of 100 bp
* 15579 17753: contig of 2175 bp in length
* 17754 17853: gap of 100 bp
* 17854 19331: contig of 1478 bp in length
* 19332 21597: contig of 2166 bp in length
* 21598 21697: gap of 100 bp
* 21698 23136: contig of 1439 bp in length
* 23137 23236: gap of 100 bp
* 23237 25903: contig of 2667 bp in length
* 25904 26003: gap of 100 bp
* 26004 29751: contig of 3648 bp in length
* 29752 33001: contig of 3250 bp in length
* 33002 33101: gap of 100 bp
* 33102 35597: contig of 2496 bp in length
* 35598 37964: contig of 2267 bp in length
* 37965 38064: gap of 100 bp
* 38065 41070: contig of 3006 bp in length
* 41071 41170: gap of 100 bp
* 41171 43345: contig of 2175 bp in length
* 43346 46364: contig of 2919 bp in length
* 46365 49323: contig of 2859 bp in length
* 49324 49423: gap of 100 bp
* 49424 52514: contig of 3091 bp in length
* 52515 56594: contig of 3980 bp in length
* 56595 60340: gap of 100 bp
* 60341 60440: gap of 100 bp
* 60441 64493: contig of 4053 bp in length
* 64494 66453: gap of 100 bp
* 66454 68745: contig of 4052 bp in length
* 68746 71501: contig of 2756 bp in length
* 71502 71601: gap of 100 bp
* 71602 74120: contig of 2519 bp in length
* 74121 78968: contig of 4748 bp in length
* 78969 79068: gap of 100 bp
* 79069 83734: contig of 4666 bp in length
* 83735 83834: gap of 100 bp
* 83835 89530: contig of 5696 bp in length
* 89531 89630: gap of 100 bp
* 89631 94947: contig of 5317 bp in length
* 94948 95047: gap of 100 bp
* 95048 100827: contig of 5780 bp in length
* 100828 100927: gap of 100 bp
* 100928 105800: contig of 4873 bp in length
* 105801 105900: gap of 100 bp
* 105901 114896: contig of 8996 bp in length
* 114897 127117: contig of 12121 bp in length
* 127118 127217: gap of 100 bp

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/db_xref="taxon:9606"
/chromosome="1"
/map="1"
/clone="RP11-275I14"
/clone_1fb="RP11 Human Male BAC"
1..1156
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gap
1157..1256
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1257..2265
/note="assembly_fragment"
gap
2266..2365
/estimated_length=100
misc_feature
2366..3576
/note="assembly_fragment"
gap
3577..3676
/estimated_length=100
misc_feature
3677..4845
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gap
4846..4945
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4946..7367
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gap
7368..7467
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misc_feature
7468..8595
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8596..8695
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misc_feature
8696..10409
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10410..10509
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10510..11838
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11839..11938
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misc_feature
11939..13792
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13793..13892
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13893..15478
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Query Match 100.0%; Score 14; DB 14; Length 140409;
Best Local Similarity 78.6%; Pred. No. 3.9e+03;
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGUACUGCAACUG 14
Db 14580 CGTACTGCACTCG 14567
RESULT 18
AP005426 148848 bp DNA linear PLN 28-JUL-2004
LOCUS Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 9,
DEFINITION PAC Clone:F0668D04.
ACCESSION AP005426
VERSION AP005426.3 GI:50725953
KEYWORDS
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

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REFERENCE  
ATTNORS  
TITLE  
JOURNAL  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
gene

1  
Sasaki, T., Matsumoto, T. and Katayose, Y.  
Oryza sativa Nipponbare (GA3) genomic DNA, chromosome 9, PAC  
clone: P0668D04  
Published Only in Database (2002)  
2 (bases 1 to 148848)  
Sasaki, T., Matsumoto, T. and Katayose, Y.  
Direct Submission  
Submitted (12-JUN-2002) Takuji Sasaki, National Institute of  
Agrobiological Sciences, Rice Genome Research Program, Kamondai  
2-1-2, Tsukuba, Ibaraki 305-8602, Japan  
(E-mail: tsasaki@nias.affrc.go.jp, URL: http://cgp.dna.affrc.go.jp/  
Tel:81-298-38-7441, Fax:81-298-38-7468)  
On Jul 27, 2004 this sequence version replaced gi:4215348.  
Genes were predicted from the integrated results of the following:  
GENSCAN (http://CCR-081.mt.edu/GENSCAN.html), FGENESH  
(http://www.softberry.com/), GeneMark.hmm  
(http://opal.biology.gatech.edu/GeneMark/), glimmer  
(http://www.tigr.org/cdb/glimmer/glmr\_form.html), RiceHMM  
(http://cgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor  
(http://bioinformatics.iasatc.edu/cgi-bin/sp.cgi), sim4  
(http://globin.cse.psu.edu/html/docs/sim4.html), gap2  
(http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The  
genomic sequence was searched against NCBI Nonredundant Protein  
database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA  
sequence database at RGP or DDBJ. Protein homologues of the coding  
regions were searched against NCBI Nonredundant protein database  
with BLASTP. ESTs represent the identified cDNA sequences using  
BLASTN with the corresponding DDBJ accession no. and RGP clone ID.  
Full-length cDNAs represent the identified cDNA sequences using  
BLASTN with the corresponding DDBJ accession no.  
A gene with identity or significant homology to a protein is  
classified based on the protein name to indicate the homology level  
such as same name, 'putative-' and '-like protein'. A gene without  
significant homology to any protein but with full-length cDNA or  
EST homology (covering almost the entire length of partial  
sequence) is classified as an 'unknown' protein. A gene predicted  
by two or more gene prediction programs is classified as a  
'hypothetical' protein according to IRGSP standard. A gene  
predicted by a single gene prediction program is also classified as a  
probable 'hypothetical' protein and is included as a  
miscellaneous feature of the sequence.  
The orientation of the sequence is from T7 to SP6 of the PAC clone.  
This sequence of P0668D04 clone has an overlap with P0701F11 (DDBJ:  
AP005429) clone at 5' end and with FJ174D06 (DDBJ: AP005579)  
clone at 3' end. Detailed information on overlap and assembly  
quality together with annotation of this entry is available at  
http://cgp.dna.affrc.go.jp/GenomesSeq.html.

FEATURES  
Source  
gene  
mRNA  
CDs  
gene

1.148848  
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/db\_xref="taxon:39947"  
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TASGGRHRFSSPHPSIHPHPTIPSSITLAIOSINVTYTKQRRRRRRGGDDHPVK  
VTRMKRRRQCIWGIVFFLPKPRMRSP"  
27300..8340

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misc_feature
|gene="P0668D04.2-2"
|join(<2793..7588,7705..7793,7901..>8340)
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|note="supported by full-length cDNA(s) : AKI21336"
2793..8340
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|note="contains full-length cDNA(s) : AKI21336
non-coding transcript
probably inactive due to including stop codon(s) in CDS"
2802..9052
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2802..9052
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|note="contains full-length cDNA(s) : AK073292
non-coding transcript
probably inactive due to including stop codon(s) in CDS"
4775..9051
|gene="P0668D04.2-3"
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|gene="P0668D04.2-3"
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probably inactive due to including stop codon(s) in CDS"
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predicted by RiceHMM
this category is not included in IRGP standard"
complement(join(133250..13596,14755..15107,15521..15709,
15814..15968,16099..16319))
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complement(join(133250..13596,14755..15107,15521..15709,
15814..15968,16099..16319))
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|note="supported by full-length cDNA(s) : AK067949"
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15814..15968,16099..16318))
|gene="P0668D04.4-1"
|note="supported by full-length cDNA(s) : AKI04860"
complement(join(13407..13596,14755..15107,15521..15709,
15814..15968,16099..16285))
|gene="P0668D04.4-1"
|note="contains BST(e) : AU086004(S10974),D46355(S10974)
contains full-length cDNA(s) : AK067949,AKI04860"
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|protein_id="BADJ3482.1"
|db_xref="GI:50725955"
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VFHTASPTDDEQVEAPVRGETSYVIKAALAEGATVRVETSSIGATMDPNRPGPDV
VNDSCWDLDFEKTCKRWVCYGRVAIVGEAKCAABRGVDLVVASPVLYGLPIQPLQPL
VNASVLIIDTSGAKKYANAVOAYDVDAHAHRVFAAPASGHILCAREVLHRR
EDVHHIKLPEPYVPFRGSDVNPQRPKYMSKKQLQDGLHFIPVSDBLYETVKS
LOEKHLPVLSKEIPERLNGVPA"
complement(join(14414..15107,15521..15709,15814..15968,
16099..16313))
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complement(join(14414..15107,15521..15709,15814..15968,
16099..16313))
|gene="P0668D04.4-2"
|note="supported by full-length cDNA(s) : AKI07198"
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16099..16285))
|gene="P0668D04.4-2"
|note="contains BST(e) : AU086004(S10974),D46355(S10974)
contains full-length cDNA(s) : AKI07198"
|codon_start=1

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/product="putative cinnamoyl CoA reductase"  
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 /db\_xref="GI:50725956"  
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 VFTTASPVTDPEQOMEPANRGTEYVYKAAEAGTTRVFTSSICATYMDPRGSDV  
 VVDSCHSDLEFCRKTKNMTCTGNAVAESDCAAEKRGVDLVVSPVAVGGLDPT  
 VNASVAHLLKLYLDSAKCYANAVQAVVDVAAAHVFAEFAEASGRHLCARVLAH  
 EDVHLIGKLFPEYPTPR"  
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 /note="predicted by GENSCAN etc."  
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 /note="predicted by GeneMark.hmm etc."  
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 /db\_xref="GI:50725958"  
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 22537..23576  
 /gene="P0668D04.7"  
 /note="probably inactive due to 5' exon missing in CDS  
 , pseudogene, En/Spm-related transposon protein"  
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 Best Local Similarity 78.6%; Pred. No. 3.8e+03;  
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 CGUACUGCAACUCG 14  
 ||:|||||:  
**Db** 19106 CGTACTGCACACTCG 19119

**RESULT 19**  
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**LOCUS** Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 9,  
**DEFINITION** PAC clone: P0701F11.  
**ACCESSION** AP005429  
**VERSION** AP005429.3 GI:50252464  
**KEYWORDS** Oryza sativa (japonica cultivar-group)  
**SOURCE** Oryza sativa (japonica cultivar-group)  
**ORGANISM** Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
**REFERENCE** 1  
**AUTHORS** Sasaki, T., Matsumoto, T. and Katayose, Y.  
**TITLE** Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, PAC  
 clone: P0701F11  
**JOURNAL** Published only in Database (2002)  
**REFERENCE** 2 (bases 1 to 154950)

# AUTHORS TITLE JOURNAL

## COMMENT

Sasaki, T., Matsumoto, T. and Katayose, Y.  
 Direct Submission  
 Submitted (12-JUN-2002) Takuji Sasaki, National Institute of  
 Agricultural Sciences, Rice Genome Research Program, Kannondai  
 2-1-2, Tsukuba, Ibaraki 305-8602, Japan  
 (E-mail: tsasaki@nias.affrc.go.jp, url: http://rtp.dna.affrc.go.jp/  
 Tel: 81-298-38-7441, Fax: 81-298-38-7468)  
 On Jul 12, 2004 this sequence version replaced gi:38347824.  
 Genes were predicted from the integrated results of the following:  
 GENSCAN (http://CCR-081.mtc.edu/GENSCAN.html), FGENESH  
 (http://opal.biology.gatech.edu/Genemark/), Glimmer  
 (http://opal.biology.gatech.edu/Genemark/), Glimmer  
 (http://www.tigr.org/tcd/glimmer/glmr\_form.html), RiceHMM  
 (http://rtp.dna.affrc.go.jp/RiceHMM/), SplicePredictor  
 (http://bioinformatics.laetate.edu/cgi-bin/sp.cgi), slm4  
 (http://globin.cse.psu.edu/html/doces/slm4.html), GAP2  
 (http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The  
 genomic sequence was searched against NCBI NonRedundant Protein  
 database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA  
 sequence database at RGP or DBJ. Protein homologues of the coding  
 regions were searched against NCBI NonRedundant Protein database  
 with BLASTP. RSTs represent the identified cDNA sequences using  
 BLASTN with the corresponding DBJ accession no. and RGP clone ID.  
 Full-length cDNAs represent the identified cDNA sequences using  
 BLASTN with the corresponding DBJ accession no.  
 A gene with identity or significant homology to a protein is  
 classified based on the protein name to indicate the homology level  
 such as same name, 'putative-' and '-like protein'. A gene without  
 significant homology to any protein but with full-length cDNA or  
 RST homology (covering almost the entire length of partial  
 sequence) is classified as an 'unknown' protein. A gene predicted  
 by two or more gene prediction programs is classified as a  
 'hypothetical' protein according to IRGSP standard. A gene  
 predicted by a single gene prediction program is also classified as a  
 probable 'hypothetical' protein and is included as a  
 miscellaneous feature of the sequence.  
 The orientation of the sequence is from SP6 to T7 of the PAC clone.  
 This sequence of P0701F11 clone has an overlap with P0014G10 (DBJ:  
 AP005784) clone at 5' end and with P0668D04 (DBJ: AP005426) clone  
 at 3' end. Detailed information on overlap and assembly quality  
 together with annotation of this entry is available at  
 http://rtp.dna.affrc.go.jp/Genomeseq.html.

## FEATURES

### source

1..154950

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="genomic DNA"

/cultivar="Nipponbare"

/db\_xref="taxon:39947"

/chromosome="9"

/clone="P0701F11"

/complement(7738..9684)

/gene="P0701F11.1"

/complement(join(7738..8259,8789..8911,9006..9338,  
 9472..9684))

/gene="P0701F11.1"

/note="supported by full-length cDNA(s): AK067834"

/complement(join(7843..8259,8789..8911,9006..9338,  
 9472..9555))

/gene="P0701F11.1"

/note="contains full-length cDNA(s): AK067834"

/codon\_start=1

/product="putative WIZZ"

/protein\_id="BAD28643.1"

/db\_xref="GI:50252465"

/translation="MDDDDGSSSPYDSSAAAGLPIFSRSPAELEKTRAPMEENA  
 RITRLDAILAHGHHQRLLAPSSPPPESTAPASVSTSCAREDAAPVAAAAA  
 STAPSRQOPPTAPRPRPVRTVRVADADADANSMARVADGVTQMRKYGQVTRDN  
 PYRAVYFCAFPACPVYKQIQRCADSRSMVAATGEGHNALSTOTTEFVAGGTTG  
 CHAGSSSPLECSISINSGRTITLDTNQGSGSICGVEAALVAGELVTVASPE  
 LARHIVERYQVLKDADEVRVAVTAVAVDVDPHVPVH"

join(11245..11304,12099..12272,12615..12681,16273..16317,  
 17030..17142,17983..18084)

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/gene="P0701F11.2"



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 17030..17142,17983..18084)  
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 predicted by GENSCAN  
 this category is not included in IRGSP standard"  
 18428..18697  
 /gene="P0701F11.3"  
 18428..18697  
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 /note="hypothetical ORF  
 predicted by Glimmerm  
 this category is not included in IRGSP standard"  
 18788..19280  
 /gene="P0701F11.4"  
 join(18788..18922,18960..19280)  
 /note="start and end point are not identified"  
 join(18788..18922,18960..19280)  
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 /note="predicted by FGENESH etc."  
 /codon\_start=1  
 /product="hypothetical protein"  
 /protein\_id="BAD28644.1"  
 /db\_xref="GI:50252466"  
 /translation="MTLQEDRAAGADAVAREGSEHRSRVPDREGAKRERVPDA  
 VANPRCRMELGRRLPKTMPPPSFLDDMDPAADREYSGSGCPAGRPRLPVE  
 EATQKRVSDSGSSVQIKREBEKVPAMASGLAKRVSKVSLAN"  
 complement(23977..25632)  
 /gene="P0701F11.5-1"  
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 /gene="P0701F11.5-1"  
 /note="supported by full-length cDNA(s): AK061220"  
 complement(23977..25509)  
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 /note="supported by full-length cDNA(s): AK061493"  
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 /note="supported by full-length cDNA(s): AK061220"  
 complement(23977..25509)  
 /gene="P0701F11.5-1"  
 /note="supported by full-length cDNA(s): AK100881"  
 complement(23977..24090,24325..25451)  
 /gene="P0701F11.5-2"  
 complement(join(23977..24090,24325..25451))  
 /gene="P0701F11.5-2"  
 /note="supported by full-length cDNA(s): AK119760"  
 complement(join(24001..24090,24325..25281))  
 /gene="P0701F11.5-2"  
 /note="contains full-length cDNA(s): AK119760"  
 /codon\_start=1  
 /product="putative CBL-interacting protein kinase"  
 /protein\_id="BAD28645.1"  
 /db\_xref="GI:50252467"  
 /translation="MVEQLAREISIMRWHPNVGIRVLAASRAAFVVMYARGSE  
 LFAKVARGRLTBEHARRYPQQLVAAVGFCGGRVARDLKEPMLLDEGRLLKVTDFG  
 LALPEQLRODGLHTOCGPAYVAEVRKRGDARADLMCGVLLVYLQGLFPG  
 OHENYAKMOKIETKAEYOVPPWSDGARSRLVLLVYDPAKRSISEIMTPMKFGK  
 VPPVPTSPVSPKMEEDVILDGSDGASPRCAAFQIISMSGFDLSGMRSEQK  
 AATVTSRAPAATVIOQLKAVGSRSLGTSATRGKMLRLBATASVQDVMSVCSFS  
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 complement(24100..25470)  
 /gene="P0701F11.5-1"  
 /note="contains EST(s): C98911(E3245), C98910(E3245)  
 contains full-length cDNA(s): AK061220, AK061433, AK100881"  
 /codon\_start=1  
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 /db\_xref="GI:50252468"  
 /translation="MARBARBEADOVERLIVGRYBIRLLGCGTFAVYVYGRDLS  
 GSEVAKVIDKALRTBEQVBEQRLREISIMRWHPNVGIRVLAASRAAFVVMYARGSE  
 ARGSELPAKVARGRLTBEHARRYPQQLVAAVGFCGGRVARDLKEPMLLDEGRLLK  
 VTDPLAALPEQLRODGLHTOCGPAYVAEVRKRGDARADLMCGVLLVYLQGLFPG  
 GFPLPHENYAKMOKIETKAEYOVPPWSDGARSRLVLLVYDPAKRSISEIMTPMK  
 FKGGFVPTSPVSPKMEEDVILDGSDGASPRCAAFQIISMSGFDLSGMRSEQK  
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 /gene="P0701F11.6"  
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 /note="start and end point are not identified"  
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 /note="predicted by Glimmerm etc."  
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 /db\_xref="GI:50252469"  
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 TIQLEAARPRGSTRVRLSSGAPYLRUGPGDDMKVLM"  
 32286..34241  
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 /note="start and end point are not identified"  
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 /note="predicted by GENSCAN etc."  
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 /protein\_id="BAD28648.1"  
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 AAVQLOLOLQAEVAVQFASGQARNRENDRRPMWDALKEKRNINASAV"  
 join(37537..37679,39125..39152,39477..39751,39967..40129)  
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 /note="hypothetical ORF  
 predicted by GeneMark.hmm  
 this category is not included in IRGSP standard"  
 misc\_feature  
 96909 CGTACTGCACTCG 96922

Query Match 100.0%; Score 14; DB 15; Length 154950;  
 Best Local Similarity 78.6%; Pred. No. 3.8e+03;  
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUG 14  
 DB 96909 CGTACTGCACTCG 96922

RESULT 20  
 LOCUS BX088687 173867 bp DNA linear VRT 29-JAN-2004  
 DEFINITION Zebrafish DNA sequence from clone CH211-206114 in linkage group 7,  
 complete sequence.  
 ACCESSION BX088687  
 VERSION BX088687.6 GI:40994808  
 KEYWORDS HTG;  
 SOURCE Danio rerio (zebrafish)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 173867)  
 Eilwood, M.  
 Direct Submission  
 Submitted (15-JAN-2004) Wellcome Trust Sanger Institute, Hinxton,  
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 zfish-help@sanger.ac.uk Clone requests: clonequest@sanger.ac.uk  
 On Jan 17, 2004 this sequence version replaced gi:37805616.  
 ----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: zfish-help@sanger.ac.uk  
 -----

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: EMBL: SW: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhifeng Bao and Sean Eddy, submitted), and those beginning 'dir' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see [http://www.sanger.ac.uk/Projects/D\\_reio/fishmask.shtml](http://www.sanger.ac.uk/Projects/D_reio/fishmask.shtml)

CH211-206114 is from a CHORI-211 BAC library  
VECTOR: PTARBAC2.1

#### FEATURES

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1. 173867  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="CH211-206114"  
/clone\_id="CHORI-211"

##### ORIGIN

Query Match 100.0%; Score 14; DB 5; Length 173867;  
Best Local Similarity 78.6%; Pred. No. 3.7e+03;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGACGCGCACTCG 14  
||:|||||:  
Db 73300 CGTACTGCACTCG 73313

RESULT 21  
AC108605/c  
LOCUS  
DEFINITION  
Rattus norvegicus clone CH230-267P22, \*\*\* SEQUENCING IN PROGRESS  
\*\*\*, 2 unordered pieces.  
AC108605 188872 bp DNA linear HTG 09-OCT-2002  
AC108605.4 GI:23195553  
HTG; HTG\_PHASE1; HTG\_DRAFT; HTG\_ENRICHED.  
KEYWORDS  
Rattus norvegicus (Norway rat)  
SOURCE  
ORGANISM  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae; Rattus.  
1 (bases 1 to 188872)  
Muzny, D., Maric, M., Metzker, M., Lee, A., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooke, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, R., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bismar, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Butrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,

#### TITLE

#### REFERENCE

#### AUTHORS

#### JOURNAL

#### COMMENT

Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, E., Gees, K., Gill, R., Grady, M., Guerrero, M., Guevara, W., Gunatirane, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlik, P., Hawes, A., Henderson, N., Hernandez, J., Herndon, S., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulik, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolyvet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowls, C., Kraft, C.L., Ledow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lornshuwa, L., Louisedge, H., Lozada, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Manwiny, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Mirza, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwokedemel, O., Okwuonu, G., Olarnpungoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfankuch, C., Plopper, F., Polidexter, A., Popovic, D., Primus, E., Pu, L.-L., Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Register, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, M., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvarcbein, A., Slason, I., Sletter, C.D., Smajls, D., Sneed, J., Sodergren, R., Song, X.-Z., Sorrelle, R., Soza, J., Steinle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trogus, Z., Uman, K., Valas, R., Vera, V., Villalana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczky, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission  
Unpublished  
2 (bases 1 to 188872)  
Worley, K.C.  
Direct Submission  
Submitted (31-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 188872)  
Rat Genome Sequencing Consortium.  
Direct Submission  
Submitted (09-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Sep 19, 2002 this sequence version replaced gi:21737677.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

Center: Baylor College of Medicine  
Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)

Center project name: GPOC  
Center clone name: CH230-267P22

## ----- Summary Statistics

Assembly program: Phrap; version 0.990329  
 Consensus quality: 17756 bases at least Q40  
 Consensus quality: 17912 bases at least Q30  
 Consensus quality: 17978 bases at least Q20  
 Estimated insert size: 191240; sum-of-contigs estimation  
 Quality coverage: 3x in Q20 bases; sum-of-contigs estimation

----- NOTE: Estimated insert size may differ from sequence length  
 \* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 2 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 185765: contig of 185765 bp in length  
 \* 185766 185865: gap of unknown length  
 \* 185866 188872: contig of 3007 bp in length.  
 Location/Qualifiers

## FEATURES

source

misc\_feature

misc\_feature

misc\_feature

misc\_feature

misc\_feature

misc\_feature

misc\_feature

## ORIGIN

Query Match 100.0%; Score 14; DB 14; Length 188872;  
 Best Local Similarity 78.6%; Prod. NO. 3.7e+03;  
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGUACUGCACTUG 14  
 Db 60100 CGTACTGCACTCG 60087

RESULT 22  
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 LOCUS AC103229 Rattus norvegicus clone CH230-217018, WORKING DRAFT SEQUENCE.  
 DEFINITION AC103229.5 GI:30578703  
 ACCESSION HTG; HTGS PHASE2; HTGS DRAFT; HTGS FULLTOP.  
 VERSION HTG; HTGS PHASE2; HTGS DRAFT; HTGS FULLTOP.  
 KEYWORDS Rattus norvegicus (Norway rat)  
 SOURCE Rattus norvegicus  
 ORGANISM Rattus norvegicus  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Muridae; Murinae; Rattus.  
 Muzny, D. Marie, Metzker, M. Lee, Abramson, S., Adams, C., Alder, J.,

## TITLE

JOURNAL  
 AUTHORS  
 TITLE  
 JOURNAL

## REFERENCE

AUTHORS  
 TITLE  
 JOURNAL

## COMMENT

Allen, C., Allen, H., Albrooks, S., Amin, A., Anguiano, D.,  
 Anylebecht, V., Ayogel, A., Ayodeji, M., Baca, E., Baden, H.,  
 Balaban, D., Bandaranaike, D., Barber, M., Barnstead, M., Benham, F.,  
 Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,  
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 Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,  
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 Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Soza, J.,  
 Steidle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C.,  
 Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umanan, K.,  
 Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,  
 Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,  
 Williams, G., Willson, R., Wleczek, R., Wooden, H., Wolley, K.,  
 Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, V.,  
 Yu, F., Zhang, J., Zhou, X., Zhou, X., Zhao, S., Dunn, D., von  
 Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,  
 Weinstock, G. and Gibbs, R.A.  
 Direct Submission  
 Unpublished  
 2 (bases 1 to 218764)  
 Worley, K.C.  
 Direct Submission  
 Submitted (24-NOV-2001) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 218764)  
 Rat Genome Sequencing Consortium.  
 Direct Submission  
 Submitted (13-MAY-2003) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On May 13, 2003 this sequence version replaced gi:2285625.  
 The sequence in this assembly is a combination of BAC based reads  
 and whole genome shotgun sequencing reads assembled using Atlas  
 (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described  
 in the feature table below represents a scaffold in the Atlas  
 assembly (a 'contig-scaffold'). Within each contig-scaffold,  
 individual sequence contigs are ordered and oriented, and separated  
 by sized gaps filled with Ns to the estimated size. The sequence  
 may extend beyond the ends of the clone and there may be sequence  
 contigs within a contig-scaffold that consist entirely of whole  
 genome shotgun sequence reads. Both end sequences and whole genome

shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)

----- Project Information  
Center project name: GUND  
Center clone name: CH230-217018

----- Summary Statistics  
Assembly program: Atlas 3.0:

Consensus quality: 211841 bases at least Q40  
Consensus quality: 213096 bases at least Q30  
Consensus quality: 213870 bases at least Q20  
Estimated insert size: 218571; sum-of-contigs estimation  
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

-----  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 1 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
1 218764: contig of 218764 bp in length.  
Location/Qualifiers  
1. 218764

FEATURES  
source  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="CH230-217018"  
1. 1339  
misc\_feature  
/note="wgs\_contig"

## ORIGIN

Query Match 100.0%; Score 14; DB 14; Length 218764;  
Best Local Similarity 78.6%; Pred. No. 3.6e+03;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUCG 14  
||:|||||:|||||  
Db 170317 CGTACTGCAACTCG 170304

RESULT 23  
BX640547 230865 bp DNA linear VRT 29-JAN-2005  
LOCUS Zebrafish DNA sequence from clone DKEX-4UJ1 in linkage group 14,  
DEFINITION complete sequence.  
ACCESSION BX640547  
VERSION BX640547.35 GI:58331761  
KEYWORDS HTG.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 230865)  
Auger,K.

REFERENCE  
AUTHORS Submitted (29-JAN-2005) Wellcome Trust Sanger Institute, Hinxton,  
JOURNAL Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
TITLE zfish-help@sanger.ac.uk Clone requests: [clonerequest@sanger.ac.uk](mailto:clonerequest@sanger.ac.uk)  
AUTHORS On Jan 29, 2005 this sequence version replaced gi:57863663.  
JOURNAL Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: <http://www.sanger.ac.uk>

Contact: [zfish-help@sanger.ac.uk](mailto:zfish-help@sanger.ac.uk)

-----  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all  
regions were either double-stranded or sequenced with an alternate  
chemistry or covered by high quality data (i.e., phred quality >= 30)  
as compressions and repeats; all regions were covered by at least  
one plasmid subclone or more than one M13 subclone; and the  
assembly was confirmed by restriction digest, except on the rare  
occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession  
numbers given in the feature table with their source databases:  
Bm: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormPeP; Information  
on the WormPeP database can be found at  
[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep)  
Zebrafish pUC subclones occasionally display inconsistency over the  
length of mononucleotide A/T runs and conserved TA repeats. Where  
this is found the longest good quality representation will be  
submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat  
discovery system (Zhifeng Bao and Sean Eddy, submitted), and those  
beginning 'drr' were identified by Rick Waterman (Stephen Johnson  
lab, Mashu). For further information see  
[http://www.sanger.ac.uk/Projects/D\\_rerio/fishmask.shtml](http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml) DKEX-4UJ1  
is from a Zebrafish BAC library  
VECTOR: pindigobac-5.  
Location/Qualifiers  
1. 230865

FEATURES  
source  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="DKEX-4UJ1"  
/clone\_1fb="DanioKey"

## ORIGIN

Query Match 100.0%; Score 14; DB 5; Length 230865;  
Best Local Similarity 78.6%; Pred. No. 3.6e+03;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUCG 14  
||:|||||:|||||  
Db 114950 CGTACTGCAACTCG 114963

RESULT 24  
AC021883 232180 bp DNA linear HTG 25-AUG-2000  
LOCUS Homo sapiens chromosome 1 clone RP11-588h15, \*\*\* SEQUENCING IN  
DEFINITION PROGRESS \*\*\*, 40 unordered pieces.  
ACCESSION AC021883  
VERSION AC021883.4 GI:9910096  
KEYWORDS HTG; HTGS PHASE1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.  
1 (bases 1 to 232180)  
Waterston,R.H.

REFERENCE  
AUTHORS The sequence of Homo sapiens clone  
JOURNAL Unpublished  
TITLE 2 (bases 1 to 232180)  
AUTHORS Waterston,R.H.  
JOURNAL Direct Submission  
Submitted (21-JAN-2000) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA

COMMENT On Aug 25, 2000 this sequence version replaced gi:9838290.

----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: http://genome.wustl.edu/gsc/index.shtml  
----- Project Information -----  
Center project name: H\_NH058H15  
----- Summary Statistics -----  
Sequencing vector: M13, 86%  
Sequencing vector: plasmid, 14%  
Chemistry: Dye-terminator Big Dye, 14% of reads  
Chemistry: Dye-terminator Big Dye, 14% of reads  
Assembly program: Phrap, version 0.990319  
Consensus quality: 211766 bases at least Q40  
Consensus quality: 211790 bases at least Q30  
Consensus quality: 221643 bases at least Q20  
Insert size: 181000; agarose-fp  
Insert size: 228280; sum-of-contigs  
Quality coverage: 6.35 in Q20 bases; agarose-fp  
Quality coverage: 4.63 in Q20 bases; sum-of-contigs  
-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 40 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1 1312: contig of 1312 bp in length  
1313 1412: gap of unknown length  
1413 2446: contig of 1034 bp in length  
2447 2546: gap of unknown length  
2547 3878: contig of 1332 bp in length  
3879 5215: contig of 1237 bp in length  
5216 5315: gap of unknown length  
5316 6544: contig of 1223 bp in length  
6545 6644: gap of unknown length  
6645 7940: contig of 1296 bp in length  
7941 8040: gap of unknown length  
8041 9190: contig of 1150 bp in length  
9191 9290: gap of unknown length  
9291 10909: contig of 1619 bp in length  
10910 11009: gap of unknown length  
11010 12203: contig of 1194 bp in length  
12204 12303: gap of unknown length  
12304 13542: contig of 1239 bp in length  
13543 13642: gap of unknown length  
13643 14982: contig of 1340 bp in length  
14983 15082: gap of unknown length  
15083 16905: contig of 1823 bp in length  
16906 17005: gap of unknown length  
17006 18051: contig of 1046 bp in length  
18052 18151: gap of unknown length  
18152 19373: contig of 1222 bp in length  
19374 19473: gap of unknown length  
19474 20668: contig of 1195 bp in length  
20669 22399: gap of unknown length  
22399 22499: contig of 1631 bp in length  
22400 22500: gap of unknown length  
22500 24300: contig of 1701 bp in length  
24301 25667: gap of unknown length  
25668 25767: gap of unknown length  
25768 27705: contig of 1938 bp in length  
27706 27805: gap of unknown length  
27806 29643: contig of 1838 bp in length  
29644 29743: gap of unknown length  
29744 31718: contig of 1975 bp in length  
31719 31818: gap of unknown length  
31819 33299: contig of 1481 bp in length

33399: gap of unknown length  
33400 33400: contig of 2189 bp in length  
33400 35588: gap of unknown length  
35589 35688: gap of unknown length  
35689 37968: contig of 2280 bp in length  
37969 38068: gap of unknown length  
38069 40341: contig of 2273 bp in length  
40342 40441: gap of unknown length  
40442 42574: contig of 2133 bp in length  
42575 42674: gap of unknown length  
42675 44938: contig of 2264 bp in length  
44939 45038: gap of unknown length  
45039 50126: contig of 5088 bp in length  
50127 50226: gap of unknown length  
50227 52594: contig of 2368 bp in length  
52595 52694: gap of unknown length  
52695 57156: contig of 4462 bp in length  
57157 57257: gap of unknown length  
57258 61310: contig of 4054 bp in length  
61311 61410: gap of unknown length  
61411 65807: contig of 4397 bp in length  
65808 65907: gap of unknown length  
65908 70160: contig of 4253 bp in length  
70161 70260: gap of unknown length  
70261 76919: contig of 6659 bp in length  
76920 77019: gap of unknown length  
77020 85764: contig of 8745 bp in length  
85765 85864: gap of unknown length  
85865 106630: contig of 20766 bp in length  
106631 134020: gap of unknown length  
134021 134120: gap of unknown length  
134121 165082: contig of 30962 bp in length  
165083 165182: gap of unknown length  
165183 196340: contig of 31058 bp in length  
196341 232180: contig of 35840 bp in length.  
Location/Qualifiers

## FEATURES

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1..332180  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="1"  
/clone="RP11-568H15"  
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/note="assembly\_name:Contig14"  
1313..1412  
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1413..2446  
/note="assembly\_name:Contig15"  
2447..2546  
/estimated\_length=unknown  
2547..3878  
/note="assembly\_name:Contig30"  
3879..3978  
/estimated\_length=unknown  
3979..5215  
/note="assembly\_name:Contig35"  
5216..5315  
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5316..6544  
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6545..6644  
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6645..7940  
/note="assembly\_name:Contig42"  
7941..8040  
/estimated\_length=unknown  
8041..9190  
/note="assembly\_name:Contig44"  
9191..9290  
/estimated\_length=unknown  
9291..10909  
/note="assembly\_name:Contig47"

```

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             /estimated_length=unknown
misc_feature 11010. .12203
             /note="assembly_name:Contig148"
gap          12204. .12303
             /estimated_length=unknown
misc_feature 12304. .13542
             /note="assembly_name:Contig152"
gap          13543. .13642
             /estimated_length=unknown
misc_feature 13643. .14582
             /note="assembly_name:Contig153"
gap          14583. .15082
             /estimated_length=unknown
misc_feature 15083. .16905
             /note="assembly_name:Contig154"
gap          16906. .17005
             /estimated_length=unknown
misc_feature 17006. .18051
             /note="assembly_name:Contig155"
gap          18052. .18151
             /estimated_length=unknown
misc_feature 18152. .19373
             /note="assembly_name:Contig156"
gap          19374. .19473
             /estimated_length=unknown
misc_feature 19474. .20668
             /note="assembly_name:Contig157"
gap          20669. .20768
             /estimated_length=unknown
misc_feature 20769. .22399
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gap          22400. .22499

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Query Match 100.0%; Score 14; DB 14; Length 232180;  
 Best Local Similarity 78.6%; Pred. No. 3.6e+03;  
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUCG 14  
 |||:|||||:  
 Db 112822 CCGTACTGCACACTCG 112809

```

RESULT 25
BX294153/c 293350 bp DNA linear BCT 17-APR-2005
LOCUS Pirellula sp. strain 1 complete genome; segment 21/24.
DEFINITION BX294153 BX119912
ACCESSION BX294153.1 GI:32447383
VERSION
KEYWORDS complete genome.
SOURCE Rhodopirellula baltica SH 1
ORGANISM Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
          Planctomycetaceae; Rhodopirellula.
REFERENCE 1 (bases 1 to 293350)
AUTHORS Glockner,F.O., Kube,M., Bauer,M., Teeling,H., Lombardot,T.,
          Ludwig,W., Gade,D., Beck,A., Borzym,K., Heilmann,K., Rabus,R.,
          Schleener,H., Aumann,R. and Reinhardt,R.
          Complete genome sequence of the marine planctomycete Pirellula sp.
          strain 1
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (14), 8298-8303 (2003)
PUBMED 12835416
REFERENCE 2 (bases 1 to 293350)
AUTHORS Kube,M., Borzym,K., Heilmann,K., Klages,S., Marguardt,I.,
          Lombardot,S., Beck,A., Pawlik,R., Reinhardt,R., Glockner,F.O.,
          Bauer,M., Teeling,H., Lombardot,T., Ludwig,W., Gade,D., Rabus,R.,
          Schleener,H. and Aumann,R.
          Direct Submission
          Submitted (21-JUN-2003) Max Planck Institute for Molecular
          Genetics, ProScience Inneustrasse 73, D-14195 Berlin, Germany
          Max Planck Institute for Marine Microbiology Celsiusstrasse 1, D-28359
          Bremen, Germany
COMMENT This project was carried out by

```

\*Max Planck Institute for Molecular Genetics, Berlin, Germany; \*Max Planck Institute for Marine Microbiology, Bremen, Germany; In the framework of the REGX-project, <http://www.regx.de> -----

Center: Max Planck Institute for Molecular Genetics  
 Center code: MPIMG

----- Summary Statistics  
 Sequencing vector: pUC19; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 7142841 bases at least Q40  
 Consensus quality: 7145138 bases at least Q30  
 Consensus quality: 7145484 bases at least Q20  
 Quality coverage: 8.03

-----  
 This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid sequence; assembly was additionally confirmed by long range PCR and cosmid end sequences.

-----  
 See <http://www.micro-genomes.mpg.de/pirellula/> for more information including minimal tiling path from a set of 220 cosmids out of 908. See the misc\_feature tag below for the boundaries of the MTP cosmids. ----- Annotation  
 Center: Max Planck Institute for Marine Microbiology  
 Celsiusstrasse 1, D-28359 Bremen, Germany.  
 Center Code: MPIMM  
 Email: [foegem@bremen.de](mailto:foegem@bremen.de)  
 Phone: +49 (0)421 2028 938 Fax: +49 (0)421 2028 580

-----  
 Three different programs (Glimmer, Critica and Orpheus) were used for ORF-prediction. A nonredundant list of ORFs was generated by suitable parsing of the results.  
 Automated annotation was done with the software package Pedant Pro (<http://www.biomax.de>). All ORF predictions and annotations were manually corrected by considering all results of the different tools applied. See <http://www.regx.de> for more information and access to supplementary information.

FEATURES

source  
 1. .293350  
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 /strain="1"  
 /db\_xref="taxon:243090"  
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 /gene="uspa"  
 /locus\_tag="RB11183"  
 complement(93. .1040)  
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 /note="PMID: 9371463 best DB hits: BLAST: pfr:A69220; conserved hypothetical protein MTH98 - Methanobacterium; E=1e-07 gb:AA046412.1; AF096262.1 (AF096262) ER6 protein (Lycopodium; E=1e-05 gb:AA04173.1; AB006246.3 (AB006246) conserved hypothetical; E=2e-05 CCG: MTH98; CCG0589 Universal stress protein UpaA and related; E=1e-08 PFAM: PF00582; Universal stress protein family; E=4e-11"  
 /codon\_start=1  
 /transl\_table=11  
 /product="conserved hypothetical protein"  
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 /db\_xref="GI:32447384"  
 /db\_xref="GOA:Q7UR82"  
 /db\_xref="InterPro:IPR006016"  
 /db\_xref="UniProt/TREMBL:Q7UR82"  
 /translation="MRVLAVDSSPYSOQAVFASHLPLRKPDVGLVVAAPMLVD TSGKMPNDPGSFALRTDRBRADAVASDKSDQDHYSYVTHPIPIGPTGSLADVA DESGADLVGAIHSAIERVLVGSVSDVVAITHADSTLVVPTSEADVPEPLQKIM ALSGREDERMLTWLRKLRPNVEHLVLRDPSYKQDLRQASDAWQAQHRQAO



ACILDEPTKLOOLGLNTEHTHPVESNHNGETLVEYARRHGCDDLAVTGDSGLTTRVFL  
GSTRVYLAHACSVLIIIRDRBRRAKRAHQIAEQSLAST"

gene  
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/db\_xref="GI:32447385"  
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/translation="MFASRWTVRAASLTASFCATPSSHLLARHSQONASWSPECK"  
complement (1231..2142)  
/gene="uspa"  
/locus\_tag="RB11185"  
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/gene="uspa"  
/locus\_tag="RB11185"  
/note="PMID: 8905231 best DB hits: BLAST:  
swisprot:P74148; YD88\_SRY33 HYPOTHETICAL 17.3 KD PROTEIN  
SLI138; E=2e-05 gb:AG20091.1; (AE005088) Vng1898c  
Halobacterium sp. NRC-1; E=5e-05 swisprot:O57951;  
Y531\_METVA HYPOTHETICAL PROTEIN MJ0531 - ----; E=7e-04 COG:  
g11388; COG0589 Universal stress protein UspA and  
related; E=2e-06 PRAM: PF00582; Universal stress protein  
family; E=0.04"  
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/transl\_table=11  
/product="conserved hypothetical protein-putative  
universal stress protein"  
/protein\_id="CAD78975.1"  
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/db\_xref="GOA:Q7UBR0"  
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/translation="MNRBNGPKRLTIGDSSAPADALQALSKTLAEACEVSLATI  
VPEPPIYTIIDTSMPIROVPSRLIEINTOLKQOGRGRSPSCRSVSQGHGR  
GLIEMSERPDADWIVGVGSHAFSRILGSDYVANSITCLVHRTITTDHPSK  
GLPSRVVIAISNASEDTLPDWALALPNCVHVAHMETHPPELHLKKVAAYM  
EYERSAMKLMETTRRLALGKVKPSLSEPHVGRVAVLEVANEHACDLIVGDQDD  
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complement (2139..3614)  
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/note="best DB hits: BLAST: gb:AG4533.1; AF273214\_1  
(AF273214) Saar [Myxococcus xanthus]; E=3e-83  
swisprot:Q06065; ATOC\_ECOLI ACETOACETATE METABOLISM  
REGULATOR; E=1e-81 gb:AC28085.1; (AF100457) response  
regulator [Myxococcus xanthus]; E=5e-80 COG: atoc; COG2204  
AAA superfamily ATPases with N-terminal receiver; E=1e-82  
PRAM: PF00072; Response regulator receiver doma; E=2.7e-32  
PF00158; Sigma-54 interaction domain; E=1.1e-119"  
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/transl\_table=11  
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/db\_xref="GOA:Q7UBR0"  
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/db\_xref="InterPro:IPR003593"  
/db\_xref="UniProt/TREMBL:Q7UBR0"  
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MGACDFLTRECSLADLEHRLVQLAQORGHAKKQKALVHRNRPSKLTGNSLAME  
LSMIAKVAATRRKVLIEGSGEKGVAASVQGGDLADRPFVITINCALPAOLVES  
ELFGHOGKSGTGAATADPGLEFVADGTLFIDEVGLPPLALGPKLRLVLEDGLRRIG

CHRRKRVRLIATNRDLSEVYKAGRFREDLYRINVLTNLPELRQEGDIELLLH  
HTRPGSFDEKALDITWQYMPGPNQVILINVERATLADHOVITMDLPBLSNLP  
SNSGSPASPIHADASHLGDUTCEDPIDESTASAPLPLAGDSSLAYDILKTHVL  
KVLRLQGNKAKTAHLGIRKQYRLRLEPPEQMPAETL"

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/function="two-component signal transduction"  
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gb:AG5806.1; AF305914\_1 (AF305914) HydH [Klebsiella

Query Match 100.0%; Score 14; DB 1; Length 293350;  
Best Local Similarity 78.6%; Pred. No. 3.5e+03;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACTCG 14  
DB 161293 CGTACTGCAACTCG 161280

RESULT 26  
COS54118 65 bp DNA linear PAT 30-JAN-2004  
LOCUS Sequence 23753 from Patent WO0210445.  
DEFINITION COS54118  
ACCESSION COS54118  
VERSION COS54118.1 GI:41520545  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE  
1 Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Faigler, S.  
Oligonucleotide library for detecting rna transcripts and splice  
variants that populate a transcriptome  
Patent: WO 0210449-A 23753 07-FEB-2002;  
Compugen Inc. (US)  
location/Qualifiers  
source 1..65  
/organism="Mus musculus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10090"

FEATURES  
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ORIGIN  
Query Match 92.9%; Score 13; DB 6; Length 65;  
Best Local Similarity 76.9%; Pred. No. 3.3e+04;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCAACTCG 14  
DB 31 GTACTGCAACTCG 43

RESULT 27  
AX988576/c  
LOCUS AX988576 100 bp DNA linear PAT 16-JAN-2004



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DEFINITION Sequence 39 from Patent EP1260592.
ACCESSION AX988576
VERSION AX988576.1 GI:40994900
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1
  AUTHORS Donner,H., Drescher,B., Huber,A. and Weber,J.
  TITLE Biochip
  JOURNAL Patent: EP 1260592-A 39 27-NOV-2002;
  MMG - Biotech AG (DE)
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    /mol_type="unassigned DNA"
    /db_xref="taxon:562"
    /note="y0jh b2211 U00096 complement(2303128_2304774)"
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Query Match          92.9%; Score 13; DB 6; Length 100;
Best Local Similarity 76.9%; Pred. No. 3.1e+04;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCACTCG 14
Db 14 GTACTGCACTCG 2

RESULT 28
AX988577/c
LOCUS AX988577 100 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 40 from Patent EP1260592.
ACCESSION AX988577
VERSION AX988577.1 GI:40994901
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1
  AUTHORS Donner,H., Drescher,B., Huber,A. and Weber,J.
  TITLE Biochip
  JOURNAL Patent: EP 1260592-A 40 27-NOV-2002;
  MMG - Biotech AG (DE)
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ORIGIN
Query Match          92.9%; Score 13; DB 6; Length 100;
Best Local Similarity 76.9%; Pred. No. 3.1e+04;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCACTCG 14
Db 52 GTACTGCACTCG 40

RESULT 29
AF069774
LOCUS AF069774 186 bp mRNA linear ROD 23-JUL-1998
DEFINITION Mus musculus chapayn-110 mRNA, partial cds.
ACCESSION AF069774
VERSION AF069774.1 GI:3335542
KEYWORDS
SOURCE
ORGANISM
  Mus musculus (house mouse)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE
  1 (bases 1 to 186)
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muridea; Muridae; Murinae; Mus.
  AUTHORS Watanabe,M.
  TITLE Mouse chapayn-110 partial cDNA
  JOURNAL Unpublished
  REFERENCE 2 (bases 1 to 186)
  Watanabe,M.
  TITLE Direct Submission
  JOURNAL Submitted (03-JUN-1998) Anatomy, Hokkaido University School of
  Medicine, N15W7, Kita-ku, Sapporo 060-8638, Japan
FEATURES
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    1..186
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    /note="channel-associated protein of synapse-110; similar
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ORIGIN
Query Match          92.9%; Score 13; DB 9; Length 186;
Best Local Similarity 76.9%; Pred. No. 2.9e+04;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCACTCG 14
Db 146 GTACTGCACTCG 158

RESULT 30
TRBPRTNB/c
LOCUS TRBPRTNB 200 bp mRNA linear INV 18-JUL-1994
DEFINITION Trypanosoma brucei clone TDPK-A2 protein kinase mRNA, partial cds.
ACCESSION L10992
VERSION L10992.1 GI:310958
KEYWORDS
SOURCE
  Trypanosoma brucei
  Trypanosoma brucei
  Trypanosoma brucei
  Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;
  Trypanosoma.
REFERENCE
  1 (bases 1 to 200)
  Hua,S.B. and Wang,C.C.
  TITLE Differential accumulation of a protein kinase homolog in
  Trypanosoma brucei
  JOURNAL J. Cell. Biochem. 54 (1), 20-31 (1994)
  PUBMED 8126084
  COMMENT Original source text: Trypanosoma brucei strain TREU667 mRNA.
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ORIGIN APEIIEGSRGHSYEDVWAFGV"

Query Match 92.9%; Score 13; DB 2; Length 200;  
 Best Local Similarity 76.9%; Pred. No. 2.9e+04;  
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13  
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 Db 116 CGTACTGCAACTC 76

RESULT 31  
 AF232912 327 bp mRNA linear PRI 12-MAR-2000  
 LOCUS Macaca mulatta clone MNAV10-1 T-cell receptor alpha chain mRNA,  
 DEFINITION partial cds.  
 ACCESSION AF232912  
 VERSION AF232912.1 GI:7229664  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Macaca mulatta (rhesus monkey)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Cercopithecoidea; Cercopithecinae; Macaca.  
 1 (bases 1 to 327)  
 Han, M., Nhu, Q., Folley, S. and Robinson, M.A.  
 REFERENCE 2 (bases 1 to 327)  
 Han, M., Nhu, Q., Folley, S. and Robinson, M.A.  
 AUTHORS Direct Submission  
 TITLES Submitted (09-FEB-2000) Laboratory of Immunogenetics, NIAID, 12441  
 JOURNAL Parklawn Drive, Rockville, MD 20852, USA  
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 GYLKAG"

ORIGIN

Query Match 92.9%; Score 13; DB 8; Length 327;  
 Best Local Similarity 76.9%; Pred. No. 2.7e+04;  
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13  
 ||:|||||:  
 Db 116 CGTACTGCAACTC 128

RESULT 32  
 AY011660 398 bp DNA linear PRI 07-FEB-2001  
 LOCUS Ateles fusciceps cAMP responsive element moderator (CREM) gene,  
 DEFINITION partial cds.  
 ACCESSION AY011660  
 VERSION AY011660.1 GI:12699921  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Ateles fusciceps (brown-headed spider monkey)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini;  
 Cebidae; Ateleinae; Ateles.  
 1 (bases 1 to 398)

REFERENCE

AUTHORS Murphy, W.J., Bizirik, B., Johnson, W.B., Zhang, Y.P., Ryder, O.A. and O'Brien, S.J.

TITLE Molecular phylogenetics and the origins of placental mammals

JOURNAL Nature 409 (6820), 614-618 (2001)

PubMed 11214319

REFERENCE 2 (bases 1 to 398)  
 Murphy, W.J., Bizirik, B., Johnson, W.B., Zhang, Y.P. and O'Brien, S.J.  
 AUTHORS Direct Submission  
 TITLES Submitted (01-NOV-2000) Laboratory of Genomic Diversity, National  
 JOURNAL Cancer Institute-FCRDC, P.O. Box B, Bldg. 560, Rm. 11-10,  
 Frederick, MD 21702, USA  
 FEATURES  
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ORIGIN

Query Match 92.9%; Score 13; DB 8; Length 398;  
 Best Local Similarity 76.9%; Pred. No. 2.7e+04;  
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCAACUG 14  
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 Db 357 GTACTGCAACTCG 345

RESULT 33  
 MACTCRAAL 406 bp mRNA linear PRI 13-JUN-1995  
 LOCUS Macaca mulatta (clone VA1089) T-cell receptor alpha (TCR A) mRNA,  
 DEFINITION 5' end of cds.  
 ACCESSION L38870  
 VERSION L38870.1 GI:623116  
 KEYWORDS T-cell receptor alpha.  
 SOURCE Macaca mulatta (rhesus monkey)  
 ORGANISM Macaca mulatta  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Cercopithecoidea; Cercopithecinae; Macaca.  
 1 (bases 1 to 406)  
 Chen, Z.W.  
 REFERENCE 1 (bases 1 to 406)  
 Chen, Z.W.  
 AUTHORS Macaca mulatta TCR alpha chain sequences  
 TITLES Unpublished (1995)  
 JOURNAL Original source text: Macaca mulatta cDNA to mRNA.  
 COMMENT  
 FEATURES  
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 1..406  
 /organism="Macaca mulatta"  
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ORIGIN  
Query Match 92.9%; Score 13; DB 8; Length 406;  
Best Local Similarity 76.9%; Pred. No. 2.7e+04;  
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116 CGTACTGCAACTC 128

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RESULT 34  
LOCUS MACTCRAAK 408 bp mRNA linear PRI 13-JAN-1995  
DEFINITION Macaca mulatta (clone VA101) T-cell receptor alpha (TCR A) mRNA, 5'  
end of cds.  
ACCESSION U38869.1 GI:623114  
VERSION T-cell receptor alpha.  
KEYWORDS Macaca mulatta (rhesus monkey)  
SOURCE Macaca mulatta  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Cercopithecoidea; Cercopitheciinae; Macaca.

REFERENCE  
AUTHORS Chen, Z.W.  
TITLE Macaca mulatta TCR alpha chain sequences  
JOURNAL Unpublished (1995)  
COMMENT Original source text: Macaca mulatta cDNA to mRNA.  
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SVFTSLQWRODLPQGVLLVLTGKEMKKQRLTFPGDRKDSLSLHTATQPDCT  
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ORIGIN  
Query Match 92.9%; Score 13; DB 8; Length 406;  
Best Local Similarity 76.9%; Pred. No. 2.7e+04;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
1 CGUACUGCAACTC 13  
116 CGTACTGCAACTC 128

RESULT 34  
LOCUS MACTCRAAK 408 bp mRNA linear PRI 13-JAN-1995  
DEFINITION Macaca mulatta (clone VA101) T-cell receptor alpha (TCR A) mRNA, 5'  
end of cds.  
ACCESSION U38869.1 GI:623114  
VERSION T-cell receptor alpha.  
KEYWORDS Macaca mulatta (rhesus monkey)  
SOURCE Macaca mulatta  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Cercopithecoidea; Cercopitheciinae; Macaca.

REFERENCE  
AUTHORS Chen, Z.W.  
TITLE Macaca mulatta TCR alpha chain sequences  
JOURNAL Unpublished (1995)  
COMMENT Original source text: Macaca mulatta cDNA to mRNA.  
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GYLCADSDSGMQLTRGSGTQLTVPDINQNPDA"

ORIGIN

Query Match 92.9%; Score 13; DB 8; Length 408;  
Best Local Similarity 76.9%; Pred. No. 2.7e+04;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
1 CGUACUGCAACTC 13  
116 CGTACTGCAACTC 128

ORIGIN

Query Match 92.9%; Score 13; DB 8; Length 408;  
Best Local Similarity 76.9%; Pred. No. 2.7e+04;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
1 CGUACUGCAACTC 13  
116 CGTACTGCAACTC 128

RESULT 35  
LOCUS AK111239 580 bp mRNA linear PLN 24-JUL-2003  
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:002-180-C10, full  
insert sequence.  
ACCESSION AK111239  
VERSION AK111239.1 GI:32966448  
KEYWORDS FLI\_CDNA; oligo capping.  
SOURCE Oryza sativa (japonica cultivar-group)

ORIGIN  
Query Match 92.9%; Score 13; DB 8; Length 408;  
Best Local Similarity 76.9%; Pred. No. 2.7e+04;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
1 CGUACUGCAACTC 13  
116 CGTACTGCAACTC 128

ORGANISM  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
SpERMATOPHYTES; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
AUTHORS  
1 The Rice Full-Length cDNA Consortium, National Institute of  
Agrobiological Sciences Rice Full-Length cDNA Project Team;  
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,  
Kishimoto, N., Yasaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,  
Kojima, K., Naito, T., Ohneda, E., Yahagi, M., Suzuki, K., Li, C.,  
Ohtsuka, K., Shishiki, T., Foundation of Advancement of International  
Science Genome Sequencing & Analysis Group, Otsu, Y., Murakami, K.,  
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,  
Kurosaki, T., Kodama, T., Maeda, H., Kobayashi, M., Xie, Q., Lu, M.,  
Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nishida, J.,  
Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Mura, J.,  
Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN,  
Kawai, J., Carrinci, P., Adachi, J., Aizawa, K., Arikawa, T., Fukuda, S.,  
Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,  
Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Otsu, N., Ota, Y.,  
Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,  
Yoshino, M., and Hayashizaki, Y.  
Collection, mapping, and annotation of over 28,000 cDNA clones from  
japonica rice  
Science 301 (5631), 376-379 (2003)  
12869764  
2 (bases 1 to 580)  
Adachi, J., Aizawa, K., Arikawa, T., Carrinci, P., Doi, K.,  
Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,  
Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hirooka, T.,  
Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K.,  
Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I.,  
Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M.,  
Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,  
Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Konda, M.,  
Koye, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M.,  
Maeda, H., Matsubara, K., Matsuyama, T., Mura, J., Miyazaki, A.,  
Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M.,  
Naito, T., Narikawa, R., Nishikawa, R., Nishikawa, M., Nishikawa, K.,  
Nunakami, R., Ohneda, E., Ohno, M., Ohtsuka, K., Oka, M., Ooka, H.,  
Otsu, N., Ota, Y., Otsu, Y., Ryu, R., Saitoh, K., Sakai, C., Sakai, K.,  
Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K.,  
Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S.,  
Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami, T., Tagami, Y.,  
Tagawa, A., Takahashi, F., Takaku-Akashiri, S., Tanaka, T., Tomaru, A.,  
Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, M.,  
Yamada, H., Yamamoto, M., Yasunishi, A., Yasaki, J., Yokomizo, S. and  
Yoshimura, A.  
Direct Submission  
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of  
Agrobiological Sciences, Department of Molecular Genetics, Head of  
Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki  
305-8602, Japan (E-mail: shikuchi@nias.affrc.go.jp,  
Tel:81-29-838-7007, Fax:81-29-838-7007)  
This clone is one of the 28K full-length cDNA clones from japonica  
rice.  
URL : <http://cdna01.dna.affrc.go.jp/cDNA/>  
NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,  
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yasaki, J.,  
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Naito, T.,  
Ohneda, E., Yahagi, M., Suzuki, K., Li, C., Ohtsuka, K., Shishiki, T. and  
Yamamoto, M.  
FAIS Genome Sequencing & Analysis Group: Otsu, Y., Iida, Y.,  
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,  
Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Maeda, H., Mura, J.,  
Mizuno, K., Narikawa, R., Nishikawa, R., Nishikawa, M., Nishikawa, K.,  
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,  
Yoshimura, A., Matsubara, K. and Murakami, K.  
Genome Exploration Research Group in Riken Genomic Sciences Center  
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,  
Arikawa, T., Carrinci, P., Fukuda, S., Hanagaki, T.,  
Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,  
Hirooka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,





than 100 NOS bases or with SNP rate > 0.01 were discarded. To exclude alignment between two copies of a single read, comparisons between two reads that share 95% of their genome alignments (>=95% bases of read A and >=95% bases of read B were placed at the same locus of human genome) were discarded.

## FEATURES

source

Location/Qualifiers  
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/mol\_type="genomic DNA"  
/sub\_species="troglodytes"  
/db\_xref="taxon:37011"  
/clone\_1ib="Noemie"  
<1..>742

## ORIGIN

STS

Query Match 92.9%; Score 13; DB 10; Length 742;  
Best Local Similarity 76.9%; Pred. No. 2.5e+04;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13  
||:|||||:  
278 CGTACTGCAACTC 266

Db 278 CGTACTGCAACTC 266

RESULT 40  
BV530657

768 bp DNA linear STS 08-APR-2005

LOCUS G591P617906R7.T0 Clint Pan troglodytes versu STS genomic, sequence

DEFINITION

tagged site.

ACCESSION BV530657

GI:62408441

VERSION

STS.

KEYWORDS

Pan troglodytes versu

ORGANISM

Pan troglodytes versu

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

TITLE

Homidae; Pan.

JOURNAL

Initial Sequence of the Chimpanzee Genome and Comparison with the

COMMENT

Human Genome

Unpublished (2005)

Contact: Michael C. Zody

Broad Institute of MIT and Harvard

320 Charles Street, Cambridge, MA 02141, USA

Tel: 6172580933

Fax: 6172580903

Email: mczody@road.mit.edu

Primer A: No sequence submitted

Primer B: No sequence submitted

STS size: 768

Protocol:

23,021,928 chimpanzee whole genome shotgun reads were aligned to

the Human genome NCBI

Build 34 (hg16, July 2003). Chimp WGS reads were from 9 donors,

including Clint (Pan

troglodytes versu), 3 other Pan troglodytes versu chimps

(Donald, Karlien, Yvonne), 3 Pan troglodytes versu chimps

(troglodytes troglodytes chimps (Noemie, Masuku, Clara) and 2 chimps

of unknown origin

(Gon, Unknown Chimp). Common names: Pan troglodytes versu is the

western chimp and Pan

troglodytes troglodytes is the central chimp. To be included in

chimpanzee SNP discovery, a

read must be at least 500bp in length, at least 50% of its base

calls must have Phred

score >= 20, at least 30% of its base calls must satisfy

SNOS(30,25) (single strand NOS, the

base in question has Phred score >= 30, the surrounding 10 bases in

the read have Phred

score >= 25), and the read must have at least 200 bp SNOS(30,25)

bases. Reads not uniquely

placed in the genome and read pairs whose two ends were not

consistently placed were

discarded. After above filtering, NOS(30,25) standard was applied

to all pairs of

overlapping reads to call NOS bases and SNPs. Alignments (between

two reads) with less

than 100 NOS bases or with SNP rate > 0.01 were discarded. To

exclude alignment between two

copies of a single read, comparisons between two reads that share

95% of their genome

alignments (>=95% bases of read A and >=95% bases of read B were

placed at the same locus

of human genome) were discarded.

Location/Qualifiers  
1..768  
/organism="Pan troglodytes versu"  
/mol\_type="genomic DNA"  
/sub\_species="versu"  
/db\_xref="taxon:37012"  
/clone\_1ib="Clint"  
<1..>768

Query Match 92.9%; Score 13; DB 10; Length 768;  
Best Local Similarity 76.9%; Pred. No. 2.5e+04;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCAACUCG 14  
||:|||||:  
701 GTACTGCAACTCG 713

Db 701 GTACTGCAACTCG 713

RESULT 41

BV530662

773 bp DNA linear STS 08-APR-2005

LOCUS G591P617904R12.T0 Clint Pan troglodytes versu STS genomic,

sequence tagged site.

ACCESSION BV530662

GI:62408446

VERSION

STS.

KEYWORDS

Pan troglodytes versu

Pan troglodytes versu

Pan troglodytes versu

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Pan.

1 (bases 1 to 773)

Mikkelsen,T.S., Hillier,W.L., Eichler,E.B., Zody,M.C. and

Jaffe,D.B.

Initial Sequence of the Chimpanzee Genome and Comparison with the

Human Genome

Unpublished (2005)

Contact: Michael C. Zody

Broad Institute of MIT and Harvard

320 Charles Street, Cambridge, MA 02141, USA

Tel: 6172580933

Fax: 6172580903

Email: mczody@road.mit.edu

Primer A: No sequence submitted

Primer B: No sequence submitted

STS size: 773

Protocol:

23,021,928 chimpanzee whole genome shotgun reads were aligned to

the Human genome NCBI

Build 34 (hg16, July 2003). Chimp WGS reads were from 9 donors,

including Clint (Pan

troglodytes versu), 3 other Pan troglodytes versu chimps

(Donald, Karlien, Yvonne), 3 Pan

troglodytes troglodytes chimps (Noemie, Masuku, Clara) and 2 chimps

of unknown origin

(Gon,Unknown Chimp). Common names: Pan troglodytes verus is the western chimp and Pan troglodytes troglodytes is the central chimp. To be included in chimpanzee SNP discovery, a read must be at least 500bp in length, at least 50% of its base calls must have Phred score  $\geq 20$ , at least 30% of its base calls must satisfy SNOS(30,25) (single strand NOS, the base in question has Phred score  $\geq 30$ , the surrounding 10 bases in the read have Phred score  $\geq 25$ ), and the read must have at least 200 bp SNOS(30,25) bases. Reads not uniquely placed in the genome and read pairs whose two ends were not consistently placed were discarded. After above filtering, NOS(30,25) standard was applied to all pairs of overlapping reads to call NOS bases and SNPs. Alignments (between two reads) with less than 100 NOS bases or with SNP rate  $> 0.01$  were discarded. To exclude alignment between two copies of a single read, comparisons between two reads that share 95% of their genome alignments ( $\geq 95\%$  bases of read A and  $\geq 95\%$  bases of read B were placed at the same locus of human genome) were discarded.

FEATURES  
source  
1. .773  
/organism="Pan troglodytes verus"  
/mol\_type="genomic DNA"  
/sub\_species="verus"  
/db\_xref="taxon:37012"  
/clone\_1fb="Clint"  
<1. .>773

ORIGIN  
STS

Query Match 92.9%; Score 13; DB 10; Length 773;  
Best Local Similarity 76.9%; Pred. No. 2.5e+04;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCAACG 14  
Db 711 GTRCTGCACTCG 723

RESULT 42  
BV530664 774 bp DNA linear STS 08-APR-2005  
LOCUS GS918617902RB6.T0 Clint Pan troglodytes verus STS genomic, sequence  
tagged site.  
ACCESSION BV530664  
VERSION BV530664.1 GI:62408448  
KEYWORDS STS.  
SOURCE Pan troglodytes verus  
ORGANISM Pan troglodytes verus  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Pan.  
1 (bases 1 to 774)  
Mikkelsen,T.S., Hillier,W.L., Richler,E.B., Zody,M.C. and Ulfte,D.B.  
Initial Sequence of the Chimpanzee Genome and Comparison with the Human Genome  
Unpublished (2005)

JOURNAL COMMENT  
Contact: Michael C. Zody  
Broad Institute of MIT and Harvard  
320 Charles Street, Cambridge, MA 02141, USA  
Tel: 6172580933  
Fax: 6172580903  
Email: mczody@broad.mit.edu  
Primer A: No sequence submitted  
Primer B: No sequence submitted  
STS size: 774

Protocol:  
23,021,928 chimpanzee whole genome shotgun reads were aligned to the Human genome NCBI Build 34 (hg16, July 2003). Chimp WGS reads were from 9 donors, including Clint (Pan troglodytes verus), 3 other Pan troglodytes verus chimps (Donald,Karlin,Yvonne), 3 Pan troglodytes troglodytes chimps (Noemie,Masuku,Clara) and 2 chimps of unknown origin (Gon,Unknown Chimp). Common names: Pan troglodytes verus is the western chimp and Pan troglodytes troglodytes is the central chimp. To be included in chimpanzee SNP discovery, a read must be at least 500bp in length, at least 50% of its base calls must have Phred score  $\geq 20$ , at least 30% of its base calls must satisfy SNOS(30,25) (single strand NOS, the base in question has Phred score  $\geq 30$ , the surrounding 10 bases in the read have Phred score  $\geq 25$ ), and the read must have at least 200 bp SNOS(30,25) bases. Reads not uniquely placed in the genome and read pairs whose two ends were not consistently placed were discarded. After above filtering, NOS(30,25) standard was applied to all pairs of overlapping reads to call NOS bases and SNPs. Alignments (between two reads) with less than 100 NOS bases or with SNP rate  $> 0.01$  were discarded. To exclude alignment between two copies of a single read, comparisons between two reads that share 95% of their genome alignments ( $\geq 95\%$  bases of read A and  $\geq 95\%$  bases of read B were placed at the same locus of human genome) were discarded.

FEATURES  
source

1. .774  
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/mol\_type="genomic DNA"  
/sub\_species="verus"  
/db\_xref="taxon:37012"  
/clone\_1fb="Clint"  
<1. .>774

ORIGIN  
STS

Query Match 92.9%; Score 13; DB 10; Length 774;  
Best Local Similarity 76.9%; Pred. No. 2.5e+04;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCAACG 14  
Db 707 GTRCTGCACTCG 719

RESULT 43  
D64054 939 bp mRNA linear VRT 01-FEB-2000  
LOCUS Myxine glutinosa mRNA for IMPX of hagfish, complete cds.  
DEFINITION D64054  
ACCESSION D64054.1 GI:1405320  
VERSION D64054.1  
KEYWORDS low molecular mass polypeptide, IMPX.  
SOURCE Myxine glutinosa (Atlantic hagfish)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Hyperoetretti; Myxiniiformes; Myxiniidae; Myxiniinae; Myxine.

JOURNAL COMMENT  
1 (bases 1 to 939)  
Kandil,B., Namlkawa,C., Nomaka,M., Greenberg,A.S., Flajnik,M.F., Ishibashi,T. and Kasahara,M.  
Isolation of low molecular mass polypeptide complementary DNA clones from primitive vertebrates. Implications for the origin of MHC class I-restricted antigen presentation  
J. Immunol. 156 (11), 4245-4253 (1996)  
PUBMED 8666794  
REFERENCE 2 (bases 1 to 939)





PI TOSHIRO MITSUNAGA, YASUHIRO TANAKA, TOYOKAZU YOSHIDA, PI  
KATSUMI MATAMABE  
PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/02, PC  
C12N15/00, C12N5/00  
CC  
FH Key Location/Qualifiers  
FT Source 1. .1197  
FT /organism="Hyphomicrobium sp."'  
Location/Qualifiers  
1. .1197  
/organism="Hyphomicrobium sp."'  
/mol\_type="genomic DNA"  
/db\_xref="taxon:82"

## ORIGIN

Query Match 92.9%; Score 13; DB 6; Length 1197;  
Best Local Similarity 76.9%; Pred. No. 2.4e+04;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGUACUGCAACUC 13  
||:|||||:  
Db 431 CGTACTGCAACTC 443

RESULT 46 1241 bp DNA linear BCT 15-APR-2005  
LOCUS Klebsiella pneumoniae ompK36 gene, strain 103624.  
DEFINITION AJ344089  
ACCESSION AJ344089  
VERSION AJ344089.2 GI:21912942  
KEYWORDS ompK36 gene; OmpK36 protein; porin.  
SOURCE Klebsiella pneumoniae  
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
Enterobacteriaceae; Klebsiella.

REFERENCE 1  
AUTHORS Crowley, B., Benedi, V.J. and Domenech-Sanchez, A.  
TITLE Expression of SHV-2 beta-lactamase and of reduced amounts of OmpK36  
porin in Klebsiella pneumoniae results in increased resistance to  
cephalosporins and carbapenems  
JOURNAL Antimicrob. Agents Chemother. 46 (11), 3679-3682 (2002)  
PUBMED 12384391

REFERENCE 2  
AUTHORS Domenech-Sanchez, A.  
TITLE Direct Submision  
JOURNAL Submitted (09-AUG-2001) Domenech-Sanchez A., Biologia, Area de  
Microbiologia, Universitat de les Illes Balears and IMEDDA  
(CSIC-UIB), Carretera de Valldemossa, km 7,5; Palma de Mallorca,  
07071, SPAIN

REMARK 3 (bases 1 to 1241)  
REFERENCE Domenech-Sanchez, A.  
AUTHORS Direct Submision  
JOURNAL Submitted (15-JUL-2002) Domenech-Sanchez A., Biologia, Area de  
Microbiologia, Universitat de les Illes Balears and IMEDDA  
(CSIC-UIB), Carretera de Valldemossa, km 7,5; Palma de Mallorca,  
07071, SPAIN

COMMENT On Jul 20, 2002 this sequence version replaced gi:15149830.  
FEATURES  
source  
Location/Qualifiers  
1. .1241  
/organism="Klebsiella pneumoniae"  
/mol\_type="genomic DNA"  
/isolate="103624"  
/db\_xref="taxon:573"  
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117. .1235  
/gene="ompK36"  
117. .1235  
/gene="ompK36"  
/function="porin"  
/codon\_start=11  
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/product="OmpK36 protein"

gene  
CDS

## ORIGIN

sig\_peptide  
mat\_peptide

/protein\_id="CAC50885.1"  
/db\_xref="GI:15149831"  
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/db\_xref="InterPro:IPR001702"  
/db\_xref="InterPro:IPR001897"  
/db\_xref="InterPro:IPR003229"  
/db\_xref="UniProt/TREMBL:Q93K39"  
/translation="MKVKVLSILVPAALVAGAAANAALYNNKDGNTLDYGIQGLHYF  
SDKSDVGGQFTMRGVKGETQINDLQYGGMEYNOANTSSSSDAQMTLAPAGL  
KRGDAGSPDYGNGVGVVYDVMSMTDLPFGDGTGSDNPLQSRANGVATVNSDFG  
LYDGLNPLQYGRKNGSISGRTSPNNRGLKONGGPGFQSLYDYDLSAGPAY  
CNSKNGQDNRLDKRGDGNARTYTGKLTDAANNITLATOYTATNATPSGSGSDSI  
SGFANKAQNFEVVAQYQDFGLRPSVAALQSGKQIEGQDDLLKLYDVGVATYFENK  
NMSTVYDYKIMLDNDNDFTRSAGISTDVALGLVYQF"  
117. .179  
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180. .1232  
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Query Match 92.9%; Score 13; DB 1; Length 1241;  
Best Local Similarity 76.9%; Pred. No. 2.4e+04;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CGUACUGCAACUC 13  
||:|||||:  
Db 766 CGTACTGCAACTC 778

RESULT 47 1330 bp DNA linear BCT 06-JUN-2003  
LOCUS Enterobacter sp. 22 partial 16S rRNA gene, isolate 22.  
DEFINITION AJ308467  
ACCESSION AJ308467  
VERSION AJ308467.1 GI:15551737  
KEYWORDS 16S ribosomal RNA; 16S rRNA gene.  
SOURCE Enterobacter sp. 22  
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
Enterobacteriaceae; Enterobacter.

REFERENCE 1  
AUTHORS Soutourina, O.A., Semenova, E.A., Parfenova, V.V., Danchin, A. and  
Berlin, P.  
TITLE Control of bacterial motility by environmental factors in polarly  
flagellated and peritrichous bacteria isolated from Lake Baikal  
JOURNAL Appl. Environ. Microbiol. 67 (9), 3852-3859 (2001)  
PUBMED 11525977

REFERENCE 2 (bases 1 to 1330)  
REFERENCE Soutourina, O.A.  
AUTHORS Direct Submision  
JOURNAL Submitted (06-FEB-2001) Soutourina O.A., Biochimie et genetique  
moleculaire, Pasteur Institute, Institut Pasteur, 28, rue du Dr.  
Roux, 75724 Paris cedex 15, FRANCE

FEATURES  
source  
Location/Qualifiers  
1. .1330  
/organism="Enterobacter sp. 22"  
/mol\_type="genomic DNA"  
/isolate="22"  
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/country="Russia:Lake Baikal"  
1. .1330  
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1. .1330  
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/product="16S ribosomal RNA"

gene  
RNA

## ORIGIN

Query Match 92.9%; Score 13; DB 1; Length 1330;  
Best Local Similarity 76.9%; Pred. No. 2.3e+04;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCACTCG 14  
 Db 1250 GTACTGCACTCG 1262

RESULT 48  
 AY985960  
 LOCUS  
 DEFINITION Uncultured bacterium clone D259 16S ribosomal RNA gene, partial  
 sequence.

ACCESSION AY985960  
 VERSION AY985960.1 GI:62765450  
 KEYWORDS ENV.  
 SOURCE uncultured bacterium  
 ORGANISM Bacteria; environmental samples.

REFERENCE 1 (bases 1 to 1347)  
 Eckburg,P.B., Bik,E.M., Bernstein,C.N., Purdom,E., Dethlefsen,L., Sargent,M., Gill,S.R., Nelson,K.E. and Relman,D.A.  
 Diversity of the human intestinal microbial flora

TITLE Unpublished  
 JOURNAL 2 (bases 1 to 1347)  
 Eckburg,P.B., Bik,E.M., Bernstein,C.N., Purdom,E., Dethlefsen,L., Sargent,M., Gill,S.R., Nelson,K.E. and Relman,D.A.  
 Direct Submission

REFERENCE Submitted (28-MAR-2005) Division of Infectious Diseases & Geographic Medicine, Stanford University School of Medicine, 300 Pasteur Drive, Palo Alto, CA 94305, USA

FEATURES  
 source  
 1.1347  
 /organism="uncultured bacterium"  
 /mol\_type="genomic DNA"  
 /isolation\_source="from human stool sample"  
 /db\_xref="taxon:77133"  
 /clone="D259"  
 /environmental\_sample  
 <1.>1347  
 /product="16S ribosomal RNA"

ORIGIN  
 rRNA  
 Query Match 92.9%; Score 13; DB 3; Length 1347;  
 Best Local Similarity 76.9%; Pred. No. 2.3e+04;  
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCACTCG 14  
 Db 1268 GTACTGCACTCG 1280

RESULT 49  
 AY985162  
 LOCUS  
 DEFINITION Uncultured bacterium clone BB86 16S ribosomal RNA gene, partial  
 sequence.

ACCESSION AY985162  
 VERSION AY985162.1 GI:62764652  
 KEYWORDS ENV.  
 SOURCE uncultured bacterium  
 ORGANISM Bacteria; environmental samples.

REFERENCE 1 (bases 1 to 1356)  
 Eckburg,P.B., Bik,E.M., Bernstein,C.N., Purdom,E., Dethlefsen,L., Sargent,M., Gill,S.R., Nelson,K.E. and Relman,D.A.  
 Diversity of the human intestinal microbial flora

TITLE Unpublished  
 JOURNAL 2 (bases 1 to 1356)  
 Eckburg,P.B., Bik,E.M., Bernstein,C.N., Purdom,E., Dethlefsen,L., Sargent,M., Gill,S.R., Nelson,K.E. and Relman,D.A.  
 Direct Submission

REFERENCE Submitted (28-MAR-2005) Division of Infectious Diseases & Geographic Medicine, Stanford University School of Medicine, 300 Pasteur Drive, Palo Alto, CA 94305, USA

FEATURES  
 Location/Qualifiers

source  
 1.1356  
 /organism="uncultured bacterium"  
 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:77133"  
 /clone="BB86"  
 /environmental\_sample  
 <1.>1356  
 /product="16S ribosomal RNA"

ORIGIN  
 rRNA  
 Query Match 92.9%; Score 13; DB 3; Length 1356;  
 Best Local Similarity 76.9%; Pred. No. 2.3e+04;  
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCACTCG 14  
 Db 1277 GTACTGCACTCG 1289

RESULT 50  
 AY986117  
 LOCUS  
 DEFINITION Uncultured bacterium clone D458 16S ribosomal RNA gene, partial  
 sequence.

ACCESSION AY986117  
 VERSION AY986117.1 GI:62765607  
 KEYWORDS ENV.  
 SOURCE uncultured bacterium  
 ORGANISM Bacteria; environmental samples.

REFERENCE 1 (bases 1 to 1357)  
 Eckburg,P.B., Bik,E.M., Bernstein,C.N., Purdom,E., Dethlefsen,L., Sargent,M., Gill,S.R., Nelson,K.E. and Relman,D.A.  
 Diversity of the human intestinal microbial flora

TITLE Unpublished  
 JOURNAL 2 (bases 1 to 1357)  
 Eckburg,P.B., Bik,E.M., Bernstein,C.N., Purdom,E., Dethlefsen,L., Sargent,M., Gill,S.R., Nelson,K.E. and Relman,D.A.  
 Direct Submission

REFERENCE Submitted (28-MAR-2005) Division of Infectious Diseases & Geographic Medicine, Stanford University School of Medicine, 300 Pasteur Drive, Palo Alto, CA 94305, USA

FEATURES  
 source  
 1.1357  
 /organism="uncultured bacterium"  
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 /db\_xref="taxon:77133"  
 /clone="D458"  
 /environmental\_sample  
 <1.>1357  
 /product="16S ribosomal RNA"

ORIGIN  
 rRNA  
 Query Match 92.9%; Score 13; DB 3; Length 1357;  
 Best Local Similarity 76.9%; Pred. No. 2.3e+04;  
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUACUGCACTCG 14  
 Db 1277 GTACTGCACTCG 1289

Search completed: March 18, 2006, 19:22:18  
 Job time : 800.308 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 18:35:44 ; Search time 1195.62 Seconds  
(without alignments)  
35.104 Million cell updates/sec

Title: US-10-800-926-1

Perfect score: 18

Sequence: 1 agagggugcagcgsgua 18

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 8023312 seqs, 115852854 residues 16046624

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications NA.New:\*  
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2: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
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7: /cgn2\_6/ptodata/1/pubpna/US13\_NEW\_PUB.seq:\*  
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10: /cgn2\_6/ptodata/1/pubpna/US16\_NEW\_PUB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US17\_NEW\_PUB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US18\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US19\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	18	100.0	18 US-10-619-279-60	Sequence 60, Appl
2	18	100.0	18 US-11-127-654-4	Sequence 4, Appl
3	15	83.3	18 US-10-497-591A-41	Sequence 41, Appl
4	15	83.3	22 US-10-310-914A-990315	Sequence 990315, Appl
5	15	83.3	7 US-10-981-334-21	Sequence 31, Appl
6	15	83.3	2162 US-11-091-883-330	Sequence 330, Appl
7	14.8	82.2	2106 US-10-750-185-55765	Sequence 55765, A
8	14.8	82.2	2106 US-10-750-623-55765	Sequence 55765, A
9	14.4	80.0	1411 US-10-750-185-37497	Sequence 37497, A
10	14.4	80.0	1411 US-10-750-623-37497	Sequence 37497, A
11	14	77.8	25 US-11-121-849-531952	Sequence 531952, A
12	14	77.8	600 US-10-750-185-4096	Sequence 4096, A
13	14	77.8	600 US-10-750-623-4096	Sequence 4096, A
14	14	77.8	1454 US-09-925-065A-552179	Sequence 552179, A
15	13.8	76.7	426 US-09-925-065A-649799	Sequence 649799, A
16	13.8	76.7	426 US-09-925-065A-99074	Sequence 99074, A
17	13.8	76.7	577 US-09-925-065A-151643	Sequence 151643, A
18	13.8	76.7	577 US-09-925-065A-151644	Sequence 151644, A
19	13.8	76.7	577 US-09-925-065A-151645	Sequence 151645, A
20	13.8	76.7	1490 US-11-096-568A-18587	Sequence 18587, A

21	13.8	76.7	1492 US-09-925-065A-709998	Sequence 709998, A
22	13.8	76.7	6866 US-10-240-708-20	Sequence 20, Appl
23	13.4	74.4	566 US-09-925-065A-74944	Sequence 74944, A
24	13.4	74.4	580 US-09-925-065A-46507	Sequence 46507, A
25	13.4	74.4	589 US-09-925-065A-299863	Sequence 299863, A
26	13.4	74.4	605 US-09-925-065A-47629	Sequence 47629, A
27	13.4	74.4	1185 US-11-136-527-1781	Sequence 1781, A
28	13.4	74.4	1213 US-10-750-185-62892	Sequence 62892, A
29	13.4	74.4	1213 US-10-750-623-62892	Sequence 62892, A
30	13.4	74.4	2954 US-11-171-701-1	Sequence 1, Appl
31	13.4	74.4	4663 US-10-912-971-1	Sequence 1, Appl
32	13.4	74.4	17384 US-11-082-154A-118	Sequence 118, Appl
33	13.4	74.4	22118 US-11-082-154A-18	Sequence 18, Appl
34	13.2	73.3	25 US-11-121-849-355753	Sequence 355753, A
35	13.2	73.3	25 US-10-933-982-106785	Sequence 106785, A
36	13.2	73.3	479 US-09-925-065A-290116	Sequence 290116, A
37	13.2	73.3	514 US-09-925-065A-354563	Sequence 354563, A
38	13.2	73.3	526 US-09-925-065A-143833	Sequence 143833, A
39	13.2	73.3	526 US-09-925-065A-143834	Sequence 143834, A
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42	13.2	73.3	550 US-09-925-065A-505693	Sequence 505693, A
43	13.2	73.3	584 US-09-925-065A-839454	Sequence 839454, A
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163	12.8	71.1	441	6	US-09-925-065A-496612	Sequence 496612,
164	12.8	71.1	441	6	US-09-925-065A-496613	Sequence 496613,
165	12.8	71.1	441	6	US-09-925-065A-496614	Sequence 496614,
166	12.8	71.1	441	6	US-09-925-065A-496615	Sequence 496615,

C 240	12.4	68.9	1279	8	US-10-750-623-44120	Sequence 44120, A	C 313	12.2	67.8	201	12	US-11-124-367A-21677	Sequence 21677, A
C 241	12.4	68.9	1290	9	US-11-096-568A-7839	Sequence 7839, Ap	C 314	12.2	67.8	201	12	US-11-124-367A-21679	Sequence 21679, A
C 242	12.4	68.9	1416	7	US-10-932-182A-3167	Sequence 3167, Ap	C 315	12.2	67.8	201	12	US-11-124-367A-21763	Sequence 21763, A
C 243	12.4	68.9	1416	7	US-10-932-182A-3167	Sequence 3167, Ap	C 316	12.2	67.8	201	12	US-11-124-367A-21767	Sequence 21767, A
C 244	12.4	68.9	1450	6	US-09-925-065A-683380	Sequence 683380, A	C 317	12.2	67.8	318	8	US-10-467-657-2857	Sequence 2857, Ap
C 245	12.4	68.9	1450	6	US-09-925-065A-683381	Sequence 683381, A	C 318	12.2	67.8	318	8	US-10-467-657-5709	Sequence 5709, Ap
C 246	12.4	68.9	1450	6	US-09-925-065A-683382	Sequence 683382, A	C 319	12.2	67.8	354	8	US-10-467-657-5107	Sequence 5107, Ap
C 247	12.4	68.9	1552	9	US-11-096-568A-12907	Sequence 12907, A	C 320	12.2	67.8	408	8	US-10-467-657-6107	Sequence 6107, Ap
C 248	12.4	68.9	1552	9	US-09-925-065A-61328	Sequence 61328, A	C 321	12.2	67.8	409	6	US-09-925-065A-8487612	Sequence 8487612, A
C 249	12.4	68.9	1643	6	US-09-925-065A-61329	Sequence 61329, A	C 322	12.2	67.8	433	6	US-09-925-065A-845068	Sequence 845068, A
C 250	12.4	68.9	1643	6	US-09-925-065A-548208	Sequence 548208, A	C 323	12.2	67.8	455	6	US-09-925-065A-289024	Sequence 289024, A
C 251	12.4	68.9	1643	6	US-09-925-065A-718277	Sequence 718277, A	C 324	12.2	67.8	456	6	US-09-925-065A-623177	Sequence 623177, A
C 252	12.4	68.9	1678	6	US-09-925-065A-70558	Sequence 70558, A	C 325	12.2	67.8	459	6	US-09-925-065A-507827	Sequence 507827, A
C 253	12.4	68.9	1678	6	US-09-925-065A-70559	Sequence 70559, A	C 326	12.2	67.8	464	6	US-09-925-065A-501353	Sequence 501353, A
C 254	12.4	68.9	1678	6	US-09-925-065A-70560	Sequence 70560, A	C 327	12.2	67.8	471	8	US-10-467-657-4359	Sequence 4359, Ap
C 255	12.4	68.9	1698	8	US-10-467-657-3301	Sequence 3301, Ap	C 328	12.2	67.8	475	6	US-09-925-065A-778034	Sequence 778034, A
C 256	12.4	68.9	1725	8	US-10-821-234-772	Sequence 772, Ap	C 329	12.2	67.8	489	6	US-09-925-065A-142400	Sequence 142400, A
C 257	12.4	68.9	1864	9	US-11-096-568A-22131	Sequence 22131, A	C 330	12.2	67.8	492	6	US-09-925-065A-500711	Sequence 500711, A
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C 260	12.4	68.9	2005	9	US-11-072-512-175	Sequence 175, Ap	C 333	12.2	67.8	494	6	US-09-925-065A-153218	Sequence 153218, A
C 261	12.4	68.9	2319	12	US-11-024-959-162	Sequence 162, Ap	C 334	12.2	67.8	497	6	US-09-925-065A-843463	Sequence 843463, A
C 262	12.4	68.9	2534	6	US-09-925-065A-76182	Sequence 76182, A	C 335	12.2	67.8	498	6	US-09-925-065A-729564	Sequence 729564, A
C 263	12.4	68.9	2537	6	US-09-925-065A-715287	Sequence 715287, A	C 336	12.2	67.8	498	6	US-09-925-065A-729564	Sequence 729564, A
C 264	12.4	68.9	2537	6	US-09-925-065A-715288	Sequence 715288, A	C 337	12.2	67.8	503	6	US-09-925-065A-115416	Sequence 115416, A
C 265	12.4	68.9	2908	12	US-11-136-527-3781	Sequence 3781, Ap	C 338	12.2	67.8	510	6	US-09-925-065A-796498	Sequence 796498, A
C 266	12.4	68.9	3870	8	US-10-947-249-58	Sequence 58, Ap	C 339	12.2	67.8	517	6	US-09-925-065A-618287	Sequence 618287, A
C 267	12.4	68.9	4185	8	US-10-821-234-196	Sequence 196, Ap	C 340	12.2	67.8	517	6	US-09-925-065A-443551	Sequence 443551, A
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C 271	12.4	68.9	78698	12	US-11-075-185-1	Sequence 1, Ap	C 344	12.2	67.8	519	6	US-09-925-065A-555395	Sequence 555395, A
C 272	12.4	68.9	150437	12	US-11-112-908-44	Sequence 44, Ap	C 345	12.2	67.8	521	6	US-09-925-065A-879076	Sequence 879076, A
C 273	12.4	68.9	150491	12	US-11-112-908-46	Sequence 46, Ap	C 346	12.2	67.8	523	6	US-09-925-065A-859457	Sequence 859457, A
C 274	12.4	68.9	155515	12	US-11-112-908-42	Sequence 42, Ap	C 347	12.2	67.8	524	6	US-09-925-065A-484219	Sequence 484219, A
C 275	12.4	68.9	164810	12	US-11-121-086-4	Sequence 4, Ap	C 348	12.2	67.8	526	6	US-09-925-065A-484220	Sequence 484220, A
C 276	12.4	68.9	175100	12	US-11-121-086-21	Sequence 21, Ap	C 349	12.2	67.8	526	6	US-09-925-065A-563087	Sequence 563087, A
C 277	12.4	68.9	177623	12	US-11-112-908-41	Sequence 41, Ap	C 350	12.2	67.8	530	6	US-09-925-065A-430408	Sequence 430408, A
C 278	12.4	68.9	179587	12	US-11-121-086-91	Sequence 91, Ap	C 351	12.2	67.8	530	6	US-09-925-065A-430409	Sequence 430409, A
C 279	12.4	68.9	189933	12	US-11-121-086-78	Sequence 78, Ap	C 352	12.2	67.8	530	6	US-09-925-065A-430410	Sequence 430410, A
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C 281	12.2	67.8	18	8	US-10-310-914A-980300	Sequence 980300, A	C 354	12.2	67.8	532	6	US-09-925-065A-146812	Sequence 146812, A
C 282	12.2	67.8	20	8	US-10-310-914A-706996	Sequence 706996, A	C 355	12.2	67.8	532	6	US-09-925-065A-768925	Sequence 768925, A
C 283	12.2	67.8	21	8	US-10-310-914A-145151	Sequence 145151, A	C 356	12.2	67.8	536	6	US-09-925-065A-210092	Sequence 210092, A
C 284	12.2	67.8	21	8	US-10-310-914A-564470	Sequence 564470, A	C 357	12.2	67.8	537	6	US-09-925-065A-788540	Sequence 788540, A
C 285	12.2	67.8	21	8	US-10-310-914A-706997	Sequence 706997, A	C 358	12.2	67.8	539	6	US-09-925-065A-138899	Sequence 138899, A
C 286	12.2	67.8	21	8	US-10-310-914A-1062689	Sequence 1062689, A	C 359	12.2	67.8	539	6	US-09-925-065A-628088	Sequence 628088, A
C 287	12.2	67.8	24	8	US-10-310-914A-145332	Sequence 145332, A	C 360	12.2	67.8	540	6	US-09-925-065A-572179	Sequence 572179, A
C 288	12.2	67.8	25	7	US-10-933-982-204585	Sequence 204585, A	C 361	12.2	67.8	540	6	US-09-925-065A-773556	Sequence 773556, A
C 289	12.2	67.8	25	7	US-10-934-048A-93793	Sequence 93793, A	C 362	12.2	67.8	540	6	US-09-925-065A-849238	Sequence 849238, A
C 290	12.2	67.8	25	12	US-11-121-849-306385	Sequence 306385, A	C 363	12.2	67.8	545	6	US-09-925-065A-458435	Sequence 458435, A
C 291	12.2	67.8	25	12	US-11-121-849-306386	Sequence 306386, A	C 364	12.2	67.8	546	6	US-09-925-065A-167379	Sequence 167379, A
C 292	12.2	67.8	25	12	US-11-121-849-306387	Sequence 306387, A	C 365	12.2	67.8	548	6	US-09-925-065A-279513	Sequence 279513, A
C 293	12.2	67.8	25	12	US-11-121-849-380723	Sequence 380723, A	C 366	12.2	67.8	549	6	US-09-925-065A-228685	Sequence 228685, A
C 294	12.2	67.8	25	12	US-11-136-527-316667	Sequence 316667, A	C 367	12.2	67.8	550	6	US-09-925-065A-402156	Sequence 402156, A
C 295	12.2	67.8	201	8	US-10-995-561-13632	Sequence 13632, A	C 368	12.2	67.8	551	6	US-09-925-065A-637489	Sequence 637489, A
C 296	12.2	67.8	201	8	US-10-995-561-30529	Sequence 30529, A	C 369	12.2	67.8	551	6	US-09-925-065A-195292	Sequence 195292, A
C 297	12.2	67.8	201	8	US-10-995-561-54859	Sequence 54859, A	C 370	12.2	67.8	553	6	US-09-925-065A-568721	Sequence 568721, A
C 298	12.2	67.8	201	8	US-10-995-561-63795	Sequence 63795, A	C 371	12.2	67.8	554	6	US-09-925-065A-18157	Sequence 18157, A
C 299	12.2	67.8	201	8	US-10-995-561-64652	Sequence 64652, A	C 372	12.2	67.8	554	6	US-09-925-065A-296545	Sequence 296545, A
C 300	12.2	67.8	201	8	US-10-995-561-65094	Sequence 65094, A	C 373	12.2	67.8	554	6	US-09-925-065A-296546	Sequence 296546, A
C 301	12.2	67.8	201	8	US-10-995-561-69056	Sequence 69056, A	C 374	12.2	67.8	554	6	US-09-925-065A-829390	Sequence 829390, A
C 302	12.2	67.8	201	8	US-10-995-561-72524	Sequence 72524, A	C 375	12.2	67.8	555	6	US-09-925-065A-747419	Sequence 747419, A
C 303	12.2	67.8	201	8	US-10-995-561-83578	Sequence 83578, A	C 376	12.2	67.8	555	6	US-09-925-065A-747420	Sequence 747420, A
C 304	12.2	67.8	201	12	US-11-124-368A-414	Sequence 414, Ap	C 377	12.2	67.8	556	6	US-09-925-065A-822312	Sequence 822312, A
C 305	12.2	67.8	201	12	US-11-124-368A-415	Sequence 415, Ap	C 378	12.2	67.8	556	6	US-09-925-065A-3508	Sequence 3508, Ap
C 306	12.2	67.8	201	12	US-11-124-368A-4600	Sequence 4600, Ap	C 379	12.2	67.8	556	6	US-09-925-065A-144197	Sequence 144197, Ap
C 307	12.2	67.8	201	12	US-11-124-368A-4601	Sequence 4601, Ap	C 380	12.2	67.8	556	6	US-09-925-065A-731726	Sequence 731726, A
C 308	12.2	67.8	201	12	US-11-124-368A-15420	Sequence 15420, A	C 381	12.2	67.8	557	6	US-09-925-065A-570807	Sequence 570807, A
C 309	12.2	67.8	201	12	US-11-124-368A-20096	Sequence 20096, A	C 382	12.2	67.8	558	6	US-09-925-065A-636310	Sequence 636310, A
C 310	12.2	67.8	201	12	US-11-124-368A-20097	Sequence 20097, A	C 383	12.2	67.8	558	6	US-09-925-065A-636310	Sequence 636310, A
C 311	12.2	67.8	201	12	US-11-124-367A-17427	Sequence 17427, A	C 384	12.2	67.8	560	6	US-09-925-065A-170080	Sequence 170080, A
C 312	12.2	67.8	201	12	US-11-124-367A-17428	Sequence 17428, A	C 385	12.2	67.8	563	6	US-09-925-065A-831282	Sequence 831282, A



C 386	12.2	67.8	555	6	US-09-925-065A-44354	Sequence 44354, A	459	12.2	67.8	623	6	US-09-925-065A-932768	Sequence 932768,
C 387	12.2	67.8	572	6	US-09-925-065A-439809	Sequence 439809,	460	12.2	67.8	624	6	US-09-925-065A-47568	Sequence 47568, A
C 388	12.2	67.8	574	6	US-09-925-065A-723380	Sequence 723380,	461	12.2	67.8	625	6	US-09-925-065A-472411	Sequence 472411,
C 389	12.2	67.8	574	6	US-09-925-065A-723380	Sequence 723380,	462	12.2	67.8	626	6	US-09-925-065A-723411	Sequence 723411,
C 390	12.2	67.8	575	6	US-09-925-065A-135033	Sequence 135033,	463	12.2	67.8	629	6	US-09-925-065A-355953	Sequence 355953,
C 391	12.2	67.8	578	6	US-09-925-065A-563330	Sequence 563330,	464	12.2	67.8	629	6	US-09-925-065A-355954	Sequence 355954,
C 392	12.2	67.8	578	6	US-09-925-065A-563331	Sequence 563331,	465	12.2	67.8	629	6	US-09-925-065A-355954	Sequence 355954,
C 393	12.2	67.8	579	6	US-09-925-065A-609039	Sequence 609039,	466	12.2	67.8	630	6	US-09-925-065A-355954	Sequence 355954,
C 394	12.2	67.8	579	6	US-09-925-065A-784522	Sequence 784522,	467	12.2	67.8	631	6	US-09-925-065A-355954	Sequence 355954,
C 395	12.2	67.8	579	6	US-09-925-065A-784522	Sequence 784522,	468	12.2	67.8	631	6	US-09-925-065A-355954	Sequence 355954,
C 396	12.2	67.8	580	6	US-09-925-065A-923112	Sequence 923112,	469	12.2	67.8	631	6	US-09-925-065A-355954	Sequence 355954,
C 397	12.2	67.8	580	6	US-09-925-065A-923112	Sequence 923112,	470	12.2	67.8	631	6	US-09-925-065A-355954	Sequence 355954,
C 398	12.2	67.8	580	6	US-09-925-065A-947283	Sequence 947283,	471	12.2	67.8	632	6	US-09-925-065A-355954	Sequence 355954,
C 399	12.2	67.8	580	12	US-11-128-061-5551	Sequence 5551, Ap	472	12.2	67.8	632	6	US-09-925-065A-355954	Sequence 355954,
C 400	12.2	67.8	580	12	US-11-128-061-5551	Sequence 5551, Ap	473	12.2	67.8	633	6	US-09-925-065A-355954	Sequence 355954,
C 401	12.2	67.8	580	12	US-11-128-049-2309	Sequence 2309, Ap	474	12.2	67.8	635	6	US-09-925-065A-559349	Sequence 559349,
C 402	12.2	67.8	580	12	US-11-128-049-2309	Sequence 2309, Ap	475	12.2	67.8	635	6	US-09-925-065A-559349	Sequence 559349,
C 403	12.2	67.8	581	6	US-09-925-065A-927721	Sequence 927721, Ap	476	12.2	67.8	635	6	US-09-925-065A-559349	Sequence 559349,
C 404	12.2	67.8	581	6	US-09-925-065A-927723	Sequence 927723,	477	12.2	67.8	637	6	US-09-925-065A-903966	Sequence 903966,
C 405	12.2	67.8	581	6	US-09-925-065A-949460	Sequence 949460,	478	12.2	67.8	638	6	US-09-925-065A-903966	Sequence 903966,
C 406	12.2	67.8	582	6	US-09-925-065A-507033	Sequence 507033,	479	12.2	67.8	638	6	US-09-925-065A-903966	Sequence 903966,
C 407	12.2	67.8	582	6	US-09-925-065A-507034	Sequence 507034,	480	12.2	67.8	639	6	US-09-925-065A-903966	Sequence 903966,
C 408	12.2	67.8	585	6	US-09-925-065A-255688	Sequence 255688,	481	12.2	67.8	640	6	US-09-925-065A-903966	Sequence 903966,
C 409	12.2	67.8	587	6	US-09-925-065A-302641	Sequence 302641,	482	12.2	67.8	642	6	US-09-925-065A-887710	Sequence 887710,
C 410	12.2	67.8	588	6	US-09-925-065A-97391	Sequence 97391, A	483	12.2	67.8	650	6	US-09-925-065A-933221	Sequence 933221,
C 411	12.2	67.8	588	6	US-09-925-065A-428270	Sequence 428270,	484	12.2	67.8	650	6	US-09-925-065A-933221	Sequence 933221,
C 412	12.2	67.8	588	6	US-09-925-065A-428271	Sequence 428271,	485	12.2	67.8	651	6	US-09-925-065A-933221	Sequence 933221,
C 413	12.2	67.8	588	6	US-09-925-065A-619345	Sequence 619345,	486	12.2	67.8	654	6	US-09-925-065A-501847	Sequence 501847,
C 414	12.2	67.8	588	6	US-09-925-065A-768327	Sequence 768327,	487	12.2	67.8	654	6	US-09-925-065A-501848	Sequence 501848,
C 415	12.2	67.8	588	6	US-09-925-065A-833964	Sequence 833964,	488	12.2	67.8	654	6	US-09-925-065A-501848	Sequence 501848,
C 416	12.2	67.8	588	6	US-10-467-657-1157	Sequence 1157, Ap	489	12.2	67.8	656	6	US-09-925-065A-501848	Sequence 501848,
C 417	12.2	67.8	588	6	US-09-925-065A-24297	Sequence 24297, A	490	12.2	67.8	657	6	US-09-925-065A-754770	Sequence 754770,
C 418	12.2	67.8	590	6	US-09-925-065A-542989	Sequence 542989,	491	12.2	67.8	659	6	US-09-925-065A-770155	Sequence 770155,
C 419	12.2	67.8	590	6	US-09-925-065A-931196	Sequence 931196,	492	12.2	67.8	669	6	US-09-925-065A-526865	Sequence 526865,
C 420	12.2	67.8	593	6	US-09-925-065A-382018	Sequence 382018,	493	12.2	67.8	669	6	US-09-925-065A-526865	Sequence 526865,
C 421	12.2	67.8	593	6	US-09-925-065A-382020	Sequence 382020,	494	12.2	67.8	674	6	US-09-925-065A-773264	Sequence 773264,
C 422	12.2	67.8	593	6	US-09-925-065A-544121	Sequence 544121,	495	12.2	67.8	681	6	US-09-925-065A-771213	Sequence 771213,
C 423	12.2	67.8	593	6	US-09-925-065A-862191	Sequence 862191,	496	12.2	67.8	682	6	US-09-925-065A-906691	Sequence 906691,
C 424	12.2	67.8	593	6	US-09-925-065A-930553	Sequence 930553,	497	12.2	67.8	683	6	US-09-925-065A-709225	Sequence 709225,
C 425	12.2	67.8	594	6	US-09-925-065A-659312	Sequence 659312,	498	12.2	67.8	683	6	US-09-925-065A-709226	Sequence 709226,
C 426	12.2	67.8	594	6	US-09-925-065A-692719	Sequence 692719,	499	12.2	67.8	689	6	US-09-925-065A-681126	Sequence 681126,
C 427	12.2	67.8	594	6	US-09-925-065A-807601	Sequence 807601,	500	12.2	67.8	702	6	US-09-925-065A-874753	Sequence 874753,
C 428	12.2	67.8	595	6	US-09-925-065A-275903	Sequence 275903,	501	12.2	67.8	702	8	US-10-750-185-60624	Sequence 60624, A
C 429	12.2	67.8	595	6	US-09-925-065A-923244	Sequence 923244,	502	12.2	67.8	702	8	US-10-750-185-60624	Sequence 60624, A
C 430	12.2	67.8	596	6	US-09-925-065A-863531	Sequence 863531,	503	12.2	67.8	704	6	US-09-925-065A-56605	Sequence 56605, A
C 431	12.2	67.8	600	6	US-09-925-065A-489929	Sequence 489929,	504	12.2	67.8	745	6	US-09-925-065A-95256	Sequence 95256, A
C 432	12.2	67.8	600	8	US-10-750-185-3305	Sequence 3305, Ap	505	12.2	67.8	745	6	US-09-925-065A-95256	Sequence 95256, A
C 433	12.2	67.8	600	8	US-10-750-185-3305	Sequence 3305, Ap	506	12.2	67.8	757	9	US-11-096-568A-25335	Sequence 25335, A
C 434	12.2	67.8	600	8	US-10-750-185-3305	Sequence 3305, Ap	507	12.2	67.8	759	6	US-09-925-065A-83969	Sequence 83969, A
C 435	12.2	67.8	600	8	US-10-750-185-3305	Sequence 3305, Ap	508	12.2	67.8	759	6	US-09-925-065A-83970	Sequence 83970, A
C 436	12.2	67.8	600	12	US-11-136-527-6714	Sequence 6714, Ap	509	12.2	67.8	759	6	US-09-925-065A-83971	Sequence 83971, A
C 437	12.2	67.8	601	6	US-09-925-065A-740118	Sequence 740118,	510	12.2	67.8	755	12	US-11-000-463-199	Sequence 199, Ap
C 438	12.2	67.8	602	6	US-09-925-065A-557356	Sequence 557356,	511	12.2	67.8	773	6	US-09-925-065A-94773	Sequence 94773, A
C 439	12.2	67.8	602	6	US-09-925-065A-652794	Sequence 652794,	512	12.2	67.8	778	6	US-09-925-065A-940108	Sequence 940108,
C 440	12.2	67.8	604	6	US-09-925-065A-729702	Sequence 729702,	513	12.2	67.8	794	8	US-10-750-185-64100	Sequence 64100, A
C 441	12.2	67.8	604	6	US-09-925-065A-729703	Sequence 729703,	514	12.2	67.8	794	8	US-10-750-185-64100	Sequence 64100, A
C 442	12.2	67.8	605	6	US-09-925-065A-774604	Sequence 774604,	515	12.2	67.8	803	12	US-11-005-822-905	Sequence 905, Ap
C 443	12.2	67.8	605	6	US-09-925-065A-775868	Sequence 775868,	516	12.2	67.8	803	12	US-11-005-822-905	Sequence 905, Ap
C 444	12.2	67.8	605	6	US-09-925-065A-837463	Sequence 837463,	517	12.2	67.8	827	6	US-09-925-065A-546952	Sequence 546952,
C 445	12.2	67.8	606	6	US-09-925-065A-492027	Sequence 492027,	518	12.2	67.8	827	6	US-09-925-065A-546953	Sequence 546953,
C 446	12.2	67.8	606	6	US-09-925-065A-812530	Sequence 812530,	519	12.2	67.8	827	6	US-09-925-065A-546954	Sequence 546954,
C 447	12.2	67.8	606	6	US-09-925-065A-844630	Sequence 844630,	520	12.2	67.8	834	7	US-10-932-182A-3518	Sequence 3518, Ap
C 448	12.2	67.8	607	6	US-09-925-065A-220430	Sequence 220430,	521	12.2	67.8	834	7	US-10-932-182A-3518	Sequence 3518, Ap
C 449	12.2	67.8	608	6	US-09-925-065A-355952	Sequence 355952,	522	12.2	67.8	840	6	US-09-925-065A-355952	Sequence 355952,
C 450	12.2	67.8	609	6	US-09-925-065A-865668	Sequence 865668,	523	12.2	67.8	852	8	US-10-467-657-22897	Sequence 22897, Ap
C 451	12.2	67.8	610	6	US-09-925-065A-294410	Sequence 294410,	524	12.2	67.8	875	6	US-09-925-065A-924936	Sequence 924936,
C 452	12.2	67.8	610	6	US-09-925-065A-609038	Sequence 609038,	525	12.2	67.8	896	6	US-09-925-065A-719063	Sequence 719063,
C 453	12.2	67.8	611	6	US-09-925-065A-668820	Sequence 668820,	526	12.2	67.8	903	6	US-09-925-065A-77088	Sequence 77088, A
C 454	12.2	67.8	616	6	US-09-925-065A-124180	Sequence 124180,	527	12.2	67.8	937	6	US-09-925-065A-97385	Sequence 97385, A
C 455	12.2	67.8	616	6	US-09-925-065A-753581	Sequence 753581,	528	12.2	67.8	938	6	US-09-925-065A-66572	Sequence 66572, A
C 456	12.2	67.8	617	6	US-09-925-065A-758114	Sequence 758114,	529	12.2	67.8	987	8	US-10-750-185-48214	Sequence 48214, A
C 457	12.2	67.8	621	6	US-09-925-065A-840121	Sequence 840121,	530	12.2	67.8	987	8	US-10-750-185-48214	Sequence 48214, A
C 458	12.2	67.8	623	6	US-09-925-065A-8120	Sequence 8120, Ap	531	12.2	67.8	990	7	US-10-932-182A-303	Sequence 303, Ap

532	12.2	67.8	990	7	US-10-932-182A-303	Sequence 303, App
533	12.2	67.8	1000	9	US-11-204-311-474	Sequence 474, App
534	12.2	67.8	1000	9	US-11-204-311-475	Sequence 475, App
535	12.2	67.8	1000	9	US-11-204-311-476	Sequence 476, App
536	12.2	67.8	1020	12	US-11-165-226-120	Sequence 120, App
537	12.2	67.8	1021	6	US-09-925-065A-69866	Sequence 69866, App
538	12.2	67.8	1039	6	US-09-925-065A-691050	Sequence 691050, App
539	12.2	67.8	1054	6	US-09-925-065A-28689	Sequence 28689, App
540	12.2	67.8	1077	9	US-11-096-568A-25933	Sequence 25933, App
541	12.2	67.8	1091	6	US-09-925-065A-65812	Sequence 65812, App
542	12.2	67.8	1091	6	US-09-925-065A-65813	Sequence 65813, App
543	12.2	67.8	1095	6	US-09-925-065A-18171	Sequence 18171, App
544	12.2	67.8	1095	6	US-09-925-065A-18172	Sequence 18172, App
545	12.2	67.8	1095	6	US-09-925-065A-18173	Sequence 18173, App
546	12.2	67.8	1106	6	US-09-925-065A-70306	Sequence 70306, App
547	12.2	67.8	1125	9	US-11-096-568A-19011	Sequence 19011, App
548	12.2	67.8	1141	6	US-09-925-065A-684793	Sequence 684793, App
549	12.2	67.8	1161	6	US-10-467-657-1159	Sequence 1159, App
550	12.2	67.8	1178	6	US-09-925-065A-22656	Sequence 22656, App
551	12.2	67.8	1178	6	US-09-925-065A-22657	Sequence 22657, App
552	12.2	67.8	1178	6	US-09-925-065A-22658	Sequence 22658, App
553	12.2	67.8	1178	6	US-09-925-065A-22659	Sequence 22659, App
554	12.2	67.8	1184	12	US-11-159-597-1	Sequence 1, App
555	12.2	67.8	1186	9	US-11-096-568A-21226	Sequence 21226, App
556	12.2	67.8	1187	6	US-09-925-065A-92527	Sequence 92527, App
557	12.2	67.8	1242	8	US-10-750-185-27164	Sequence 27164, App
558	12.2	67.8	1242	8	US-10-750-623-27164	Sequence 27164, App
559	12.2	67.8	1281	6	US-09-925-065A-726078	Sequence 726078, App
560	12.2	67.8	1310	6	US-09-925-065A-715731	Sequence 715731, App
561	12.2	67.8	1310	6	US-09-925-065A-715732	Sequence 715732, App
562	12.2	67.8	1333	12	US-11-000-688-1047	Sequence 1047, App
563	12.2	67.8	1331	7	US-10-932-182A-3951	Sequence 3951, App
564	12.2	67.8	1341	7	US-10-932-182A-3951	Sequence 3951, App
565	12.2	67.8	1386	12	US-11-055-822-365	Sequence 365, App
566	12.2	67.8	1386	12	US-11-055-822-365	Sequence 365, App
567	12.2	67.8	1386	12	US-11-055-822-365	Sequence 365, App
568	12.2	67.8	1396	6	US-09-925-065A-711903	Sequence 711903, App
569	12.2	67.8	1396	6	US-09-925-065A-711904	Sequence 711904, App
570	12.2	67.8	1406	9	US-11-096-568A-26444	Sequence 26444, App
571	12.2	67.8	1413	8	US-10-750-185-64359	Sequence 64359, App
572	12.2	67.8	1413	8	US-10-750-623-64359	Sequence 64359, App
573	12.2	67.8	1429	8	US-10-750-185-38898	Sequence 38898, App
574	12.2	67.8	1429	8	US-10-750-623-38898	Sequence 38898, App
575	12.2	67.8	1434	9	US-11-096-568A-17985	Sequence 17985, App
576	12.2	67.8	1467	9	US-11-096-568A-22361	Sequence 22361, App
577	12.2	67.8	1485	6	US-09-925-065A-670109	Sequence 670109, App
578	12.2	67.8	1485	6	US-09-925-065A-714347	Sequence 714347, App
579	12.2	67.8	1485	6	US-09-925-065A-714348	Sequence 714348, App
580	12.2	67.8	1500	8	US-10-750-185-57734	Sequence 57734, App
581	12.2	67.8	1500	8	US-10-750-623-57734	Sequence 57734, App
582	12.2	67.8	1516	6	US-09-925-065A-88603	Sequence 88603, App
583	12.2	67.8	1525	6	US-09-925-065A-680299	Sequence 680299, App
584	12.2	67.8	1525	6	US-09-925-065A-680300	Sequence 680300, App
585	12.2	67.8	1525	6	US-09-925-065A-680301	Sequence 680301, App
586	12.2	67.8	1533	8	US-10-750-185-29904	Sequence 29904, App
587	12.2	67.8	1533	8	US-10-750-623-29904	Sequence 29904, App
588	12.2	67.8	1541	6	US-09-925-065A-87111	Sequence 87111, App
589	12.2	67.8	1556	6	US-09-925-065A-692921	Sequence 692921, App
590	12.2	67.8	1573	6	US-09-925-065A-692928	Sequence 692928, App
591	12.2	67.8	1591	8	US-10-750-185-61656	Sequence 61656, App
592	12.2	67.8	1591	8	US-10-750-623-61656	Sequence 61656, App
593	12.2	67.8	1623	6	US-09-925-065A-697964	Sequence 697964, App
594	12.2	67.8	1642	9	US-11-096-568A-25999	Sequence 25999, App
595	12.2	67.8	1677	9	US-11-096-568A-26216	Sequence 26216, App
596	12.2	67.8	1686	6	US-09-925-065A-88839	Sequence 88839, App
597	12.2	67.8	1686	6	US-10-750-185-42554	Sequence 42554, App
598	12.2	67.8	1686	6	US-10-750-623-42554	Sequence 42554, App
599	12.2	67.8	1693	9	US-11-096-568A-12609	Sequence 12609, App
600	12.2	67.8	1703	9	US-11-096-568A-20081	Sequence 20081, App
601	12.2	67.8	1761	6	US-09-925-065A-546861	Sequence 546861, App
602	12.2	67.8	1806	9	US-11-096-568A-19454	Sequence 19454, App
603	12.2	67.8	1831	8	US-10-750-185-62445	Sequence 62445, App
604	12.2	67.8	1831	8	US-10-750-623-62445	Sequence 62445, App
605	12.2	67.8	1856	9	US-11-096-568A-19630	Sequence 19630, App
606	12.2	67.8	1883	8	US-10-750-185-32058	Sequence 32058, App
607	12.2	67.8	1885	8	US-10-750-623-32059	Sequence 32059, App
608	12.2	67.8	1885	8	US-10-750-185-56447	Sequence 56447, App
609	12.2	67.8	1915	8	US-10-750-623-56447	Sequence 56447, App
610	12.2	67.8	1915	8	US-10-750-185-47637	Sequence 47637, App
611	12.2	67.8	1945	8	US-10-750-623-47637	Sequence 47637, App
612	12.2	67.8	1945	8	US-10-750-623-47637	Sequence 47637, App
613	12.2	67.8	1953	7	US-10-932-182A-79419	Sequence 79419, App
614	12.2	67.8	1953	7	US-10-932-182A-79419	Sequence 79419, App
615	12.2	67.8	1953	7	US-10-750-185-37926	Sequence 37926, App
616	12.2	67.8	1953	7	US-10-750-623-37926	Sequence 37926, App
617	12.2	67.8	2085	7	US-10-932-182A-78109	Sequence 78109, App
618	12.2	67.8	2085	7	US-10-932-182A-78109	Sequence 78109, App
619	12.2	67.8	2085	7	US-11-072-512-1055	Sequence 1055, App
620	12.2	67.8	2127	7	US-10-932-182A-338	Sequence 338, App
621	12.2	67.8	2127	7	US-10-932-182A-338	Sequence 338, App
622	12.2	67.8	2127	7	US-11-136-527-2618	Sequence 2618, App
623	12.2	67.8	2323	12	US-11-186-284-62	Sequence 62, App
624	12.2	67.8	2323	12	US-11-186-284-62	Sequence 62, App
625	12.2	67.8	2344	6	US-09-925-065A-73261	Sequence 73261, App
626	12.2	67.8	2348	12	US-11-136-527-3691	Sequence 3691, App
627	12.2	67.8	2362	12	US-11-136-527-522	Sequence 522, App
628	12.2	67.8	2388	12	US-11-072-512-1207	Sequence 1207, App
629	12.2	67.8	2538	9	US-11-072-512-751	Sequence 751, App
630	12.2	67.8	2626	9	US-11-072-512-751	Sequence 751, App
631	12.2	67.8	2635	6	US-09-925-065A-728054	Sequence 728054, App
632	12.2	67.8	2641	8	US-10-947-249-179	Sequence 179, App
633	12.2	67.8	2660	6	US-11-200-296B-5	Sequence 5, App
634	12.2	67.8	2661	12	US-11-000-463-4	Sequence 4, App
635	12.2	67.8	2823	9	US-11-072-512-854	Sequence 854, App
636	12.2	67.8	2841	9	US-11-200-296B-9	Sequence 9, App
637	12.2	67.8	2886	7	US-10-932-182A-865	Sequence 865, App
638	12.2	67.8	2906	6	US-09-925-065A-712308	Sequence 712308, App
639	12.2	67.8	2906	6	US-09-925-065A-712309	Sequence 712309, App
640	12.2	67.8	2929	9	US-10-524-919-3	Sequence 3, App
641	12.2	67.8	2929	9	US-11-072-512-181	Sequence 181, App
642	12.2	67.8	2936	9	US-11-072-512-482	Sequence 482, App
643	12.2	67.8	3513	7	US-10-932-182A-865	Sequence 865, App
644	12.2	67.8	3513	7	US-10-932-182A-865	Sequence 865, App
645	12.2	67.8	3632	6	US-09-925-065A-708670	Sequence 708670, App
646	12.2	67.8	3632	6	US-09-925-065A-708671	Sequence 708671, App
647	12.2	67.8	3969	12	US-11-000-688-1407	Sequence 1407, App
648	12.2	67.8	4095	12	US-11-136-527-2030	Sequence 2030, App
649	12.2	67.8	4385	12	US-11-000-463-776	Sequence 476, App
650	12.2	67.8	4392	8	US-10-750-185-33960	Sequence 33960, App
651	12.2	67.8	4432	8	US-10-750-623-33960	Sequence 33960, App
652	12.2	67.8	4437	8	US-10-750-185-54999	Sequence 54999, App
653	12.2	67.8	4437	8	US-10-750-623-54999	Sequence 54999, App
654	12.2	67.8	4437	8	US-10-750-623-54999	Sequence 54999, App
655	12.2	67.8	4539	9	US-11-051-720-97	Sequence 97, App
656	12.2	67.8	4828	8	US-10-750-185-56813	Sequence 56813, App
657	12.2	67.8	4828	8	US-10-750-623-56813	Sequence 56813, App
658	12.2	67.8	4877	12	US-11-169-041-51	Sequence 51, App
659	12.2	67.8	5005	8	US-10-750-185-37507	Sequence 37507, App
660	12.2	67.8	5005	8	US-10-750-623-37507	Sequence 37507, App
661	12.2	67.8	5306	9	US-11-072-175-51	Sequence 51, App
662	12.2	67.8	5307	12	US-11-035-105-1	Sequence 1, App
663	12.2	67.8	5707	12	US-11-136-527-7026	Sequence 2026, App
664	12.2	67.8	7304	8	US-10-240-708-43	Sequence 43, App
665	12.2	67.8	10011	9	US-11-245-147-188	Sequence 188, App
666	12.2	67.8	15804	8	US-10-995-561-13294	Sequence 13294, App
667	12.2	67.8	16637	8	US-10-995-561-13508	Sequence 13508, App
668	12.2	67.8	16637	8	US-10-995-561-13467	Sequence 13467, App
669	12.2	67.8	21605	12	US-11-124-367A-5092	Sequence 5092, App
670	12.2	67.8	21991	12	US-11-124-367A-5092	Sequence 5092, App
671	12.2	67.8	23046	12	US-11-124-368A-2925	Sequence 2925, App
672	12.2	67.8	29260	7	US-10-330-773-165	Sequence 165, App
673	12.2	67.8	33019	8	US-10-995-561-13371	Sequence 13371, App
674	12.2	67.8	37705	12	US-11-124-367A-5060	Sequence 5060, App
675	12.2	67.8	40000	8	US-10-995-561-13513	Sequence 13513, App
676	12.2	67.8	42811	7	US-10-330-773-925	Sequence 925, App
677	12.2	67.8	47460	12	US-11-124-368A-2877	Sequence 2877, App

C 678	12.2	67.8	49312	9	US-11-204-311-485	Sequence 485, App	751	12.2	67.8	1080000	8	US-10-928-446A-195	Sequence 195, App
679	12.2	67.8	50484	7	US-10-930-483-63	Sequence 63, App	752	12.2	67.8	1080000	8	US-10-928-446A-195	Sequence 195, App
680	12.2	67.8	61739	7	US-10-330-773-320	Sequence 320, App	753	12.2	67.8	1080000	8	US-10-928-446A-197	Sequence 197, App
C 681	12.2	67.8	66916	8	US-10-995-561-13374	Sequence 13374, A	C 754	12.2	67.8	1080000	8	US-10-928-446A-197	Sequence 197, App
C 682	12.2	67.8	70708	7	US-10-330-773-554	Sequence 554, App	C 755	12.2	67.8	1080000	8	US-10-928-446A-199	Sequence 199, App
C 683	12.2	67.8	73930	7	US-10-330-773-554	Sequence 554, App	C 756	12.2	67.8	1080000	8	US-10-928-446A-199	Sequence 199, App
C 684	12.2	67.8	75007	8	US-10-995-561-13194	Sequence 13194, A	C 757	12.2	67.8	1080000	8	US-10-928-446A-201	Sequence 201, App
C 685	12.2	67.8	76589	8	US-10-995-561-13322	Sequence 13322, A	C 758	12.2	67.8	1080000	8	US-10-928-446A-201	Sequence 201, App
C 686	12.2	67.8	79548	8	US-10-330-773-741	Sequence 741, App	C 759	12.2	67.8	1082144	12	US-11-117-187-211	Sequence 211, App
C 687	12.2	67.8	83712	8	US-10-995-561-13366	Sequence 13366, A	C 760	12	66.7	25	12	US-11-175-859-20864	Sequence 20864, A
C 688	12.2	67.8	86149	7	US-10-330-773-239	Sequence 239, App	C 761	12	66.7	50	12	US-10-995-561-15380	Sequence 15380, A
C 689	12.2	67.8	88607	7	US-10-330-773-625	Sequence 625, App	C 762	12	66.7	201	8	US-10-995-561-37698	Sequence 37698, A
C 690	12.2	67.8	91561	12	US-11-124-368A-2896	Sequence 2896, App	C 763	12	66.7	201	8	US-11-102-883-13	Sequence 13, App
C 691	12.2	67.8	93112	8	US-10-995-561-13334	Sequence 13334, A	C 764	12	66.7	450	12	US-09-925-065A-346240	Sequence 346240, A
C 692	12.2	67.8	100000	12	US-11-124-368A-2901	Sequence 2901, App	C 765	12	66.7	490	6	US-09-925-065A-505181	Sequence 505181, A
C 693	12.2	67.8	100864	7	US-10-330-773-239	Sequence 239, App	C 766	12	66.7	591	6	US-09-925-065A-505181	Sequence 505181, A
C 694	12.2	67.8	103661	7	US-10-330-773-689	Sequence 689, App	C 767	12	66.7	591	6	US-09-925-065A-505182	Sequence 505182, A
C 695	12.2	67.8	103661	7	US-10-330-773-689	Sequence 689, App	C 768	12	66.7	600	12	US-11-136-527-4307	Sequence 4307, App
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C 697	12.2	67.8	115935	8	US-10-775-169-241	Sequence 241, App	C 770	12	66.7	767	12	US-11-136-527-211	Sequence 211, App
C 698	12.2	67.8	118544	7	US-10-330-773-76	Sequence 76, App	C 771	12	66.7	855	6	US-09-925-065A-29182	Sequence 29182, A
C 699	12.2	67.8	126552	12	US-11-121-086-1	Sequence 1, App	C 772	12	66.7	855	6	US-09-925-065A-29183	Sequence 29183, A
C 700	12.2	67.8	134499	12	US-11-117-187-192	Sequence 192, App	C 773	12	66.7	855	6	US-09-925-065A-29184	Sequence 29184, A
C 701	12.2	67.8	138627	7	US-10-330-773-159	Sequence 159, App	C 774	12	66.7	870	12	US-11-102-883-1	Sequence 1, App
C 702	12.2	67.8	145985	7	US-10-330-773-140	Sequence 140, App	C 775	12	66.7	2991	6	US-09-925-065A-31308	Sequence 31308, A
C 703	12.2	67.8	150038	12	US-11-112-908-23	Sequence 23, App	C 776	12	66.7	2991	6	US-09-925-065A-31309	Sequence 31309, A
C 704	12.2	67.8	150481	12	US-11-112-908-37	Sequence 37, App	C 777	12	66.7	2991	6	US-09-925-065A-31310	Sequence 31310, A
C 705	12.2	67.8	150481	12	US-11-112-908-37	Sequence 37, App	C 778	12	66.7	2991	6	US-09-925-065A-31311	Sequence 31311, A
C 706	12.2	67.8	153142	12	US-11-121-086-27	Sequence 27, App	C 779	12	66.7	2991	6	US-09-925-065A-31312	Sequence 31312, A
C 707	12.2	67.8	159497	12	US-11-112-908-61	Sequence 61, App	C 780	12	66.7	173995	8	US-10-995-561-13277	Sequence 13277, A
C 708	12.2	67.8	160170	12	US-11-121-086-32	Sequence 32, App	C 781	12	66.7	321019	8	US-10-995-561-13204	Sequence 13204, A
C 709	12.2	67.8	163162	12	US-11-121-086-66	Sequence 66, App	C 782	12	66.7	321019	8	US-10-995-561-13204	Sequence 13204, A
C 710	12.2	67.8	164810	12	US-11-121-086-4	Sequence 4, App	C 783	11.8	65.6	19	8	US-10-310-914A-335370	Sequence 335370, A
C 711	12.2	67.8	167891	12	US-11-121-086-14	Sequence 14, App	C 784	11.8	65.6	19	8	US-10-310-914A-377129	Sequence 377129, A
C 712	12.2	67.8	168516	12	US-11-121-086-3	Sequence 3, App	C 785	11.8	65.6	19	8	US-10-310-914A-41248	Sequence 41248, A
C 713	12.2	67.8	171152	12	US-11-112-908-38	Sequence 38, App	C 786	11.8	65.6	19	10	US-11-101-244-430485	Sequence 430485, A
C 714	12.2	67.8	171152	12	US-11-112-908-38	Sequence 38, App	C 787	11.8	65.6	19	10	US-11-101-244-430485	Sequence 430485, A
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C 717	12.2	67.8	173602	12	US-11-121-086-25	Sequence 25, App	C 790	11.8	65.6	20	8	US-10-310-914A-460569	Sequence 460569, A
C 718	12.2	67.8	175673	12	US-11-121-086-55	Sequence 55, App	C 791	11.8	65.6	20	8	US-10-310-914A-460569	Sequence 460569, A
C 719	12.2	67.8	179487	7	US-10-330-773-664	Sequence 664, App	C 792	11.8	65.6	21	8	US-10-310-914A-118640	Sequence 118640, A
C 720	12.2	67.8	179777	12	US-11-121-086-106	Sequence 106, App	C 793	11.8	65.6	21	8	US-10-310-914A-118640	Sequence 118640, A
C 721	12.2	67.8	179892	12	US-11-112-908-39	Sequence 39, App	C 794	11.8	65.6	21	8	US-10-310-914A-1186965	Sequence 1186965, A
C 722	12.2	67.8	187786	8	US-10-995-561-13474	Sequence 13474, A	C 795	11.8	65.6	22	8	US-10-310-914A-1249930	Sequence 1249930, A
C 723	12.2	67.8	187986	8	US-10-995-561-13474	Sequence 13474, A	C 796	11.8	65.6	22	8	US-10-310-914A-558043	Sequence 558043, A
C 724	12.2	67.8	191091	12	US-11-121-086-60	Sequence 60, App	C 797	11.8	65.6	23	8	US-10-310-914A-1187018	Sequence 1187018, A
C 725	12.2	67.8	194186	7	US-10-330-773-395	Sequence 395, App	C 798	11.8	65.6	24	8	US-10-310-914A-377116	Sequence 377116, A
C 726	12.2	67.8	197096	12	US-11-121-086-107	Sequence 107, App	C 799	11.8	65.6	24	8	US-10-310-914A-511758	Sequence 511758, A
C 727	12.2	67.8	197781	12	US-11-112-908-34	Sequence 34, App	C 800	11.8	65.6	24	8	US-10-310-914A-511758	Sequence 511758, A
C 728	12.2	67.8	217623	12	US-11-112-908-33	Sequence 33, App	C 801	11.8	65.6	25	7	US-10-932-182A-62376	Sequence 62376, A
C 729	12.2	67.8	218821	12	US-11-121-086-31	Sequence 31, App	C 802	11.8	65.6	25	7	US-10-932-182A-62376	Sequence 62376, A
C 730	12.2	67.8	248999	7	US-10-330-773-342	Sequence 342, App	C 803	11.8	65.6	25	7	US-10-932-182A-62376	Sequence 62376, A
C 731	12.2	67.8	257645	7	US-10-330-773-266	Sequence 266, App	C 804	11.8	65.6	25	7	US-10-932-182A-62376	Sequence 62376, A
C 732	12.2	67.8	268685	8	US-10-933-025-22	Sequence 22, App	C 805	11.8	65.6	25	7	US-10-932-182A-62376	Sequence 62376, A
C 733	12.2	67.8	318488	9	US-11-114-798-58	Sequence 58, App	C 806	11.8	65.6	25	7	US-10-933-982-67281	Sequence 67281, A
C 734	12.2	67.8	390183	7	US-10-330-773-937	Sequence 937, App	C 807	11.8	65.6	25	7	US-10-933-982-67281	Sequence 67281, A
C 735	12.2	67.8	1080000	8	US-10-928-446A-1	Sequence 1, App	C 808	11.8	65.6	25	7	US-10-933-982-67281	Sequence 67281, A
C 736	12.2	67.8	1080000	8	US-10-928-446A-1	Sequence 1, App	C 809	11.8	65.6	25	7	US-10-933-982-67281	Sequence 67281, A
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C 739	12.2	67.8	1080000	8	US-10-928-446A-183	Sequence 183, App	C 812	11.8	65.6	25	12	US-11-121-0849-561330	Sequence 561330, A
C 740	12.2	67.8	1080000	8	US-10-928-446A-183	Sequence 183, App	C 813	11.8	65.6	25	12	US-11-121-0849-561330	Sequence 561330, A
C 741	12.2	67.8	1080000	8	US-10-928-446A-185	Sequence 185, App	C 814	11.8	65.6	25	12	US-11-121-0849-561330	Sequence 561330, A
C 742	12.2	67.8	1080000	8	US-10-928-446A-185	Sequence 185, App	C 815	11.8	65.6	25	12	US-11-121-0849-561330	Sequence 561330, A
C 743	12.2	67.8	1080000	8	US-10-928-446A-187	Sequence 187, App	C 816	11.8	65.6	32	8	US-10-939-294A-15780	Sequence 15780, A
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C 997 11.8 65.6 1164 12 US-11-137-465-24 Sequence 24, Appl
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## ALIGNMENTS

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RESULT 1
US-10-619-279-60/c
; Sequence 60, Application US/10619279
; Publication No. US20050267057A1
; GENERAL INFORMATION:
; APPLICANT: Kries, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7023/HCL
; CURRENT APPLICATION NUMBER: US/10/619,279
; PRIOR FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US 08/960,774
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-619-279-60
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Best Local Similarity 88.9%; Pred. No.1.2;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Db 18 AGAGGUGCGACCGCGUA 1
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RESULT 2
US-11-127-654-4/c
; Sequence 4, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Kries, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; FILE REFERENCE: C1039, 70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-4
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Query Match 100.0%; Score 18; DB 12; Length 18;
Best Local Similarity 88.9%; Pred. No.1.2;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
US-10-497-591A-41/c
; Sequence 41, Application US/10497591A
; Publication No. US20050250716A1
; GENERAL INFORMATION:
; APPLICANT: SCHMIDT, MALTE
; APPLICANT: SCHLACK, CAROLA
; APPLICANT: EGYED, ALENA
; APPLICANT: LINGNAU, KAREN
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES
; FILE REFERENCE: SONN/045US
; CURRENT APPLICATION NUMBER: US/10/497,591A
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: PCT/EP02/13791
; PRIOR FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: A 1924/2001
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.1
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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; NAME/KEY: modified base
; LOCATION: (5)..(11)
; OTHER INFORMATION: n = inosine or uracil
US-10-497-591A-41
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Query Match 83.3%; Score 15; DB 8; Length 18;
Best Local Similarity 72.2%; Pred. No. 57;
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RESULT 4  
US-10-310-914A-990315/C

Sequence 990315, Application US/10310914A  
Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shiller, Kviatatz

TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

FILE REFERENCE: 06087,0200,CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

NUMBER OF SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 990315

LENGTH: 22

TYPE: RNA

ORGANISM: Human

US-10-310-914A-990315

Query Match 83.3%; Score 15; DB 8; Length 22;  
Best Local Similarity 93.3%; Pred. No. 57;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGCGG 16

DB 19 GAGGUGCGACGCGG 5

RESULT 5  
US-10-981-334-21

Sequence 21, Application US/10981334

Publication No. US20060008816A1

GENERAL INFORMATION:

APPLICANT: Lu, Yi-Ping et al.

TITLE OF INVENTION: PROMOTER, PROMOTER CONTROL ELEMENTS, AND COMBINATIONS, AND USES

FILE REFERENCE: 2750-1581PUS2

CURRENT APPLICATION NUMBER: US/10/981,334

NUMBER OF SEQ ID NOS: 68

SOFTWARE: PatentIn version 3.3

SEQ ID NO 21

LENGTH: 935

TYPE: DNA

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Promoter and/or promoter control element identified from

US-10-981-334-21

Query Match 83.3%; Score 15; DB 7; Length 935;  
Best Local Similarity 86.7%; Pred. No. 52;

Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGGUGCGACGCGGU 17

DB 864 AGGUGCGACGCGGT 878

RESULT 6  
US-11-091-883-330/C

Sequence 330, Application US/11091883

Publication No. US20060024693A1

GENERAL INFORMATION:

APPLICANT: CIBELLI, JOSE

APPLICANT: FERNANDEZ, EMILIO O.

APPLICANT: JORDAO DE MEGALHANS, GUILHERME

APPLICANT: KOCABAS, ARIF

APPLICANT: CROSBY, JAVIER A.

TITLE OF INVENTION: IDENTIFICATION OF GENES OR POLYPEPTIDES THE EXPRESSION OF WHICH  
CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEBORN

TITLE OF INVENTION: VIABILITY

FILE REFERENCE: 53942US

CURRENT APPLICATION NUMBER: US/11/091,883

CURRENT FILING DATE: 2005-03-29

PRIOR APPLICATION NUMBER: 60/556,875

PRIOR FILING DATE: 2004-03-29

NUMBER OF SEQ ID NOS: 513

SOFTWARE: PatentIn version 3.3

SEQ ID NO 330

LENGTH: 2162

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: modified base

LOCATION: (909)..(909)

OTHER INFORMATION: a, c, g, or t

FEATURE:

NAME/KEY: modified base

LOCATION: (1400)..(1400)

OTHER INFORMATION: a, c, g, or t

FEATURE:

NAME/KEY: modified base

LOCATION: (2051)..(2053)

OTHER INFORMATION: a, c, g, or t

FEATURE:

NAME/KEY: modified base

LOCATION: (2056)..(2056)

OTHER INFORMATION: a, c, g, or t

FEATURE:

NAME/KEY: modified base

LOCATION: (2072)..(2074)

OTHER INFORMATION: a, c, g, or t

US-11-091-883-330

Query Match 83.3%; Score 15; DB 12; Length 2162;  
Best Local Similarity 93.3%; Pred. No. 51;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGCGG 16

DB 2035 GAGGUGCGACGCGG 2021

RESULT 7  
US-10-750-185-55765

Sequence 55765, Application US/10750185

Publication No. US20050260603A1

GENERAL INFORMATION:

APPLICANT: MMT GENOMICS, INC.

APPLICANT: DENISE, Sue K.

APPLICANT: KERR, Richard

APPLICANT: ROSENFELD, David

APPLICANT: HOLM, Tom

APPLICANT: BATES, Stephen

APPLICANT: PANTIN, Dennis

TITLE OF INVENTION: COMPOSITIONS FOR IMPROVING BOVINE TRAITS

FILE REFERENCE: MM1100-2

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT FILING DATE: 2003-12-31

PRIOR APPLICATION NUMBER: US 60/437,482

PRIOR FILING DATE: 2002-12-31

NUMBER OF SEQ ID NOS: 64922

SOFTWARE: PatentIn version 3.1

SEQ ID NO 55765

LENGTH: 2106

TYPE: DNA

ORGANISM: Bovine

US-10-750-185-55765

Query Match 82.2%; Score 14.8; DB 8; Length 2106;  
Best Local Similarity 77.8%; Pred. No. 66;



Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 1 AGAGGUCGCGACGGGUA 18  
|||||:|||||:|||||:  
Db 831 AGAGGCTCGCATCGGTA 848

RESULT 8  
US-10-750-623-55765  
; Sequence 55765, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMT GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: PANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM11100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; PRIOR FILING DATE: 2003-12-31  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 55765  
; LENGTH: 2106  
; TYPE: DNA  
; ORGANISM: Bovine 19866881318594  
US-10-750-623-55765

Query Match 82.2%; Score 14.8; DB 8; Length 2106;  
Best Local Similarity 77.8%; Pred. No. 66;  
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGAGGUCGCGACGGGUA 18  
|||||:|||||:|||||:  
Db 831 AGAGGCTCGCATCGGTA 848

RESULT 9  
US-10-750-185-37497/c  
; Sequence 37497, Application US/10750185  
; Publication No. US200502603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMT GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: PANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM11100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; PRIOR FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 37497  
; LENGTH: 1411  
; TYPE: DNA  
; ORGANISM: Bovine 19866881318594  
US-10-750-185-37497

Query Match 80.0%; Score 14.4; DB 8; Length 1411;  
Best Local Similarity 93.8%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 AGAGGUCGCGACGGG 16

Db 655 AGAGGGCGCGACGGG 640  
|||||:|||||:|||||:  
|||||:|||||:|||||:

RESULT 10  
US-10-750-623-37497/c  
; Sequence 37497, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMT GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: PANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM11100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; PRIOR FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 37497  
; LENGTH: 1411  
; TYPE: DNA  
; ORGANISM: Bovine 19866881318594  
US-10-750-623-37497

Query Match 80.0%; Score 14.4; DB 8; Length 1411;  
Best Local Similarity 93.8%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUCGCGACGGG 16  
|||||:|||||:|||||:  
Db 655 AGAGGGCGCGACGGG 640

RESULT 11  
US-11-121-849-531952  
; Sequence 531952, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded se  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; PRIOR FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 531952  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-531952

Query Match 77.8%; Score 14; DB 12; Length 25;  
Best Local Similarity 92.9%; Pred. No. 2.1e+02;  
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUCGCGACGGG 15  
|||||:|||||:|||||:  
Db 12 GAGGCTCGCATCGG 25

RESULT 12  
US-10-750-185-4096/c  
; Sequence 4096, Application US/10750185  
; Publication No. US200502603A1



GENERAL INFORMATION:  
APPLICANT: MMI GENOMICS, INC.  
APPLICANT: DENISE, Sue K.  
APPLICANT: KERR, Richard  
APPLICANT: ROSENFELD, David  
APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen  
APPLICANT: PANTIN, Dennis  
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
FILE REFERENCE: M11100-2  
CURRENT APPLICATION NUMBER: US/10/750,185  
PRIOR FILING DATE: 2003-12-31  
PRIOR APPLICATION NUMBER: US 60/437,482  
PRIOR FILING DATE: 2002-12-31  
NUMBER OF SEQ ID NOS: 64922  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4096  
LENGTH: 600  
TYPE: DNA  
ORGANISM: Bovine MMBT19288  
US-10-750-185-4096

Query Match 77.8%; Score 14; DB 8; Length 600;  
Best Local Similarity 87.5%; Pred. No. 1.9e+02;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACCGCG 16  
DB 307 AGAGGGGCGACCGCG 292

RESULT 13  
US-10-750-623-4096/C  
Sequence 4096, Application US/10750623  
Publication No. US20050287531A1  
GENERAL INFORMATION:  
APPLICANT: MMI GENOMICS, INC.  
APPLICANT: DENISE, Sue K.  
APPLICANT: KERR, Richard  
APPLICANT: ROSENFELD, David  
APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen  
APPLICANT: PANTIN, Dennis  
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
FILE REFERENCE: M11100-1  
CURRENT APPLICATION NUMBER: US/10/750,623  
PRIOR FILING DATE: 2003-12-31  
PRIOR APPLICATION NUMBER: US 60/437,482  
PRIOR FILING DATE: 2002-12-31  
NUMBER OF SEQ ID NOS: 64922  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4096  
LENGTH: 600  
TYPE: DNA  
ORGANISM: Bovine MMBT19288  
US-10-750-623-4096

Query Match 77.8%; Score 14; DB 8; Length 600;  
Best Local Similarity 87.5%; Pred. No. 1.9e+02;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACCGCG 16  
DB 307 AGAGGGGCGACCGCG 292

RESULT 14  
US-09-925-065A-552179/C  
Sequence 552179, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 552179  
LENGTH: 1454  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-552179

Query Match 77.8%; Score 14; DB 6; Length 1454;  
Best Local Similarity 92.9%; Pred. No. 1.9e+02;  
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGGUGCGACCGCG 16  
DB 422 AGGTCGCGACCGCG 409

RESULT 15  
US-09-925-065A-649799  
Sequence 649799, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 649799  
LENGTH: 414  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-649799

Query Match 76.7%; Score 13.8; DB 6; Length 414;  
Best Local Similarity 76.5%; Pred. No. 2.5e+02;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGGUGCGACCGCGUA 18  
DB 292 GAGGTCGCGACCGCGTA 308

RESULT 16  
US-09-925-065A-99074/C  
Sequence 99074, Application US/09925065A  
Publication No. US20040181048A1

```

; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99074
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-99074

```

```

Query Match          76.7%; Score 13.8; DB 6; Length 426;
Best Local Similarity 76.5%; Pred. No. 2.5e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 AGAGGGUCGACGCCGGU 17
    |||||:|||||:
DB 24 AGAGGGTCGAACGCCGT 8

```

```

RESULT 17
US-09-925-065A-151643
; Sequence 151643, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151643
; LENGTH: 577
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-151643

```

```

Query Match          76.7%; Score 13.8; DB 6; Length 577;
Best Local Similarity 76.5%; Pred. No. 2.5e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 AGAGGGUCGACGCCGGU 17
    |||||:|||||:
DB 118 AGAGGGTCGAACGCCGT 134

```

RESULT 18

```

US-09-925-065A-151644
; Sequence 151644, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151644
; LENGTH: 577
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-151644

```

```

Query Match          76.7%; Score 13.8; DB 6; Length 577;
Best Local Similarity 76.5%; Pred. No. 2.5e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 AGAGGGUCGACGCCGGU 17
    |||||:|||||:
DB 118 AGAGGGTCGAACGCCGT 134

```

```

RESULT 19
US-09-925-065A-151645
; Sequence 151645, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151645
; LENGTH: 577
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-151645

```

```

Query Match          76.7%; Score 13.8; DB 6; Length 577;
Best Local Similarity 76.5%; Pred. No. 2.5e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 AGAGGGUCGACGCCGGU 17
    |||||:|||||:
DB 118 AGAGGGTCGAACGCCGT 134

```

```
RESULT 20
US-11-096-568A-18587/c
; Sequence 18587, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nicholas et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592P052
; CURRENT APPLICATION NUMBER: US/11/096,568A
; PRIOR FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 18587
; LENGTH: 1490
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1490)
; OTHER INFORMATION: Ceres Seq. ID no. 12365955
US-11-096-568A-18587

Query Match          76.7%; Score 13.8; DB 9; Length 1490;
Best Local Similarity 76.5%; Pred. No. 2.4e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 AGAGGUGCGACCGCGU 17
    |||||:|||||:
Db 876 AGCGGTCGACGCGGT 860
```

```
RESULT 21
US-09-925-065A-709998
; Sequence 709998, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 709998
; LENGTH: 1492
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-709998
```

```
Query Match          76.7%; Score 13.8; DB 6; Length 1492;
Best Local Similarity 76.5%; Pred. No. 2.4e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 AGAGGUGCGACCGCGU 17
    |||||:|||||:
Db 451 AGAGGTCGACGCGGT 467
```

```
RESULT 22
US-10-240-708-20
```

```
; Sequence 20, Application US/10240708
; Publication No. US20050282157A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: BERENBERG, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/240,708
; PRIOR FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 20
; LENGTH: 6866
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-708-20
```

```
Query Match          76.7%; Score 13.8; DB 8; Length 6866;
Best Local Similarity 76.5%; Pred. No. 2.3e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 AGAGGUGCGACCGCGU 17
    |||||:|||||:
Db 4008 ATAGGTCGACGCGGT 4024
```

```
RESULT 23
US-09-925-065A-74944
; Sequence 74944, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74944
; LENGTH: 566
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-74944
```

```
Query Match          74.4%; Score 13.4; DB 6; Length 566;
Best Local Similarity 76.5%; Pred. No. 4.2e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 AGAGGUGCGACCGCGU 17
```

Db 273 AGAGGCGCAGCGCGT 289

RESULT 24  
US-09-925-065A-46507

/ Sequence 46507, Application US/09925065A  
/ Publication No. US20040181048A1

/ GENERAL INFORMATION:

/ APPLICANT: Wang, David G.

/ TITLE OF INVENTION: Identification and Mapping of Single

/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

/ FILE REFERENCE: 108827.135

/ CURRENT APPLICATION NUMBER: US/09/925,065A

/ PRIOR FILING DATE: 2001-08-08

/ PRIOR APPLICATION NUMBER: US 60/243,096

/ PRIOR FILING DATE: 2000-10-24

/ PRIOR APPLICATION NUMBER: US 60/252,147

/ PRIOR FILING DATE: 2000-11-20

/ PRIOR APPLICATION NUMBER: US 60/250,092

/ PRIOR FILING DATE: 2000-11-30

/ PRIOR APPLICATION NUMBER: US 60/261,766

/ PRIOR FILING DATE: 2001-01-16

/ PRIOR APPLICATION NUMBER: US 60/289,846

/ PRIOR FILING DATE: 2001-05-09

/ NUMBER OF SEQ ID NOS: 957086

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 46507

/ LENGTH: 580

/ TYPE: DNA

/ ORGANISM: Homo sapiens

/ US-09-925-065A-46507

Query Match 74.4%; Score 13.4; DB 6; Length 580;

Best Local Similarity 93.3%; Pred. No. 4.2e+02; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGCGCGCAGCGCG 16

Db 123 GAGGCGCGCAGCGCG 137

RESULT 25  
US-09-925-065A-299863/C

/ Sequence 299863, Application US/09925065A

/ Publication No. US20040181048A1

/ GENERAL INFORMATION:

/ APPLICANT: Wang, David G.

/ TITLE OF INVENTION: Identification and Mapping of Single

/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

/ FILE REFERENCE: 108827.135

/ CURRENT APPLICATION NUMBER: US/09/925,065A

/ PRIOR FILING DATE: 2001-08-08

/ PRIOR APPLICATION NUMBER: US 60/243,096

/ PRIOR FILING DATE: 2000-10-24

/ PRIOR APPLICATION NUMBER: US 60/252,147

/ PRIOR FILING DATE: 2000-11-20

/ PRIOR APPLICATION NUMBER: US 60/250,092

/ PRIOR FILING DATE: 2000-11-30

/ PRIOR APPLICATION NUMBER: US 60/261,766

/ PRIOR FILING DATE: 2001-01-16

/ PRIOR APPLICATION NUMBER: US 60/289,846

/ PRIOR FILING DATE: 2001-05-09

/ NUMBER OF SEQ ID NOS: 957086

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 299863

/ LENGTH: 589

/ TYPE: DNA

/ ORGANISM: Homo sapiens

/ US-09-925-065A-299863

Query Match 74.4%; Score 13.4; DB 6; Length 589;

Best Local Similarity 80.0%; Pred. No. 4.2e+02; Indels 0; Gaps 0;

Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGGCGCGCAGCGCGU 17

Db 528 AGGCGCGCAGCGCGT 514

RESULT 26  
US-09-925-065A-47629

/ Sequence 47629, Application US/09925065A

/ Publication No. US20040181048A1

/ GENERAL INFORMATION:

/ APPLICANT: Wang, David G.

/ TITLE OF INVENTION: Identification and Mapping of Single

/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

/ FILE REFERENCE: 108827.135

/ CURRENT APPLICATION NUMBER: US/09/925,065A

/ PRIOR FILING DATE: 2001-08-08

/ PRIOR APPLICATION NUMBER: US 60/243,096

/ PRIOR FILING DATE: 2000-10-24

/ PRIOR APPLICATION NUMBER: US 60/252,147

/ PRIOR FILING DATE: 2000-11-20

/ PRIOR APPLICATION NUMBER: US 60/250,092

/ PRIOR FILING DATE: 2000-11-30

/ PRIOR APPLICATION NUMBER: US 60/261,766

/ PRIOR FILING DATE: 2001-01-16

/ PRIOR APPLICATION NUMBER: US 60/289,846

/ PRIOR FILING DATE: 2001-05-09

/ NUMBER OF SEQ ID NOS: 957086

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 47629

/ LENGTH: 605

/ TYPE: DNA

/ ORGANISM: Homo sapiens

/ US-09-925-065A-47629

Query Match 74.4%; Score 13.4; DB 6; Length 605;

Best Local Similarity 93.3%; Pred. No. 4.2e+02; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGCGCGCAGCGCG 16

Db 123 GAGGCGCGCAGCGCG 137

RESULT 27  
US-11-136-527-1781/C

/ Sequence 1781, Application US/11136527

/ Publication No. US20050287570A1

/ GENERAL INFORMATION:

/ APPLICANT: Wyeth

/ APPLICANT: Mounts, William M

/ TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

/ FILE REFERENCE: 031896-041000 (AM101086)

/ CURRENT APPLICATION NUMBER: US/11/136,527

/ PRIOR FILING DATE: 2005-05-25

/ PRIOR APPLICATION NUMBER: US 60/574,294

/ PRIOR FILING DATE: 2005-05-26

/ NUMBER OF SEQ ID NOS: 362830

/ SOFTWARE: Patentin version 3.2

/ SEQ ID NO 1781

/ LENGTH: 1185

/ TYPE: DNA

/ ORGANISM: Rattus norvegicus

/ US-11-136-527-1781

Query Match 74.4%; Score 13.4; DB 12; Length 1185;

Best Local Similarity 80.0%; Pred. No. 4.1e+02; Indels 0; Gaps 0;

Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGGCGCGCAGCGCGU 17

Db 907 AGGCGCGCAGCGCGT 893

## RESULT 28

US-10-750-185-62892/c  
; Sequence 62892, Application US/10750185  
; Publication No. US2005026063A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: PANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM11100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 62892  
; LENGTH: 1213  
; TYPE: DNA  
; ORGANISM: Bovine 19866880761026  
US-10-750-185-62892

Query Match 74.4%; Score 13.4; DB 8; Length 1213;  
Best Local Similarity 80.0%; Pred. No. 4.1e+02;  
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGUGCGACGCGGTA 18  
|||:|||||:  
Db 775 GGGTGCGACGCGTA 761

## RESULT 29

US-10-750-623-62892/c  
; Sequence 62892, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: PANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM11100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 62892  
; LENGTH: 1213  
; TYPE: DNA  
; ORGANISM: Bovine 19866880761026  
US-10-750-623-62892

Query Match 74.4%; Score 13.4; DB 8; Length 1213;  
Best Local Similarity 80.0%; Pred. No. 4.1e+02;  
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGUGCGACGCGGTA 18  
|||:|||||:  
Db 775 GGGTGCGACGCGTA 761

## RESULT 30

## US-11-171-701-1/c

; Sequence 1, Application US/11171701  
; Publication No. US20060008879A1  
; GENERAL INFORMATION:  
; APPLICANT: Ocani, Suzanne  
; APPLICANT: Blinkovsky, Alexander  
; APPLICANT: Ge, Haiyan  
; APPLICANT: Harris, Paul  
; APPLICANT: Yaver, Debbie  
; TITLE OF INVENTION: Polypeptides Having Alpha-Glucosidase Activity And  
; TITLE OF INVENTION: Polynucleotides Encoding Same  
; FILE REFERENCE: 10655.200-US  
; CURRENT APPLICATION NUMBER: US/11/171,701  
; CURRENT FILING DATE: 2005-06-29  
; PRIOR APPLICATION NUMBER: 60/585,336  
; PRIOR FILING DATE: 2005-06-29  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 2954  
; TYPE: DNA  
; ORGANISM: Aspergillus fumigatus  
US-11-171-701-1

Query Match 74.4%; Score 13.4; DB 12; Length 2954;  
Best Local Similarity 86.7%; Pred. No. 4e+02;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGCGG 16  
|||:|||||:  
Db 2741 GAGGUGCGACGCGG 2727

## RESULT 31

US-10-912-971-1/c  
; Sequence 1, Application US/10912971  
; Publication No. US20060029546A1  
; GENERAL INFORMATION:  
; APPLICANT: Gurney, et al.  
; TITLE OF INVENTION: MATERIALS AND METHODS FOR IDENTIFYING ANTI-SCHIZOPHRENIC AGENTS  
; FILE REFERENCE: 30847/40237  
; CURRENT APPLICATION NUMBER: US/10/912,971  
; CURRENT FILING DATE: 2004-08-06  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 4663  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-912-971-1

Query Match 74.4%; Score 13.4; DB 7; Length 4663;  
Best Local Similarity 86.7%; Pred. No. 4e+02;  
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 GGUGCGACGCGGTA 18  
|||:|||||:  
Db 1164 GGGTGCGACGCGCA 1150

## RESULT 32

US-11-082-154A-118/c  
; Sequence 118, Application US/11082154A  
; Publication No. US20060024820A1  
; GENERAL INFORMATION:  
; APPLICANT: Perkins, Edward  
; APPLICANT: Perez, Carl  
; APPLICANT: Lindenbaum, Michael  
; APPLICANT: Greene, Amy  
; APPLICANT: Leung, Josephine  
; APPLICANT: Fleming, Siena  
; APPLICANT: Stewart, Sandra  
; APPLICANT: Shellard, Joan

QY 4 GGUGCGACGCGGTA 18  
|||:|||||:  
Db 1164 GGGTGCGACGCGCA 1150

US-10-933-982-106785  
; Sequence 106785, Application US/10933982  
; Publication No. US20060051769A1  
; GENERAL INFORMATION:  
; APPLICANT: Barts, Jennifer  
; TITLE OF INVENTION: Methods of Genetic Analysis of E. coli  
; FILE REFERENCE: 3700  
; CURRENT APPLICATION NUMBER: US/10/933,982  
; PRIOR FILING DATE: 2004-09-03  
; NUMBER OF SEQ ID NOS: 224976  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 106785  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: E. coli  
US-10-933-982-106785

Query Match 73.3%; Score 13.2; DB 7; Length 25;  
Best Local Similarity 72.2%; Pred. No. 5.8e+02;  
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18  
DB 3 ATATGCTCGACGCTGTGA 20

RESULT 35  
US-11-121-849-355753  
; Sequence 355753, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded ss  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; PRIOR FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949  
; PRIOR FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 673904  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 355753  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-355753

Query Match 73.3%; Score 13.2; DB 12; Length 25;  
Best Local Similarity 77.8%; Pred. No. 5.8e+02;  
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18  
DB 5 AGAGGACTCTGCGCGCA 22

RESULT 36  
US-09-925-065A-290316  
; Sequence 290316, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30

Query Match 74.4%; Score 13.4; DB 12; Length 22118;  
Best Local Similarity 93.3%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGG 15  
DB 7580 AGAGGACGCGACGCG 7566

RESULT 34

```

; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 290316
; LENGTH: 479
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-290316

Query Match
Best Local Similarity 73.3%; Score 13.2; DB 6; Length 479;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGUGCCACGCGGUA 18
DB 224 AGAGGCTGCGACGAGCTA 241

RESULT 37
US-09-925-065A-354563
; Sequence 354563, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 354563
; LENGTH: 514
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-354563

Query Match
Best Local Similarity 73.3%; Score 13.2; DB 6; Length 514;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGUGCCACGCGGUA 18
DB 330 AGAGGCTGCGTGGCAGCTA 347

RESULT 38
US-09-925-065A-143833
; Sequence 143833, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
```

```

; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 143833
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-143833

Query Match
Best Local Similarity 73.3%; Score 13.2; DB 6; Length 526;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGUGCCACGCGGUA 18
DB 35 AGAGGCTGCGACGAGCTA 52

RESULT 39
US-09-925-065A-143834
; Sequence 143834, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 143834
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-143834

Query Match
Best Local Similarity 73.3%; Score 13.2; DB 6; Length 526;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGUGCCACGCGGUA 18
DB 35 AGAGGCTGCGACGAGCTA 52

RESULT 40
US-10-475-075-758
; Sequence 758, Application US/10475075
; Publication No. US20060053498A1
; GENERAL INFORMATION:
; APPLICANT: Bejani, Stephanie
; APPLICANT: Tanaka, Hiroaki
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Jobert, Severin
; APPLICANT: Giordano, Jean-Yves
; TITLE OF INVENTION: Full-length human cDNAs encoding potentially secreted proteins
```



```
FILE REFERENCE: G-081US03PCT
CURRENT APPLICATION NUMBER: US/10/475,075
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: PCT/IB01/00914
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 918
SOFTWARE: Patent.pm
SEQ ID NO 758
LENGTH: 543
TYPE: DNA
ORGANISM: Homo sapiens
US-10-475-075-758

Query Match
Best Local Similarity 73.3%; Score 13.2; DB 6; Length 543;
Pred. No. 5.4e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACCGGUA 18
Db 285 AAAGGTCACACGGGTA 302

RESULT 41
US-09-925-065A-742789/C
Sequence 742789, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 742789
LENGTH: 548
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-742789

Query Match
Best Local Similarity 73.3%; Score 13.2; DB 6; Length 548;
Pred. No. 5.4e+02;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACCGGUA 18
Db 173 ACAGGGCCGACACGGTA 156

RESULT 42
US-09-925-065A-505693/C
Sequence 505693, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
```

```
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 505693
LENGTH: 550
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-505693

Query Match
Best Local Similarity 73.3%; Score 13.2; DB 6; Length 550;
Pred. No. 5.4e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACCGGUA 18
Db 292 AGAGGTCACACGGTGA 275

RESULT 43
US-09-925-065A-839454
Sequence 839454, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 839454
LENGTH: 584
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-839454

Query Match
Best Local Similarity 73.3%; Score 13.2; DB 6; Length 584;
Pred. No. 5.4e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACCGGUA 18
Db 14 AGAGGTCACCTGTA 31

RESULT 44
US-09-925-065A-847993/C
Sequence 847993, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
```

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; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 847993
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-847993

Query Match
Best Local Similarity 73.3%; Score 13.2; DB 6; Length 585;
Best Local Similarity 72.2%; Pred. No. 5.4e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGUGCCACCGCGUA 18
    |||||:|||||:|
Db 574 AGAGGCTCTCACTTGTA 557

RESULT 45
US-09-925-065A-516742
; Sequence 516742, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 516742
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-516742

Query Match
Best Local Similarity 73.3%; Score 13.2; DB 6; Length 594;
Best Local Similarity 72.2%; Pred. No. 5.4e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGUGCCACCGCGUA 18
    |||||:|||||:|
Db 429 AGAGGTGGCACCTGTGA 446

RESULT 46
US-09-925-065A-516743
; Sequence 516743, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
```

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; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 516743
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-516743

Query Match
Best Local Similarity 73.3%; Score 13.2; DB 6; Length 594;
Best Local Similarity 72.2%; Pred. No. 5.4e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGUGCCACCGCGUA 18
    |||||:|||||:|
Db 429 AGAGGTGGCACCTGTGA 446

RESULT 47
US-09-925-065A-516744
; Sequence 516744, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 516744
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-516744

Query Match
Best Local Similarity 73.3%; Score 13.2; DB 6; Length 594;
Best Local Similarity 72.2%; Pred. No. 5.4e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAGGUGCCACCGCGUA 18
    |||||:|||||:|
Db 429 AGAGGTGGCACCTGTGA 446

RESULT 48
US-09-925-065A-151923
; Sequence 151923, Application US/09925065A
; Publication No. US20040181048A1
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; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151923
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-151923

```

```

Query Match      73.3%; Score 13.2; DB 6; Length 603;
Best Local Similarity 72.2%; Pred. No. 5.4e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      1 AGAGGGUCCGACGCGGUA 18
Db      492 AGAGGGTGGCATGTGGTA 509

```

```

RESULT 49
; US-09-925-065A-841497
; Sequence 841497, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 841497
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-841497

```

```

Query Match      73.3%; Score 13.2; DB 6; Length 625;
Best Local Similarity 72.2%; Pred. No. 5.4e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      1 AGAGGGUCCGACGCGGUA 18
Db      457 AGAGGGTGGCATGTGGTA 474

```

RESULT 50

```

US-09-925-065A-821405
; Sequence 821405, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 821405
; LENGTH: 629
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-821405

```

```

Query Match      73.3%; Score 13.2; DB 6; Length 629;
Best Local Similarity 72.2%; Pred. No. 5.4e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

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QY      1 AGAGGGUCCGACGCGGUA 18
Db      461 AGAGGGTGGCATGTGGTA 478

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Search completed: March 19, 2006, 05:42:21  
Job time : 1217.62 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 18:35:47 ; Search time 2695.85 Seconds  
(without alignments)  
55.214 Million cell updates/sec

Title: US-10-800-926-1

Sequence: 1 agagggucgacgcgsgua 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database :

Published Applications NA.Main:\*  
1: /cgn2\_6/prodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/prodata/1/pubpna/US08\_PUBCOMB.seq:\*  
3: /cgn2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq:\*  
4: /cgn2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq:\*  
5: /cgn2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*  
6: /cgn2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*  
7: /cgn2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*  
8: /cgn2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*  
9: /cgn2\_6/prodata/1/pubpna/US10\_PUBCOMB.seq:\*  
10: /cgn2\_6/prodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	18	100.0	18	3	US-09-824-468-60 Sequence 60, Appl
C 2	18	100.0	18	3	US-09-888-326-485 Sequence 485, Appl
C 3	18	100.0	18	3	US-09-776-479-4 Sequence 4, Appl
C 4	18	100.0	18	3	US-09-776-479-4 Sequence 56, Appl
C 5	18	100.0	18	3	US-09-954-9878-67 Sequence 67, Appl
C 6	18	100.0	18	3	US-09-776-479-4 Sequence 4, Appl
C 7	18	100.0	18	3	US-09-776-479-4 Sequence 56, Appl
C 8	18	100.0	18	3	US-10-112-653-4 Sequence 4, Appl
C 9	18	100.0	18	3	US-10-017-995-4 Sequence 56, Appl
C 10	18	100.0	18	3	US-10-017-995-4 Sequence 56, Appl
C 11	18	100.0	18	3	US-10-161-229-54 Sequence 54, Appl
C 12	18	100.0	18	3	US-10-187-264A-60 Sequence 60, Appl
C 13	18	100.0	18	3	US-10-265-072-75 Sequence 75, Appl
C 14	18	100.0	18	3	US-10-06-522-60 Sequence 60, Appl
C 15	18	100.0	18	3	US-10-314-578-4 Sequence 56, Appl
C 16	18	100.0	18	3	US-10-314-578-4 Sequence 56, Appl
C 17	18	100.0	18	3	US-10-373-381-47 Sequence 47, Appl
C 18	18	100.0	18	3	US-10-719-493-60 Sequence 60, Appl
C 19	18	100.0	18	3	US-10-627-331-60 Sequence 60, Appl
C 20	18	100.0	18	3	US-10-877-369-47 Sequence 47, Appl
C 21	18	100.0	18	3	US-10-831-778-4 Sequence 4, Appl
C 22	18	100.0	18	3	US-10-831-778-4 Sequence 56, Appl
C 23	18	100.0	18	3	US-10-876-892-47 Sequence 47, Appl

C 24	18	100.0	18	8	US-10-876-965-47 Sequence 47, Appl
C 25	18	100.0	18	8	US-10-800-926-1 Sequence 1, Appl
C 26	18	100.0	18	9	US-10-627-413-60 Sequence 60, Appl
C 27	18	100.0	18	9	US-10-921-086-60 Sequence 60, Appl
C 28	18	100.0	18	10	US-11-084-777-67 Sequence 67, Appl
C 29	18	100.0	18	10	US-11-071-836-60 Sequence 60, Appl
C 30	18	100.0	18	10	US-11-110-189-60 Sequence 43, Appl
C 31	18	100.0	17	6	US-10-053-645A-43 Sequence 9, Appl
C 32	17	94.4	17	6	US-10-053-645A-9 Sequence 5, Appl
C 33	17	94.4	17	9	US-10-822-205-5 Sequence 9, Appl
C 34	17	94.4	17	9	US-10-961-458-9 Sequence 9, Appl
C 35	16.4	91.1	20	3	US-09-781-980-4 Sequence 4, Appl
C 36	16	88.9	16	10	US-11-021-729-58 Sequence 58, Appl
C 37	16	88.9	32	3	US-09-965-116A-79 Sequence 79, Appl
C 38	16	88.9	32	3	US-09-965-116A-80 Sequence 80, Appl
C 39	16	88.9	32	8	US-10-694-075-79 Sequence 79, Appl
C 40	16	88.9	32	8	US-10-694-075-80 Sequence 80, Appl
C 41	16	88.9	32	8	US-10-694-383-79 Sequence 79, Appl
C 42	16	88.9	32	8	US-10-694-383-80 Sequence 80, Appl
C 43	16	88.9	32	8	US-10-694-418-79 Sequence 79, Appl
C 44	16	88.9	32	8	US-10-694-418-80 Sequence 80, Appl
C 45	15	83.3	17	6	US-10-053-645A-8 Sequence 8, Appl
C 46	15	83.3	17	9	US-10-961-458-8 Sequence 8, Appl
C 47	15	83.3	337	8	US-10-723-860-668 Sequence 668, Appl
C 48	15	83.3	337	9	US-10-756-149-689 Sequence 689, Appl
C 49	15	83.3	363	7	US-10-918-995-126012 Sequence 126012, A
C 50	15	83.3	381	7	US-09-918-995-36640 Sequence 36640, A
C 51	15	83.3	588	7	US-10-767-701-4082 Sequence 4082, A
C 52	15	83.3	779	8	US-10-478-914-58 Sequence 58, Appl
C 53	15	83.3	1936	3	US-09-954-456-1138 Sequence 1138, A
C 54	15	83.3	1936	8	US-10-843-641A-4165 Sequence 4165, A
C 55	15	83.3	3870	8	US-10-723-860-5301 Sequence 5301, A
C 56	14.8	82.2	18	3	US-09-734-846-69 Sequence 69, Appl
C 57	14.8	82.2	18	6	US-10-302-262-69 Sequence 69, Appl
C 58	14.8	82.2	1512	7	US-10-425-114-26340 Sequence 26340, A
C 59	14.8	82.2	2140405	5	US-10-027-632-76212 Sequence 76212, A
C 60	14.8	82.2	2140405	6	US-10-027-632-76212 Sequence 76212, A
C 61	14.4	80.0	25	8	US-10-719-900-359937 Sequence 359937, A
C 62	14.4	80.0	25	10	US-11-036-317-604153 Sequence 604153, A
C 63	14.4	80.0	378	9	US-10-779-543-11148 Sequence 11148, A
C 64	14.4	80.0	821	8	US-10-425-115-18852 Sequence 18852, A
C 65	14.4	80.0	886	8	US-10-425-115-16778 Sequence 16778, A
C 66	14.4	80.0	957	8	US-10-425-115-16779 Sequence 16779, A
C 67	14.4	80.0	1532	7	US-10-767-701-13328 Sequence 13328, A
C 68	14.4	80.0	2000	3	US-09-938-842A-3764 Sequence 3764, A
C 69	14.4	80.0	2000	3	US-09-938-842A-3764 Sequence 3764, A
C 70	14.4	80.0	2103	7	US-10-767-701-13076 Sequence 13076, A
C 71	14.4	80.0	2193	3	US-09-997-722-55 Sequence 55, Appl
C 72	14.4	80.0	27846	3	US-09-952-060-31 Sequence 31, Appl
C 73	14.4	80.0	36620	7	US-10-380-641-31 Sequence 31, Appl
C 74	14.4	80.0	36620	9	US-10-636-730-31 Sequence 31, Appl
C 75	14.4	80.0	36620	9	US-10-636-730-31 Sequence 31, Appl
C 76	14.4	80.0	37474	3	US-09-952-060-26 Sequence 26, Appl
C 77	14.4	80.0	37474	3	US-10-380-641-26 Sequence 26, Appl
C 78	14.4	80.0	37474	8	US-10-645-883A-8 Sequence 8, Appl
C 79	14.4	80.0	37474	8	US-10-645-187-7 Sequence 7, Appl
C 80	14.4	80.0	37474	9	US-10-636-730-26 Sequence 26, Appl
C 81	14.4	80.0	37474	9	US-10-507-098-3 Sequence 3, Appl
C 82	14.4	80.0	38519	3	US-09-952-060-29 Sequence 29, Appl
C 83	14.4	80.0	38519	7	US-10-380-641-29 Sequence 29, Appl
C 84	14.4	80.0	38519	7	US-10-636-730-29 Sequence 29, Appl
C 85	14.4	80.0	104729	8	US-10-723-860-1334 Sequence 1334, A
C 86	14.4	80.0	104729	8	US-10-723-860-1334 Sequence 1334, A
C 87	14.4	80.0	13117	8	US-10-779-591-1 Sequence 1, Appl
C 88	14.4	80.0	13117	8	US-10-779-591-1 Sequence 1, Appl
C 89	14.4	80.0	1331719	9	US-10-297-465A-1 Sequence 1, Appl
C 90	14	77.8	17	6	US-10-053-645A-10 Sequence 10, Appl
C 91	14	77.8	17	9	US-10-961-458-10 Sequence 10, Appl
C 92	14	77.8	384	7	US-10-424-599-76033 Sequence 76033, A
C 93	14	77.8	389	7	US-10-424-599-76033 Sequence 76033, A
C 94	14	77.8	1454	4	US-09-925-065A-552179 Sequence 552179, A
C 95	14	77.8	1498	7	US-10-425-114-12591 Sequence 12591, A
C 96	14	77.8	1498	8	US-10-425-115-114887 Sequence 114887, A

C 97	14	77.8	1752	8	US-10-425-115-53432	Sequence 53432, A	170	13.8	76.7	2663	5	US-10-087-110-1	Sequence 1, Appl1
98	14	77.8	1791	7	US-10-425-114-24178	Sequence 24178, A	C 171	13.8	76.7	2951	10	US-11-097-143-18478	Sequence 18478, A
99	14	77.8	2293	8	US-10-425-115-53442	Sequence 53442, A	C 172	13.8	76.7	3076	8	US-10-425-115-177044	Sequence 177044, A
100	14	77.8	2463	8	US-10-425-115-170656	Sequence 170656, A	C 173	13.8	76.7	3129	7	US-10-437-963-98363	Sequence 98363, A
101	14	77.8	4317	7	US-10-697-036-69	Sequence 69, Appl1	C 174	13.8	76.7	4542	7	US-10-437-963-18105	Sequence 18105, A
C 102	14	77.8	6276	10	US-11-097-143-42070	Sequence 42070, A	C 175	13.8	76.7	4569	6	US-10-156-761-7339	Sequence 7339, Ap
103	14	77.8	15362	3	US-09-764-877-2856	Sequence 2856, Ap	C 176	13.8	76.7	5973	10	US-11-097-143-33221	Sequence 33221, A
104	14	77.8	15362	6	US-10-442-515-2856	Sequence 2856, Ap	C 177	13.8	76.7	6497	10	US-11-097-143-18136	Sequence 18136, A
105	14	77.8	15535	3	US-09-764-877-2855	Sequence 2855, Ap	C 178	13.8	76.7	6816	6	US-09-935-541-1	Sequence 1, Appl1
106	14	77.8	15535	6	US-10-442-515-2855	Sequence 2855, Ap	C 179	13.8	76.7	6816	6	US-10-425-800-1	Sequence 1, Appl1
C 107	13.8	76.7	211	8	US-10-425-115-53619	Sequence 53619, A	C 180	13.8	76.7	6855	3	US-09-935-541-3	Sequence 3, Appl1
C 108	13.8	76.7	225	7	US-10-437-963-97910	Sequence 97910, A	C 181	13.8	76.7	6855	6	US-10-425-800-3	Sequence 3, Appl1
C 109	13.8	76.7	287	8	US-10-425-115-164021	Sequence 164021, A	C 182	13.8	76.7	6866	6	US-10-311-453-640	Sequence 640, App
C 110	13.8	76.7	310	8	US-10-425-115-11406	Sequence 11406, A	C 183	13.8	76.7	8346	6	US-10-240-453-201	Sequence 201, App
C 111	13.8	76.7	386	9	US-10-756-149-4367	Sequence 4367, Ap	C 184	13.8	76.7	9302	6	US-09-764-870-646	Sequence 646, App
112	13.8	76.7	406	7	US-10-424-599-133031	Sequence 133031, A	C 185	13.8	76.7	9302	5	US-10-125-540-646	Sequence 646, App
113	13.8	76.7	414	4	US-09-925-065A-133031	Sequence 649794, A	C 186	13.8	76.7	10016	10	US-11-097-143-33224	Sequence 23224, A
C 114	13.8	76.7	426	4	US-09-925-065A-99074	Sequence 99074, A	C 187	13.8	76.7	14180	10	US-11-097-143-33227	Sequence 23227, A
C 115	13.8	76.7	430	7	US-10-424-599-79765	Sequence 79765, A	C 188	13.8	76.7	1062	10	US-11-097-143-18487	Sequence 18487, A
C 116	13.8	76.7	442	8	US-10-425-115-173258	Sequence 173258, A	C 189	13.8	76.7	25617	9	US-10-485-710-7	Sequence 7, Appl1
C 117	13.8	76.7	450	3	US-09-918-995-5084	Sequence 5084, Ap	C 190	13.8	76.7	50000	5	US-10-063-763-4	Sequence 4, Appl1
C 118	13.8	76.7	480	9	US-10-915-740A-694	Sequence 694, App	C 191	13.8	76.7	50000	5	US-10-060-763-4	Sequence 110, App
C 119	13.8	76.7	486	7	US-10-437-963-88924	Sequence 88924, A	C 192	13.8	76.7	50000	7	US-10-423-543-110	Sequence 58, Appl
C 120	13.8	76.7	501	5	US-10-437-963-42589	Sequence 42589, A	C 193	13.8	76.7	61103	5	US-10-087-192-58	Sequence 1, Appl1
C 121	13.8	76.7	527	5	US-10-027-632-288223	Sequence 288223, A	C 194	13.8	76.7	149430	8	US-10-626-832-1	Sequence 1, Appl1
C 122	13.8	76.7	527	6	US-10-027-632-288223	Sequence 288223, A	C 195	13.8	76.7	150223	7	US-10-624-149A-1	Sequence 1, Appl1
C 123	13.8	76.7	538	8	US-10-425-115-155585	Sequence 155585, A	C 196	13.8	76.7	203654	3	US-09-820-905-3	Sequence 3, Appl1
C 124	13.8	76.7	577	4	US-09-925-065A-151643	Sequence 151643, A	C 197	13.8	76.7	203654	8	US-10-473-338A-3	Sequence 3, Appl1
C 125	13.8	76.7	577	4	US-09-925-065A-151644	Sequence 151644, A	C 198	13.8	76.7	337344	8	US-10-388-838-58	Sequence 58, Appl
C 126	13.8	76.7	577	4	US-09-925-065A-151645	Sequence 151645, A	C 199	13.8	76.7	347001	7	US-10-319-908-16	Sequence 16, Appl
C 127	13.8	76.7	592	8	US-10-363-345A-23309	Sequence 23309, A	C 200	13.8	76.7	401433	9	US-10-737-082-79	Sequence 79, Appl
C 128	13.8	76.7	592	8	US-10-363-345A-23310	Sequence 23310, A	C 201	13.8	76.7	401433	9	US-10-765-790-79	Sequence 79, Appl
C 129	13.8	76.7	592	9	US-10-363-483A-23309	Sequence 23309, A	C 202	13.8	76.7	902608	6	US-10-156-761-1	Sequence 1, Appl1
C 130	13.8	76.7	592	9	US-10-363-483A-23310	Sequence 23310, A	C 203	13.8	76.7	902608	6	US-10-156-761-1	Sequence 1, Appl1
C 131	13.8	76.7	593	5	US-10-027-632-264177	Sequence 264177, A	C 204	13.4	74.4	25	7	US-10-719-966-43523	Sequence 43523, A
C 132	13.8	76.7	593	5	US-10-027-632-264178	Sequence 264178, A	C 205	13.4	74.4	165	6	US-10-156-761-6310	Sequence 6310, Ap
C 133	13.8	76.7	593	6	US-10-027-632-264177	Sequence 264177, A	C 206	13.4	74.4	293	6	US-09-294-093B-1786	Sequence 1786, Ap
C 134	13.8	76.7	593	6	US-10-027-632-264178	Sequence 264178, A	C 207	13.4	74.4	314	7	US-10-424-599-113658	Sequence 113658, A
C 135	13.8	76.7	599	9	US-10-972-079-61333	Sequence 61333, A	C 208	13.4	74.4	325	8	US-10-425-115-4932	Sequence 4932, A
C 136	13.8	76.7	599	9	US-10-972-079-61334	Sequence 61334, A	C 209	13.4	74.4	382	8	US-10-856-499-1949	Sequence 1949, App
C 137	13.8	76.7	599	9	US-10-972-079-61335	Sequence 61335, A	C 210	13.4	74.4	426	3	US-09-960-355-9997	Sequence 9997, Ap
C 138	13.8	76.7	604	7	US-10-767-701-31426	Sequence 31426, A	C 211	13.4	74.4	431	8	US-10-425-115-115494	Sequence 115494, A
C 139	13.8	76.7	690	8	US-10-425-115-119505	Sequence 119505, A	C 212	13.4	74.4	442	3	US-09-960-355-4560	Sequence 4360, Ap
C 140	13.8	76.7	725	8	US-10-463-345A-33203	Sequence 33203, A	C 213	13.4	74.4	448	10	US-11-006-098-81	Sequence 81, Appl
C 141	13.8	76.7	725	8	US-10-463-345A-33204	Sequence 33204, A	C 214	13.4	74.4	471	3	US-09-738-626-33087	Sequence 33087, Ap
C 142	13.8	76.7	725	9	US-10-463-483A-33204	Sequence 33204, A	C 215	13.4	74.4	496	3	US-09-918-995-33847	Sequence 33847, A
C 143	13.8	76.7	725	9	US-10-463-483A-33204	Sequence 33204, A	C 216	13.4	74.4	545	7	US-10-856-499-252	Sequence 85153, A
C 144	13.8	76.7	750	7	US-10-425-114-1441	Sequence 1441, Ap	C 217	13.4	74.4	563	8	US-10-437-963-85153	Sequence 252, App
C 145	13.8	76.7	920	6	US-10-594-006-25	Sequence 25, Appl	C 218	13.4	74.4	566	4	US-09-925-065A-74944	Sequence 74944, A
C 146	13.8	76.7	920	7	US-10-594-006-25	Sequence 25, Appl	C 219	13.4	74.4	580	4	US-09-925-065A-74944	Sequence 74944, A
C 147	13.8	76.7	927	6	US-10-594-006-25	Sequence 25, Appl	C 220	13.4	74.4	589	4	US-09-925-065A-74944	Sequence 74944, A
C 148	13.8	76.7	1000	7	US-10-594-006-25	Sequence 25, Appl	C 221	13.4	74.4	594	10	US-11-006-098-79	Sequence 79, Appl
C 149	13.8	76.7	1105	8	US-10-425-115-41103	Sequence 41103, A	C 222	13.4	74.4	605	4	US-09-925-065A-74949	Sequence 74949, A
C 150	13.8	76.7	1212	6	US-10-156-761-2154	Sequence 2154, Ap	C 223	13.4	74.4	610	8	US-10-363-345A-37479	Sequence 37480, A
C 151	13.8	76.7	1215	7	US-10-482-122A-40326	Sequence 40326, A	C 224	13.4	74.4	610	8	US-10-363-345A-37479	Sequence 37480, A
C 152	13.8	76.7	1222	6	US-10-369-493-32790	Sequence 32790, A	C 225	13.4	74.4	610	9	US-10-363-483A-37480	Sequence 37480, A
C 153	13.8	76.7	1287	5	US-10-369-493-26680	Sequence 26680, A	C 226	13.4	74.4	610	9	US-10-363-483A-37480	Sequence 37480, A
C 154	13.8	76.7	1289	5	US-10-137-473-10	Sequence 10, Appl	C 227	13.4	74.4	627	7	US-10-021-332-8883	Sequence 8883, Ap
C 155	13.8	76.7	1338	10	US-11-097-143-41837	Sequence 41837, A	C 228	13.4	74.4	628	5	US-10-027-632-288222	Sequence 288222, A
C 156	13.8	76.7	1351	6	US-10-425-114-32758	Sequence 32758, A	C 229	13.4	74.4	628	5	US-10-027-632-288222	Sequence 288222, A
C 157	13.8	76.7	1351	6	US-10-477-161-72	Sequence 72, Appl	C 230	13.4	74.4	687	7	US-10-351-242-43	Sequence 43, Appl
C 158	13.8	76.7	1375	3	US-09-915-925-3	Sequence 3, Appl1	C 231	13.4	74.4	712	9	US-10-487-804-343	Sequence 343, App
C 159	13.8	76.7	1375	6	US-10-294-006-3	Sequence 3, Appl1	C 232	13.4	74.4	712	9	US-10-487-804-350	Sequence 350, App
C 160	13.8	76.7	1402	6	US-10-369-493-34393	Sequence 34393, A	C 233	13.4	74.4	741	7	US-10-767-701-8983	Sequence 8983, Ap
C 161	13.8	76.7	1492	4	US-09-925-065A-709998	Sequence 709998, A	C 234	13.4	74.4	1046	5	US-10-027-632-100954	Sequence 100954, A
C 162	13.8	76.7	1629	9	US-10-450-763-17705	Sequence 17705, A	C 235	13.4	74.4	1046	5	US-10-027-632-100955	Sequence 100955, A
C 163	13.8	76.7	1629	9	US-10-450-763-25131	Sequence 25131, A	C 236	13.4	74.4	1046	6	US-10-027-632-100955	Sequence 100955, A
C 164	13.8	76.7	1662	8	US-10-425-115-56344	Sequence 56344, A	C 237	13.4	74.4	1046	6	US-10-027-632-100955	Sequence 100955, A
C 165	13.8	76.7	1671	6	US-10-469-493-24437	Sequence 24437, A	C 238	13.4	74.4	1297	8	US-10-437-963-29466	Sequence 29466, A
C 166	13.8	76.7	1753	3	US-09-814-353-20009	Sequence 20009, A	C 239	13.4	74.4	1297	8	US-10-363-345A-19085	Sequence 19085, A
C 167	13.8	76.7	1937	10	US-11-097-143-23222	Sequence 23222, A	C 240	13.4	74.4	1297	8	US-10-363-345A-19086	Sequence 19086, A
C 168	13.8	76.7	2349	5	US-10-087-110-5	Sequence 5, Appl1	C 241	13.4	74.4	1297	9	US-10-363-483A-19086	Sequence 19086, A
C 169	13.8	76.7	2364	7	US-10-437-963-70634	Sequence 70634, A	C 242	13.4	74.4	1297	9	US-10-363-483A-19086	Sequence 19086, A

C 243	13.4	74.4	1358	8	US-10-856-499-473	Sequence 473, App	C 316	13.4	74.4	4361	5	US-10-007-747-23	Sequence 23, Appl
C 244	13.4	74.4	1377	7	US-10-437-963-21080	Sequence 21080, A	C 317	13.4	74.4	4361	5	US-10-038-937-23	Sequence 23, Appl
C 245	13.4	74.4	1401	6	US-10-369-493-26591	Sequence 26591, A	C 318	13.4	74.4	4659	5	US-10-243-740-9	Sequence 9, Appl
C 246	13.4	74.4	1457	6	US-10-172-118-1713	Sequence 1713, Ap	C 319	13.4	74.4	4659	5	US-10-146-806-10	Sequence 10, Appl
C 247	13.4	74.4	1457	7	US-10-342-887-1713	Sequence 1713, Ap	C 320	13.4	74.4	4780	7	US-10-437-963-29469	Sequence 29469, A
C 248	13.4	74.4	1457	9	US-10-287-436A-270	Sequence 270, App	C 321	13.4	74.4	6690	10	US-11-097-143-22394	Sequence 22394, A
C 249	13.4	74.4	1457	9	US-10-287-436A-1376	Sequence 1276, Ap	C 322	13.4	74.4	7282	5	US-10-213-948-11	Sequence 11, Appl
C 250	13.4	74.4	1503	7	US-10-437-963-38395	Sequence 38395, A	C 323	13.4	74.4	7796	6	US-10-348-155-12	Sequence 12, Appl
C 251	13.4	74.4	1506	6	US-10-156-761-5829	Sequence 5829, Ap	C 324	13.4	74.4	8663	3	US-09-764-878-397	Sequence 397, App
C 252	13.4	74.4	1506	9	US-10-450-763-6845	Sequence 6845, Ap	C 325	13.4	74.4	8663	3	US-10-079-854-337	Sequence 397, App
C 253	13.4	74.4	1506	9	US-10-450-763-28207	Sequence 28207, A	C 326	13.4	74.4	17384	6	US-10-161-403-118	Sequence 118, App
C 254	13.4	74.4	1548	3	US-09-986-480-145	Sequence 145, App	C 327	13.4	74.4	22118	10	US-11-006-076-118	Sequence 118, App
C 255	13.4	74.4	1548	3	US-10-863-332-145	Sequence 145, App	C 328	13.4	74.4	22118	3	US-09-799-462A-16	Sequence 16, Appl
C 256	13.4	74.4	1611	9	US-10-510-021-28	Sequence 28, Appl	C 329	13.4	74.4	22118	3	US-09-815-991-5	Sequence 5, Appl
C 257	13.4	74.4	1684	9	US-10-450-763-26528	Sequence 26528, A	C 330	13.4	74.4	22118	3	US-09-836-911A-16	Sequence 16, Appl
C 258	13.4	74.4	1752	9	US-10-487-804-363	Sequence 363, App	C 331	13.4	74.4	22118	3	US-09-815-979-5	Sequence 5, Appl
C 259	13.4	74.4	1752	8	US-10-425-115-17692	Sequence 363, App	C 332	13.4	74.4	22118	5	US-10-125-767-16	Sequence 16, Appl
C 260	13.4	74.4	1762	10	US-11-097-143-6592	Sequence 174692, A	C 333	13.4	74.4	22118	5	US-10-151-061-16	Sequence 16, Appl
C 261	13.4	74.4	1911	5	US-10-152-886-40	Sequence 6992, Ap	C 334	13.4	74.4	22118	5	US-10-287-313-16	Sequence 16, Appl
C 262	13.4	74.4	1911	10	US-11-053-052-40	Sequence 40, Appl	C 335	13.4	74.4	22118	5	US-10-219-694-16	Sequence 16, Appl
C 263	13.4	74.4	1911	10	US-11-053-052-40	Sequence 40, Appl	C 336	13.4	74.4	22118	5	US-10-235-119-5	Sequence 5, Appl
C 264	13.4	74.4	1914	6	US-10-369-493-40681	Sequence 40681, A	C 337	13.4	74.4	22118	6	US-10-161-403-18	Sequence 18, Appl
C 265	13.4	74.4	1986	7	US-10-767-701-14605	Sequence 14605, A	C 338	13.4	74.4	22118	6	US-10-086-745-5	Sequence 5, Appl
C 266	13.4	74.4	2340	3	US-09-815-242-7995	Sequence 7995, Ap	C 339	13.4	74.4	22118	6	US-10-428-653-5	Sequence 5, Appl
C 267	13.4	74.4	2340	7	US-10-282-122A-30620	Sequence 30620, A	C 340	13.4	74.4	22118	9	US-10-808-689-16	Sequence 16, Appl
C 268	13.4	74.4	2576	7	US-10-473-574-52	Sequence 52, Appl	C 341	13.4	74.4	22118	9	US-10-976-394-5	Sequence 5, Appl
C 269	13.4	74.4	2763	6	US-10-369-493-32734	Sequence 32734, A	C 342	13.4	74.4	22118	9	US-10-976-394-5	Sequence 5, Appl
C 270	13.4	74.4	2888	10	US-11-097-143-22478	Sequence 22478, A	C 343	13.4	74.4	22118	10	US-10-151-078A-16	Sequence 16, Appl
C 271	13.4	74.4	3007	3	US-09-945-901-33	Sequence 33, Appl	C 344	13.4	74.4	22118	10	US-11-006-076-18	Sequence 18, Appl
C 272	13.4	74.4	3007	5	US-10-007-747-33	Sequence 33, Appl	C 345	13.4	74.4	22115	7	US-09-997-722-118	Sequence 118, App
C 273	13.4	74.4	3007	5	US-10-038-937-33	Sequence 33, Appl	C 346	13.4	74.4	24883	7	US-10-322-281-1	Sequence 1, Appl
C 274	13.4	74.4	3070	5	US-09-945-901-39	Sequence 39, Appl	C 347	13.4	74.4	26729	6	US-10-283-247-6	Sequence 6, Appl
C 275	13.4	74.4	3070	5	US-10-007-747-39	Sequence 39, Appl	C 348	13.4	74.4	26729	6	US-10-283-247-6	Sequence 6, Appl
C 276	13.4	74.4	3109	6	US-10-038-937-39	Sequence 39, Appl	C 349	13.4	74.4	2833	5	US-11-143-787-6	Sequence 6, Appl
C 277	13.4	74.4	3109	6	US-10-101-510-449	Sequence 449, App	C 350	13.4	74.4	31808	9	US-10-087-192-651	Sequence 691, App
C 278	13.4	74.4	3135	6	US-10-156-761-2721	Sequence 2721, Ap	C 351	13.4	74.4	47670	10	US-11-097-143-22477	Sequence 22477, A
C 279	13.4	74.4	3155	5	US-09-945-901-13	Sequence 13, Appl	C 352	13.4	74.4	47670	10	US-11-097-143-22477	Sequence 22477, A
C 280	13.4	74.4	3155	5	US-10-007-747-13	Sequence 13, Appl	C 353	13.4	74.4	65958	7	US-10-316-242-11	Sequence 11, Appl
C 281	13.4	74.4	3155	5	US-10-038-937-13	Sequence 13, Appl	C 354	13.4	74.4	70383	7	US-10-283-247-3	Sequence 3, Appl
C 282	13.4	74.4	3211	3	US-09-945-901-21	Sequence 21, Appl	C 355	13.4	74.4	70383	10	US-11-143-787-3	Sequence 3, Appl
C 283	13.4	74.4	3211	5	US-10-007-747-21	Sequence 21, Appl	C 356	13.4	74.4	71887	8	US-10-087-192-1654	Sequence 1654, Ap
C 284	13.4	74.4	3211	5	US-10-038-937-21	Sequence 21, Appl	C 357	13.4	74.4	149430	8	US-10-626-832-1	Sequence 1, Appl
C 285	13.4	74.4	3274	3	US-09-945-901-37	Sequence 37, Appl	C 358	13.4	74.4	150223	7	US-10-624-149A-1	Sequence 1, Appl
C 286	13.4	74.4	3274	5	US-10-007-747-37	Sequence 37, Appl	C 359	13.4	74.4	156387	8	US-10-741-600-17574	Sequence 17574, A
C 287	13.4	74.4	3274	5	US-10-038-937-37	Sequence 37, Appl	C 360	13.4	74.4	2940917	5	US-10-027-632-174763	Sequence 174763, A
C 288	13.4	74.4	3546	10	US-11-097-143-16228	Sequence 16228, A	C 361	13.4	74.4	2940917	5	US-10-027-632-174763	Sequence 174763, A
C 289	13.4	74.4	3622	10	US-11-097-143-16270	Sequence 16270, A	C 362	13.4	74.4	3309400	3	US-09-738-626-1	Sequence 1, Appl
C 290	13.4	74.4	3633	8	US-10-526-832-155	Sequence 155, App	C 363	13.2	73.3	25	5	US-10-098-263B-81315	Sequence 81315, A
C 291	13.4	74.4	3731	5	US-09-945-901-31	Sequence 31, Appl	C 364	13.2	73.3	100	9	US-10-476-264-150	Sequence 150, App
C 292	13.4	74.4	3731	5	US-10-007-747-31	Sequence 31, Appl	C 365	13.2	73.3	100	9	US-10-476-264-151	Sequence 151, App
C 293	13.4	74.4	3731	5	US-10-038-937-31	Sequence 31, Appl	C 366	13.2	73.3	192	9	US-10-617-320-603	Sequence 603, App
C 294	13.4	74.4	3794	3	US-09-945-901-27	Sequence 27, Appl	C 367	13.2	73.3	197	9	US-10-450-763-467	Sequence 467, App
C 295	13.4	74.4	3794	5	US-10-007-747-27	Sequence 27, Appl	C 368	13.2	73.3	197	9	US-10-450-763-2830	Sequence 2830, Ap
C 296	13.4	74.4	3794	5	US-10-038-937-27	Sequence 27, Appl	C 369	13.2	73.3	197	9	US-10-450-763-4798	Sequence 4798, Ap
C 297	13.4	74.4	3831	7	US-10-382-122A-30485	Sequence 30485, A	C 370	13.2	73.3	197	9	US-10-450-763-15890	Sequence 15890, A
C 298	13.4	74.4	3935	3	US-09-945-901-19	Sequence 19, Appl	C 371	13.2	73.3	197	9	US-10-450-763-23944	Sequence 23944, A
C 299	13.4	74.4	3935	3	US-10-007-747-19	Sequence 19, Appl	C 372	13.2	73.3	201	8	US-10-719-993-31811	Sequence 31811, A
C 300	13.4	74.4	3935	5	US-10-038-937-19	Sequence 19, Appl	C 373	13.2	73.3	206	9	US-10-476-264-57	Sequence 57, Appl
C 301	13.4	74.4	3998	5	US-09-945-901-35	Sequence 35, Appl	C 374	13.2	73.3	234	7	US-10-437-963-55616	Sequence 55616, A
C 302	13.4	74.4	3998	5	US-10-007-747-35	Sequence 35, Appl	C 375	13.2	73.3	237	7	US-10-424-559-101021	Sequence 101021, A
C 303	13.4	74.4	3998	5	US-10-038-937-35	Sequence 35, Appl	C 376	13.2	73.3	250	8	US-10-425-115-49884	Sequence 49884, A
C 304	13.4	74.4	3998	10	US-11-097-143-37984	Sequence 37984, A	C 377	13.2	73.3	251	7	US-10-424-559-27681	Sequence 27681, A
C 305	13.4	74.4	4094	5	US-09-945-901-29	Sequence 29, Appl	C 378	13.2	73.3	269	8	US-10-425-115-121476	Sequence 121476, A
C 306	13.4	74.4	4094	5	US-10-007-747-29	Sequence 29, Appl	C 379	13.2	73.3	301	8	US-10-422-115-26250	Sequence 26250, A
C 307	13.4	74.4	4094	5	US-10-038-937-29	Sequence 29, Appl	C 380	13.2	73.3	327	3	US-09-974-300-3682	Sequence 3682, Ap
C 308	13.4	74.4	4157	3	US-09-945-901-25	Sequence 25, Appl	C 381	13.2	73.3	331	8	US-10-425-115-15831	Sequence 15831, A
C 309	13.4	74.4	4157	5	US-10-007-747-25	Sequence 25, Appl	C 382	13.2	73.3	333	3	US-09-974-300-7073	Sequence 7073, Ap
C 310	13.4	74.4	4157	5	US-10-038-937-25	Sequence 25, Appl	C 383	13.2	73.3	339	8	US-10-425-115-153696	Sequence 153696, A
C 311	13.4	74.4	4287	10	US-11-097-143-6991	Sequence 6991, Ap	C 384	13.2	73.3	380	8	US-10-858-707-8	Sequence 8, Appl
C 312	13.4	74.4	4298	3	US-09-945-901-1	Sequence 1, Appl	C 385	13.2	73.3	394	9	US-10-450-763-486	Sequence 486, App
C 313	13.4	74.4	4298	3	US-10-007-747-1	Sequence 1, Appl	C 386	13.2	73.3	394	9	US-10-450-763-2829	Sequence 2829, Ap
C 314	13.4	74.4	4298	5	US-10-038-937-1	Sequence 1, Appl	C 387	13.2	73.3	394	9	US-10-450-763-23943	Sequence 23943, A
C 315	13.4	74.4	4361	3	US-09-945-901-23	Sequence 23, Appl	C 388	13.2	73.3	399	8	US-10-425-115-11367	Sequence 11367, A

389	13.2	73.3	400	9	US-10-498-978-5	Sequence 5, Appl1
390	13.2	73.3	402	3	US-09-214-474A-3	Sequence 7, Appl1
391	13.2	73.3	402	3	US-09-214-474A-7	Sequence 7, Appl1
392	13.2	73.3	426	8	US-10-425-115-118550	Sequence 118550
393	13.2	73.3	432	7	US-10-437-963-38264	Sequence 38264, A
394	13.2	73.3	451	7	US-10-437-963-3135	Sequence 3135, Ap
395	13.2	73.3	457	7	US-09-338-626-597	Sequence 597, App
396	13.2	73.3	468	3	US-09-732-627A-1668	Sequence 1668, Ap
397	13.2	73.3	474	3	US-10-242-535A-33948	Sequence 33948, A
398	13.2	73.3	476	7	US-10-085-783A-33948	Sequence 33948, A
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415	13.2	73.3	514	8	US-10-363-345A-5511	Sequence 5511, Ap
416	13.2	73.3	514	9	US-10-363-483A-5511	Sequence 5511, Ap
417	13.2	73.3	514	9	US-10-363-483A-5511	Sequence 5511, Ap
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426	13.2	73.3	525	9	US-10-363-483A-25831	Sequence 25831, A
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428	13.2	73.3	526	4	US-09-925-065A-143833	Sequence 143833, A
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430	13.2	73.3	531	6	US-09-925-065A-742789	Sequence 742789, A
431	13.2	73.3	530	4	US-09-925-065A-505693	Sequence 505693, A
432	13.2	73.3	531	7	US-10-767-701-328	Sequence 328, App
433	13.2	73.3	533	9	US-10-972-079-74608	Sequence 74608, A
434	13.2	73.3	533	9	US-10-972-079-74608	Sequence 74608, A
435	13.2	73.3	533	9	US-10-363-345A-207481	Sequence 207481, A
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461	13.2	73.3	533	9	US-10-363-345A-207481	Sequence 207481, A



535	13.2	73.3	1434	9	US-10-450-763-1457	Sequence 1457, App	608	13.2	73.3	20190	7	US-10-287-190-167	Sequence 167, App
536	13.2	73.3	1434	9	US-10-450-763-22463	Sequence 22463, A	609	13.2	73.3	20190	7	US-10-307-817-153	Sequence 153, App
537	13.2	73.3	1434	9	US-10-450-763-28866	Sequence 28866, A	610	13.2	73.3	22614	6	US-10-085-117-199	Sequence 199, App
538	13.2	73.3	1432	6	US-10-369-493-34366	Sequence 34366, A	611	13.2	73.3	33303	9	US-10-915-740A-61	Sequence 61, Appl
539	13.2	73.3	1544	7	US-10-437-963-4593	Sequence 4593, Ap	612	13.2	73.3	33531	8	US-10-719-993-8846	Sequence 6846, Ap
540	13.2	73.3	1445	8	US-10-425-115-106700	Sequence 106700, A	613	13.2	73.3	39541	7	US-10-741-601-5736	Sequence 5736, Ap
541	13.2	73.3	1511	8	US-10-723-860-6070	Sequence 6070, Ap	614	13.2	73.3	47941	8	US-10-742-600-17880	Sequence 17880, A
542	13.2	73.3	1617	9	US-10-450-763-28868	Sequence 28868, A	615	13.2	73.3	51837	7	US-10-322-281-598	Sequence 598, App
543	13.2	73.3	1636	4	US-09-925-065A-715347	Sequence 715347, A	616	13.2	73.3	51929	5	US-10-087-192-823	Sequence 823, App
544	13.2	73.3	1636	4	US-09-925-065A-715348	Sequence 715348, A	617	13.2	73.3	51137	5	US-10-087-192-679	Sequence 679, App
545	13.2	73.3	1756	8	US-10-450-763-4806	Sequence 4806, Ap	618	13.2	73.3	55540	5	US-10-087-192-1189	Sequence 1189, Ap
546	13.2	73.3	1756	8	US-10-357-930-25567	Sequence 25567, A	619	13.2	73.3	71292	5	US-10-087-192-1942	Sequence 1942, Ap
547	13.2	73.3	1779	7	US-10-282-122A-13080	Sequence 13080, A	620	13.2	73.3	87001	8	US-10-741-600-17792	Sequence 17792, A
548	13.2	73.3	1815	7	US-10-439-703-43	Sequence 43, Appl	621	13.2	73.3	102145	8	US-10-331-053-73	Sequence 53, Appl
549	13.2	73.3	1854	6	US-10-369-493-42949	Sequence 42949, A	622	13.2	73.3	106644	7	US-10-433-287-79	Sequence 79, Appl
550	13.2	73.3	1867	3	US-09-967-768A-115	Sequence 115, App	623	13.2	73.3	123920	5	US-10-087-192-1453	Sequence 1453, Ap
551	13.2	73.3	1867	9	US-10-843-641A-6260	Sequence 6260, Ap	624	13.2	73.3	128668	5	US-10-087-192-340	Sequence 340, App
552	13.2	73.3	1883	9	US-10-450-763-4809	Sequence 4809, Ap	625	13.2	73.3	135005	8	US-10-723-860-5230	Sequence 230, App
553	13.2	73.3	1888	7	US-10-205-331-79	Sequence 79, Appl	626	13.2	73.3	135005	9	US-10-756-149-1719	Sequence 1719, Ap
554	13.2	73.3	1901	9	US-10-450-763-18273	Sequence 18273, A	627	13.2	73.3	152501	7	US-10-316-231-4	Sequence 4, Appl
555	13.2	73.3	1901	6	US-10-087-080-9	Sequence 9, Appl	628	13.2	73.3	170489	7	US-10-316-231-380	Sequence 380, App
556	13.2	73.3	1981	10	US-11-097-143-22943	Sequence 22943, A	629	13.2	73.3	171096	8	US-10-612-869-8	Sequence 8, Appl
557	13.2	73.3	2044	6	US-10-369-493-27133	Sequence 27133, A	630	13.2	73.3	227448	9	US-10-461-862-53	Sequence 53, Appl
558	13.2	73.3	2155	9	US-10-481-032A-647	Sequence 647, App	631	13.2	73.3	325348	6	US-10-085-117-358	Sequence 358, App
559	13.2	73.3	2155	9	US-10-481-032A-700	Sequence 700, App	632	13.2	73.3	339234	7	US-10-322-696-73	Sequence 73, Appl
560	13.2	73.3	2166	5	US-10-027-632-102986	Sequence 102986, A	633	13.2	73.3	421609	7	US-10-367-094-122	Sequence 122, App
561	13.2	73.3	2166	6	US-10-027-632-102986	Sequence 102986, A	634	13.2	73.3	438892	5	US-10-087-192-454	Sequence 454, App
562	13.2	73.3	2191	7	US-10-437-963-75900	Sequence 75900, A	635	13.2	73.3	651591	8	US-10-087-192-208	Sequence 20, Appl
563	13.2	73.3	2212	9	US-10-450-763-2840	Sequence 2840, Ap	636	13.2	73.3	7322598	8	US-10-472-928-4979	Sequence 479, Ap
564	13.2	73.3	2271	3	US-09-919-585-2	Sequence 2, Appl	637	13.2	73.3	2242716	9	US-10-915-740A-1068	Sequence 1068, Ap
565	13.2	73.3	2322	10	US-11-073-550-31	Sequence 31, Appl	638	13.2	73.3	3309400	3	US-09-738-626-1	Sequence 1, Appl
566	13.2	73.3	2322	10	US-11-073-550-52	Sequence 52, Appl	639	13.2	73.3	20	5	US-10-022-598-13	Sequence 13, Appl
567	13.2	73.3	2413	9	US-10-450-763-28861	Sequence 28861, A	640	13.2	73.3	20	7	US-10-777-838-13	Sequence 13, Appl
568	13.2	73.3	2504	6	US-10-369-493-24527	Sequence 24527, A	641	13.2	73.3	20	8	US-10-793-497-13	Sequence 13, Appl
569	13.2	73.3	2504	6	US-10-067-632-63	Sequence 63, Appl	642	13.2	73.3	25	10	US-11-036-317-464441	Sequence 46441, A
570	13.2	73.3	2546	7	US-10-403-571-95	Sequence 95, Appl	643	13.2	73.3	25	10	US-11-036-317-750630	Sequence 750630, A
571	13.2	73.3	2650	9	US-10-994-138-1	Sequence 1, Appl	644	13.2	73.3	234	3	US-09-864-408A-8671	Sequence 8671, Ap
572	13.2	73.3	2684	10	US-11-097-143-4667	Sequence 4667, Ap	645	13.2	73.3	237	6	US-10-156-761-5933	Sequence 5933, Ap
573	13.2	73.3	2747	10	US-11-097-143-13304	Sequence 13304, A	646	13.2	73.3	282	7	US-10-424-559-55964	Sequence 55964, A
574	13.2	73.3	2987	7	US-10-276-774-398	Sequence 398, App	647	13.2	73.3	521	9	US-10-972-079-21267	Sequence 21267, A
575	13.2	73.3	3319	9	US-10-450-763-5102	Sequence 5102, App	648	13.2	73.3	571	8	US-10-425-115-59398	Sequence 59398, A
576	13.2	73.3	3321	9	US-10-450-763-21396	Sequence 21396, A	649	13.2	73.3	607	8	US-10-425-115-147678	Sequence 147678, A
577	13.2	73.3	3367	3	US-09-745-763-105	Sequence 105, App	650	13.2	73.3	732	4	US-10-425-115-115375	Sequence 115375, A
578	13.2	73.3	3369	2	US-08-961-527-42	Sequence 42, Appl	651	13.2	73.3	732	8	US-09-925-055A-9190	Sequence 9190, Ap
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580	13.2	73.3	3420	6	US-10-369-493-34226	Sequence 34226, A	653	13.2	73.3	849	9	US-10-627-476-587	Sequence 587, App
581	13.2	73.3	3658	9	US-10-320-797-214	Sequence 214, App	654	13.2	73.3	972	7	US-10-627-476-587	Sequence 587, App
582	13.2	73.3	3794	7	US-10-450-763-28871	Sequence 28871, A	655	13.2	73.3	1260	7	US-10-437-963-24189	Sequence 24189, A
583	13.2	73.3	3907	7	US-10-320-797-215	Sequence 215, App	656	13.2	73.3	1357	8	US-10-425-115-166442	Sequence 166442, A
584	13.2	73.3	3922	7	US-10-437-963-18656	Sequence 18656, A	657	13.2	73.3	1401	7	US-10-437-963-24188	Sequence 24188, A
585	13.2	73.3	4237	9	US-10-450-763-22464	Sequence 22464, A	658	13.2	73.3	1608	7	US-10-437-963-18753	Sequence 18753, A
586	13.2	73.3	4268	9	US-10-450-763-2844	Sequence 2844, Ap	659	13.2	73.3	1617	7	US-10-282-122A-17559	Sequence 27559, A
587	13.2	73.3	4340	10	US-11-097-143-22942	Sequence 22942, A	660	13.2	73.3	2019	6	US-10-431-273-9	Sequence 9, Appl
588	13.2	73.3	4860	9	US-10-450-763-20698	Sequence 20698, A	661	13.2	73.3	2039	6	US-10-437-963-25329	Sequence 25329, A
589	13.2	73.3	4874	7	US-10-467-397-11	Sequence 11, Appl	662	13.2	73.3	2160	7	US-10-398-221-3350	Sequence 3350, Ap
590	13.2	73.3	4927	7	US-10-467-397-20	Sequence 20, Appl	663	13.2	73.3	2478	7	US-10-109-310-31	Sequence 31, Appl
591	13.2	73.3	4986	10	US-11-097-143-13303	Sequence 13303, A	664	13.2	73.3	3285	3	US-09-712-363-143	Sequence 143, App
592	13.2	73.3	5197	6	US-09-860-670-248	Sequence 248, App	665	13.2	73.3	3612	10	US-10-745-237-125	Sequence 125, App
593	13.2	73.3	5197	6	US-10-227-646-248	Sequence 248, App	666	13.2	73.3	3612	10	US-11-097-143-26798	Sequence 26798, A
594	13.2	73.3	5891	6	US-10-311-455-1412	Sequence 1412, Ap	667	13.2	73.3	6324	10	US-11-097-143-26797	Sequence 26797, A
595	13.2	73.3	13154	10	US-11-097-143-26042	Sequence 26042, A	668	13.2	73.3	30000	3	US-09-980-217-3	Sequence 3, Appl
596	13.2	73.3	14417	3	US-09-860-670-251	Sequence 251, App	669	13.2	73.3	31328	7	US-10-109-310-19	Sequence 19, Appl
597	13.2	73.3	14417	6	US-10-227-646-251	Sequence 251, App	670	13.2	73.3	104514	5	US-10-087-192-1981	Sequence 1981, App
598	13.2	73.3	14426	3	US-09-860-670-249	Sequence 249, App	671	13.2	73.3	137560	8	US-10-481-112-1	Sequence 1, Appl
599	13.2	73.3	14426	6	US-09-860-670-252	Sequence 252, App	672	12.8	71.1	25	7	US-10-719-996-678540	Sequence 678540, A
600	13.2	73.3	14426	6	US-10-227-646-249	Sequence 249, App	673	12.8	71.1	25	8	US-10-719-990-359936	Sequence 359936, A
601	13.2	73.3	14426	6	US-10-227-646-252	Sequence 252, App	674	12.8	71.1	25	8	US-10-719-990-760102	Sequence 760102, A
602	13.2	73.3	14448	3	US-09-860-670-250	Sequence 250, App	675	12.8	71.1	25	8	US-10-719-990-774327	Sequence 774327, A
603	13.2	73.3	14448	6	US-10-227-646-250	Sequence 250, App	676	12.8	71.1	25	10	US-11-036-317-604152	Sequence 604152, A
604	13.2	73.3	14451	3	US-09-860-670-253	Sequence 253, App	677	12.8	71.1	35	7	US-10-422-366-27	Sequence 27, Appl
605	13.2	73.3	14451	6	US-10-227-646-253	Sequence 253, App	678	12.8	71.1	35	9	US-10-925-216-27	Sequence 27, Appl
606	13.2	73.3	16680	10	US-11-097-143-26041	Sequence 26041, A	679	12.8	71.1	35	9	US-10-903-582-27	Sequence 27, Appl
607	13.2	73.3	20190	3	US-09-996-015-3	Sequence 3, Appl	680	12.8	71.1	35	9	US-10-918-401A-27	Sequence 27, Appl

681	12.8	71.1	35	9	US-10-969-245-27	Sequence 27, Appl	c 754	12.8	71.1	465	8	US-10-425-115-126433	Sequence 126433,
c 682	12.8	71.1	45	8	US-10-776-399A-7	Sequence 7, Appl1	755	12.8	71.1	466	8	US-10-425-115-12048	Sequence 12048, A
c 683	12.8	71.1	50	6	US-10-131-827-4053	Sequence 4053, Ap	756	12.8	71.1	467	4	US-09-925-065A-253979	Sequence 253979,
684	12.8	71.1	132	3	US-09-783-590-11092	Sequence 11092, A	c 757	12.8	71.1	476	9	US-10-779-543-5085	Sequence 5085, Ap
c 685	12.8	71.1	132	7	US-10-437-963-97133	Sequence 97133, A	c 758	12.8	71.1	480	4	US-09-925-065A-630197	Sequence 630197,
686	12.8	71.1	132	8	US-10-425-115-4816	Sequence 4816, Ap	c 759	12.8	71.1	480	4	US-09-925-065A-630198	Sequence 630198,
687	12.8	71.1	156	7	US-10-437-963-51792	Sequence 51792, A	c 760	12.8	71.1	482	7	US-10-767-701-31414	Sequence 31414, A
c 688	12.8	71.1	160	8	US-10-425-115-29205	Sequence 29205, A	c 761	12.8	71.1	484	7	US-10-021-332-7475	Sequence 7475, Ap
c 689	12.8	71.1	173	8	US-10-425-115-67732	Sequence 67732, A	c 762	12.8	71.1	485	3	US-09-867-701-6696	Sequence 6696, Ap
c 690	12.8	71.1	186	8	US-10-425-115-27981	Sequence 27981, A	c 763	12.8	71.1	485	4	US-09-925-065A-534776	Sequence 534776,
c 691	12.8	71.1	194	7	US-10-437-963-81722	Sequence 81722, A	c 764	12.8	71.1	485	3	US-10-424-599-108624	Sequence 108624,
c 692	12.8	71.1	197	8	US-10-425-115-149611	Sequence 149611, A	c 765	12.8	71.1	486	3	US-09-918-995-2543	Sequence 2543, Ap
c 693	12.8	71.1	201	8	US-10-719-993-13532	Sequence 13532, A	c 766	12.8	71.1	492	4	US-09-925-065A-480818	Sequence 480818,
c 694	12.8	71.1	208	6	US-10-46-953-1	Sequence 1, Appl1	c 767	12.8	71.1	492	6	US-10-029-386-20218	Sequence 20218, A
c 695	12.8	71.1	220	7	US-10-437-963-79269	Sequence 79269, A	c 768	12.8	71.1	493	4	US-09-925-065A-779738	Sequence 779738,
c 696	12.8	71.1	226	7	US-10-242-535A-3404	Sequence 3404, Ap	c 769	12.8	71.1	493	6	US-10-029-386-21257	Sequence 21257, A
c 697	12.8	71.1	226	7	US-10-085-783A-3404	Sequence 3404, Ap	c 770	12.8	71.1	494	3	US-09-918-995-25095	Sequence 25095, A
c 698	12.8	71.1	239	8	US-10-425-115-53860	Sequence 53860, A	c 771	12.8	71.1	498	7	US-10-767-701-20464	Sequence 20464, A
c 699	12.8	71.1	240	7	US-10-242-535A-16497	Sequence 16497, A	c 772	12.8	71.1	499	8	US-10-357-930-11646	Sequence 11646, A
c 700	12.8	71.1	240	7	US-10-085-783A-16497	Sequence 16497, A	c 773	12.8	71.1	501	4	US-09-925-065A-531881	Sequence 531881,
c 701	12.8	71.1	244	7	US-10-469-285-496	Sequence 496, App	c 774	12.8	71.1	505	4	US-10-437-963-46120	Sequence 46120, A
c 702	12.8	71.1	249	7	US-10-437-963-7457	Sequence 7457, Ap	c 775	12.8	71.1	505	4	US-09-925-065A-545160	Sequence 545160,
c 703	12.8	71.1	253	7	US-10-424-599-123028	Sequence 123028	c 776	12.8	71.1	505	4	US-09-925-065A-445163	Sequence 445163,
c 704	12.8	71.1	255	7	US-10-242-535A-9501	Sequence 9501, Ap	c 777	12.8	71.1	507	3	US-09-925-300-835	Sequence 835, App
c 705	12.8	71.1	255	7	US-10-085-783A-9501	Sequence 9501, Ap	c 778	12.8	71.1	510	8	US-10-363-345A-28783	Sequence 28783, A
c 706	12.8	71.1	266	8	US-10-425-115-166684	Sequence 166684,	c 779	12.8	71.1	510	8	US-10-363-345A-28784	Sequence 28784, A
c 707	12.8	71.1	270	8	US-10-425-115-1586	Sequence 1586, Ap	c 780	12.8	71.1	510	9	US-10-363-483A-28783	Sequence 28783,
c 708	12.8	71.1	290	7	US-10-242-535A-48438	Sequence 48438, A	c 781	12.8	71.1	510	9	US-10-363-483A-28784	Sequence 28784,
c 709	12.8	71.1	290	7	US-10-085-783A-48438	Sequence 48438, A	c 782	12.8	71.1	513	6	US-10-029-386-66488	Sequence 66488,
c 710	12.8	71.1	300	5	US-10-076-555-25	Sequence 25, Appl	c 783	12.8	71.1	513	8	US-10-425-115-21797	Sequence 21797, A
c 711	12.8	71.1	300	9	US-10-779-543-25	Sequence 25, Appl	c 784	12.8	71.1	514	8	US-10-425-115-21782	Sequence 21782, A
c 712	12.8	71.1	303	8	US-10-767-795-5661	Sequence 5661, Ap	c 785	12.8	71.1	527	5	US-10-027-633-266513	Sequence 266513,
c 713	12.8	71.1	304	5	US-10-027-632-104451	Sequence 104451,	c 786	12.8	71.1	527	5	US-10-027-633-266514	Sequence 266514,
c 714	12.8	71.1	304	6	US-10-027-632-325581	Sequence 325581,	c 787	12.8	71.1	527	5	US-10-027-633-266515	Sequence 266515,
c 715	12.8	71.1	304	6	US-10-027-632-104451	Sequence 104451,	c 788	12.8	71.1	527	6	US-10-027-633-266514	Sequence 266514,
c 716	12.8	71.1	304	6	US-10-027-632-325581	Sequence 325581,	c 789	12.8	71.1	527	6	US-10-027-633-266515	Sequence 266515,
c 717	12.8	71.1	315	8	US-10-723-860-1488	Sequence 1488, Ap	c 790	12.8	71.1	527	6	US-10-027-633-266515	Sequence 266515,
c 718	12.8	71.1	319	3	US-09-814-353-1860	Sequence 1860, Ap	c 791	12.8	71.1	528	6	US-10-156-761-5233	Sequence 5233, Ap
c 719	12.8	71.1	319	3	US-09-814-353-8207	Sequence 8207, Ap	c 792	12.8	71.1	528	6	US-10-156-761-5233	Sequence 5233, Ap
c 720	12.8	71.1	338	7	US-10-424-599-103789	Sequence 103789,	c 793	12.8	71.1	528	8	US-10-363-345A-11545	Sequence 11545, A
c 721	12.8	71.1	340	3	US-09-783-590-749	Sequence 749, App	c 794	12.8	71.1	528	9	US-10-363-483A-11545	Sequence 11545, A
c 722	12.8	71.1	342	7	US-10-437-963-73220	Sequence 73220, A	c 795	12.8	71.1	528	9	US-10-363-483A-11546	Sequence 11546,
c 723	12.8	71.1	343	3	US-09-864-408A-4747	Sequence 4747, Ap	c 796	12.8	71.1	529	5	US-10-027-633-266687	Sequence 266687,
c 724	12.8	71.1	346	8	US-10-425-115-17481	Sequence 17481, A	c 797	12.8	71.1	529	6	US-10-027-633-266687	Sequence 266687,
c 725	12.8	71.1	356	8	US-10-425-115-68270	Sequence 68270, A	c 798	12.8	71.1	535	6	US-10-029-386-13557	Sequence 13557, A
c 726	12.8	71.1	356	8	US-10-425-115-139050	Sequence 139050,	c 799	12.8	71.1	537	6	US-10-156-761-735	Sequence 735, App
c 727	12.8	71.1	361	8	US-10-357-930-37070	Sequence 37070, A	c 800	12.8	71.1	537	6	US-10-156-761-7348	Sequence 7348,
c 728	12.8	71.1	365	6	US-10-046-953-3	Sequence 3, Appl1	c 801	12.8	71.1	538	8	US-10-363-345A-36255	Sequence 36255, A
c 729	12.8	71.1	372	7	US-10-437-963-41453	Sequence 41453, A	c 802	12.8	71.1	538	8	US-10-363-345A-36256	Sequence 36256, A
c 730	12.8	71.1	378	3	US-09-854-867-235	Sequence 235, App	c 803	12.8	71.1	538	9	US-10-363-483A-36255	Sequence 36255, A
c 731	12.8	71.1	378	9	US-10-786-970A-235	Sequence 235, App	c 804	12.8	71.1	538	9	US-10-363-483A-36256	Sequence 36256, A
c 732	12.8	71.1	382	7	US-10-767-701-20874	Sequence 20874, A	c 805	12.8	71.1	540	3	US-09-764-891-62	Sequence 62, Appl
c 733	12.8	71.1	387	9	US-10-779-543-9419	Sequence 9419, Ap	c 806	12.8	71.1	540	7	US-10-437-963-68587	Sequence 68587, A
c 734	12.8	71.1	390	7	US-10-282-122A-11114	Sequence 11114, A	c 807	12.8	71.1	541	7	US-10-437-963-53706	Sequence 53706, A
c 735	12.8	71.1	390	7	US-10-282-122A-11837	Sequence 11837, A	c 808	12.8	71.1	544	4	US-09-925-065A-810563	Sequence 810563,
c 736	12.8	71.1	391	9	US-10-721-922A-295	Sequence 295, App	c 809	12.8	71.1	546	4	US-09-925-065A-874585	Sequence 874585,
c 737	12.8	71.1	395	8	US-10-425-115-121566	Sequence 121566,	c 810	12.8	71.1	546	4	US-09-925-065A-904381	Sequence 904381,
c 738	12.8	71.1	396	7	US-10-437-963-25995	Sequence 25995, A	c 811	12.8	71.1	546	8	US-10-425-115-4332	Sequence 4332, Ap
c 739	12.8	71.1	397	3	US-09-925-299-658	Sequence 658, App	c 812	12.8	71.1	549	4	US-09-925-065A-870454	Sequence 870454,
c 740	12.8	71.1	397	3	US-09-925-299-658	Sequence 658, App	c 813	12.8	71.1	549	4	US-09-925-065A-801725	Sequence 801725,
c 741	12.8	71.1	399	7	US-10-437-963-67787	Sequence 67787, A	c 814	12.8	71.1	552	8	US-10-723-860-7777	Sequence 7777, Ap
c 742	12.8	71.1	402	3	US-09-864-408A-53	Sequence 53, Appl	c 815	12.8	71.1	553	3	US-10-437-963-18855	Sequence 18855, A
c 743	12.8	71.1	403	7	US-10-424-599-38428	Sequence 38428, A	c 816	12.8	71.1	555	3	US-09-764-891-5500	Sequence 5500, Ap
c 744	12.8	71.1	410	7	US-10-437-963-45748	Sequence 45748, A	c 817	12.8	71.1	555	4	US-09-925-065A-639143	Sequence 639143,
c 745	12.8	71.1	410	7	US-10-437-963-45748	Sequence 45748, A	c 818	12.8	71.1	555	4	US-09-925-065A-639144	Sequence 639144,
c 746	12.8	71.1	414	3	US-09-925-299-284	Sequence 284, App	c 819	12.8	71.1	555	4	US-09-925-065A-639145	Sequence 639145,
c 747	12.8	71.1	414	3	US-09-925-299-284	Sequence 284, App	c 820	12.8	71.1	555	8	US-10-425-115-65735	Sequence 65735, A
c 748	12.8	71.1	414	7	US-10-424-599-79719	Sequence 79719, A	c 821	12.8	71.1	558	4	US-09-925-065A-994057	Sequence 994057,
c 749	12.8	71.1	427	8	US-10-357-930-7101	Sequence 7101, Ap	c 822	12.8	71.1	562	8	US-10-363-345A-39149	Sequence 39149, A
c 750	12.8	71.1	441	8	US-09-925-065A-496543	Sequence 496543,	c 823	12.8	71.1	562	8	US-10-363-345A-39150	Sequence 39150, A
c 751	12.8	71.1	441	4	US-09-925-065A-496544	Sequence 496544,	c 824	12.8	71.1	562	9	US-10-363-483A-39150	Sequence 39150, A
c 752	12.8	71.1	441	8	US-10-425-115-61389	Sequence 61389, A	c 825	12.8	71.1	562	9	US-10-363-483A-39150	Sequence 39150, A
c 753	12.8	71.1	459	3	US-09-918-995-1785	Sequence 1785, Ap	c 826	12.8	71.1	569	8	US-10-363-345A-7659	Sequence 7659, Ap

C 827	12.8	71.1	569	8	US-10-363-345A-7660	Sequence 7660, Ap	C 900	12.8	71.1	701	6	US-10-125-968-683	Sequence 683, App
C 828	12.8	71.1	569	9	US-10-363-483A-7659	Sequence 7659, Ap	C 901	12.8	71.1	702	7	US-10-437-963-65734	Sequence 65734, A
C 829	12.8	71.1	569	9	US-10-363-483A-7660	Sequence 7660, Ap	C 902	12.8	71.1	705	7	US-10-437-963-6548	Sequence 6548, Ap
C 830	12.8	71.1	573	7	US-10-260-238-109	Sequence 109, App	C 903	12.8	71.1	716	8	US-10-425-115-7897	Sequence 7897, Ap
C 831	12.8	71.1	573	8	US-10-363-345A-9851	Sequence 9851, Ap	C 904	12.8	71.1	717	4	US-09-927-065A-694910	Sequence 694910, A
C 832	12.8	71.1	573	8	US-10-363-345A-9852	Sequence 9852, Ap	C 905	12.8	71.1	717	4	US-10-437-966-64737	Sequence 64737, A
C 833	12.8	71.1	573	9	US-10-363-483A-9851	Sequence 9851, Ap	C 906	12.8	71.1	734	8	US-10-363-345A-12753	Sequence 12753, A
C 834	12.8	71.1	573	9	US-10-363-483A-9852	Sequence 9852, Ap	C 907	12.8	71.1	734	8	US-10-363-345A-12754	Sequence 12754, A
C 835	12.8	71.1	578	6	US-10-125-968-746	Sequence 746, App	C 908	12.8	71.1	734	9	US-10-363-483A-12753	Sequence 12753, A
C 836	12.8	71.1	578	6	US-10-425-115-105353	Sequence 105353, A	C 909	12.8	71.1	734	9	US-10-363-483A-12754	Sequence 12754, A
C 837	12.8	71.1	579	6	US-10-156-761-3828	Sequence 3828, Ap	C 910	12.8	71.1	751	8	US-10-363-345A-4891	Sequence 4891, Ap
C 838	12.8	71.1	579	8	US-10-363-345A-29493	Sequence 29493, A	C 911	12.8	71.1	751	8	US-10-363-345A-4892	Sequence 4892, Ap
C 839	12.8	71.1	579	8	US-10-363-345A-29494	Sequence 29494, A	C 912	12.8	71.1	751	9	US-10-363-483A-4891	Sequence 4891, Ap
C 840	12.8	71.1	579	9	US-10-363-483A-29493	Sequence 29493, A	C 913	12.8	71.1	751	9	US-10-363-483A-4892	Sequence 4892, Ap
C 841	12.8	71.1	579	9	US-10-363-483A-29494	Sequence 29494, A	C 914	12.8	71.1	757	7	US-10-188-248-63	Sequence 63, App
C 842	12.8	71.1	583	6	US-10-264-049-1543	Sequence 1543, Ap	C 915	12.8	71.1	757	7	US-10-027-632-19272	Sequence 19272, A
C 843	12.8	71.1	583	8	US-10-653-047-1897	Sequence 1897, Ap	C 916	12.8	71.1	757	6	US-10-188-248-65	Sequence 65, App
C 844	12.8	71.1	585	8	US-10-363-345A-22749	Sequence 22749, A	C 917	12.8	71.1	762	7	US-10-027-632-19272	Sequence 65, App
C 845	12.8	71.1	585	8	US-10-363-345A-22750	Sequence 22750, A	C 918	12.8	71.1	763	8	US-10-684-422-247	Sequence 247, App
C 846	12.8	71.1	585	9	US-10-363-483A-22749	Sequence 22749, A	C 919	12.8	71.1	764	8	US-10-425-115-155478	Sequence 155478, A
C 847	12.8	71.1	585	9	US-10-363-483A-22750	Sequence 22750, A	C 920	12.8	71.1	771	6	US-10-363-483A-4592	Sequence 4592, A
C 848	12.8	71.1	588	6	US-10-156-761-2056	Sequence 2056, Ap	C 921	12.8	71.1	771	8	US-10-425-115-16164	Sequence 16164, A
C 849	12.8	71.1	589	3	US-09-919-580-209	Sequence 209, App	C 922	12.8	71.1	784	8	US-10-363-345A-23875	Sequence 23875, A
C 850	12.8	71.1	594	4	US-09-925-065A-542729	Sequence 542729, A	C 923	12.8	71.1	784	9	US-10-363-483A-23875	Sequence 23875, A
C 851	12.8	71.1	594	8	US-10-363-345A-36405	Sequence 36405, A	C 924	12.8	71.1	784	9	US-10-363-483A-23876	Sequence 23876, A
C 852	12.8	71.1	594	8	US-10-363-345A-36406	Sequence 36406, A	C 925	12.8	71.1	785	3	US-09-853-386-60	Sequence 60, App
C 853	12.8	71.1	594	9	US-10-363-483A-36405	Sequence 36405, A	C 926	12.8	71.1	785	6	US-10-414-080-11	Sequence 11, App
C 854	12.8	71.1	594	9	US-10-363-483A-36406	Sequence 36406, A	C 927	12.8	71.1	785	6	US-10-313-542-267	Sequence 267, App
C 855	12.8	71.1	596	4	US-09-925-065A-756408	Sequence 756408, A	C 928	12.8	71.1	787	6	US-10-425-115-1812	Sequence 1812, App
C 856	12.8	71.1	596	7	US-10-767-701-28146	Sequence 28146, A	C 929	12.8	71.1	787	8	US-10-425-115-49766	Sequence 49766, A
C 857	12.8	71.1	599	9	US-10-972-079-36306	Sequence 36306, A	C 930	12.8	71.1	790	8	US-10-425-115-49765	Sequence 49765, A
C 858	12.8	71.1	599	9	US-10-972-079-36307	Sequence 36307, A	C 931	12.8	71.1	796	7	US-10-027-632-173135	Sequence 173135, A
C 859	12.8	71.1	600	6	US-10-156-761-4768	Sequence 4768, Ap	C 932	12.8	71.1	801	5	US-10-027-632-173135	Sequence 173135, A
C 860	12.8	71.1	600	9	US-10-972-079-42696	Sequence 42696, A	C 933	12.8	71.1	801	6	US-10-027-632-173135	Sequence 173135, A
C 861	12.8	71.1	601	8	US-10-363-345A-36709	Sequence 36709, A	C 934	12.8	71.1	805	4	US-09-925-065A-952164	Sequence 952164, A
C 862	12.8	71.1	601	8	US-10-363-483A-36710	Sequence 36710, A	C 935	12.8	71.1	807	7	US-10-437-963-64782	Sequence 64782, A
C 863	12.8	71.1	601	9	US-10-363-483A-36709	Sequence 36709, A	C 936	12.8	71.1	838	4	US-09-925-065A-944180	Sequence 944180, A
C 864	12.8	71.1	601	9	US-10-363-483A-36710	Sequence 36710, A	C 937	12.8	71.1	839	7	US-10-437-963-43692	Sequence 43692, A
C 865	12.8	71.1	607	6	US-10-264-049-338	Sequence 338, App	C 938	12.8	71.1	845	8	US-10-363-345A-4195	Sequence 4195, Ap
C 866	12.8	71.1	607	7	US-10-424-599-59368	Sequence 59368, A	C 939	12.8	71.1	845	8	US-10-363-345A-4196	Sequence 4196, Ap
C 867	12.8	71.1	609	3	US-09-764-891-403	Sequence 403, App	C 940	12.8	71.1	845	9	US-10-363-483A-4195	Sequence 4195, Ap
C 868	12.8	71.1	609	5	US-10-405-428-37	Sequence 37, App	C 941	12.8	71.1	845	9	US-10-363-483A-4196	Sequence 4196, Ap
C 869	12.8	71.1	617	8	US-10-425-115-170715	Sequence 170715, A	C 942	12.8	71.1	858	9	US-10-450-763-13705	Sequence 13705, A
C 870	12.8	71.1	621	4	US-09-925-065A-710818	Sequence 710818, A	C 943	12.8	71.1	867	3	US-09-764-891-5501	Sequence 5501, Ap
C 871	12.8	71.1	623	7	US-10-437-963-8470	Sequence 8470, Ap	C 944	12.8	71.1	879	7	US-10-424-599-16413	Sequence 16413, A
C 872	12.8	71.1	624	3	US-10-767-701-2287	Sequence 2287, App	C 945	12.8	71.1	881	8	US-10-425-114-14477	Sequence 14477, A
C 873	12.8	71.1	629	3	US-09-867-550-667	Sequence 667, App	C 946	12.8	71.1	881	8	US-10-425-114-14477	Sequence 14477, A
C 874	12.8	71.1	631	8	US-10-425-115-98219	Sequence 98219, A	C 947	12.8	71.1	886	8	US-10-490-314-7	Sequence 314-7, A
C 875	12.8	71.1	644	8	US-10-425-115-86009	Sequence 86009, A	C 948	12.8	71.1	896	7	US-10-437-963-45464	Sequence 45464, A
C 876	12.8	71.1	660	4	US-09-925-065A-672967	Sequence 672967, A	C 949	12.8	71.1	900	8	US-10-695-155-95	Sequence 95, App
C 877	12.8	71.1	660	8	US-10-425-115-109041	Sequence 109041, A	C 950	12.8	71.1	914	8	US-10-425-115-17338	Sequence 17338, A
C 878	12.8	71.1	660	8	US-10-363-345A-20437	Sequence 20437, A	C 951	12.8	71.1	925	7	US-10-767-701-672	Sequence 672, App
C 879	12.8	71.1	660	8	US-10-363-345A-20438	Sequence 20438, A	C 952	12.8	71.1	933	7	US-10-767-701-9241	Sequence 9241, Ap
C 880	12.8	71.1	660	8	US-10-363-345A-25599	Sequence 25599, A	C 953	12.8	71.1	933	7	US-10-437-963-83937	Sequence 83937, A
C 881	12.8	71.1	660	8	US-10-363-345A-25600	Sequence 25600, A	C 954	12.8	71.1	952	3	US-09-791-171-41	Sequence 41, App
C 882	12.8	71.1	660	9	US-10-363-483A-20437	Sequence 20437, A	C 955	12.8	71.1	952	3	US-09-804-980-41	Sequence 41, App
C 883	12.8	71.1	660	9	US-10-363-483A-20438	Sequence 20438, A	C 956	12.8	71.1	952	7	US-10-620-246-41	Sequence 41, App
C 884	12.8	71.1	660	9	US-10-363-483A-25599	Sequence 25599, A	C 957	12.8	71.1	953	8	US-10-425-115-160389	Sequence 160389, A
C 885	12.8	71.1	660	9	US-10-363-483A-25600	Sequence 25600, A	C 958	12.8	71.1	955	8	US-10-425-115-160389	Sequence 160389, A
C 886	12.8	71.1	660	10	US-10-097-143-725	Sequence 725, App	C 959	12.8	71.1	957	6	US-10-156-761-6624	Sequence 6624, Ap
C 887	12.8	71.1	663	7	US-10-437-963-2631	Sequence 2631, Ap	C 960	12.8	71.1	967	8	US-10-363-345A-29215	Sequence 29215, A
C 888	12.8	71.1	673	7	US-10-767-701-12646	Sequence 12646, A	C 961	12.8	71.1	967	8	US-10-363-345A-29216	Sequence 29216, A
C 889	12.8	71.1	674	3	US-10-425-115-53804	Sequence 53804, A	C 962	12.8	71.1	967	9	US-10-363-345A-29216	Sequence 29216, A
C 890	12.8	71.1	675	3	US-09-712-363-43	Sequence 43, App	C 963	12.8	71.1	967	9	US-10-363-483A-29216	Sequence 29216, A
C 891	12.8	71.1	682	8	US-10-363-345A-649	Sequence 649, App	C 964	12.8	71.1	970	6	US-10-330-051A-11	Sequence 31, App
C 892	12.8	71.1	682	8	US-10-363-345A-650	Sequence 650, App	C 965	12.8	71.1	970	6	US-10-437-963-12003	Sequence 12003, A
C 893	12.8	71.1	682	9	US-10-363-483A-649	Sequence 649, App	C 966	12.8	71.1	971	8	US-10-363-345A-2832	Sequence 2832, Ap
C 894	12.8	71.1	682	9	US-10-363-483A-650	Sequence 650, App	C 967	12.8	71.1	971	8	US-10-363-345A-2832	Sequence 2832, Ap
C 895	12.8	71.1	685	7	US-10-437-963-75371	Sequence 75371, A	C 968	12.8	71.1	971	8	US-10-363-483A-2831	Sequence 2831, Ap
C 896	12.8	71.1	692	8	US-10-425-115-110648	Sequence 110648, A	C 969	12.8	71.1	971	9	US-10-363-483A-2832	Sequence 2832, Ap
C 897	12.8	71.1	695	7	US-10-424-599-93312	Sequence 93312, A	C 970	12.8	71.1	990	7	US-10-767-701-11463	Sequence 11463, A
C 898	12.8	71.1	696	7	US-10-437-963-5561	Sequence 5561, Ap	C 971	12.8	71.1	990	7	US-10-767-701-11463	Sequence 11463, A
C 899	12.8	71.1	696	7	US-10-437-963-9350	Sequence 9350, Ap	C 972	12.8	71.1	996	7	US-10-437-963-67783	Sequence 67783, A

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c 973 12.8 71.1 996 9 US-10-200-545-35 Sequence 35, Appl
c 974 12.8 71.1 999 7 US-10-425-114-980 Sequence 980, App
c 975 12.8 71.1 1008 3 US-09-873-367C-313 Sequence 313, App
c 976 12.8 71.1 1008 8 US-10-370-715B-203 Sequence 203, App
c 977 12.8 71.1 1008 8 US-10-843-641A-313 Sequence 313, App
c 978 12.8 71.1 1015 5 US-10-037-270-734 Sequence 734, App
c 979 12.8 71.1 1015 6 US-10-117-722-734 Sequence 734, App
c 980 12.8 71.1 1015 6 US-10-122-851-734 Sequence 734, App
c 981 12.8 71.1 1018 3 US-09-925-298-279 Sequence 279, App
c 982 12.8 71.1 1018 5 US-10-102-806-279 Sequence 279, App
c 983 12.8 71.1 1023 7 US-10-641-643-663 Sequence 663, App
c 984 12.8 71.1 1023 7 US-10-282-122A-13828 Sequence 13828, A
c 985 12.8 71.1 1029 6 US-10-156-761-4339 Sequence 4339, App
c 986 12.8 71.1 1032 6 US-10-156-761-4351 Sequence 4351, App
c 987 12.8 71.1 1037 7 US-10-437-963-32660 Sequence 32660, A
c 988 12.8 71.1 1041 4 US-10-767-701-5877 Sequence 5877, App
c 989 12.8 71.1 1043 4 US-09-925-065A-707999 Sequence 70799, A
c 990 12.8 71.1 1043 4 US-09-925-065A-707999 Sequence 70799, A
c 991 12.8 71.1 1043 9 US-10-887-553A-837 Sequence 837, App
c 992 12.8 71.1 1047 9 US-10-450-763-20815 Sequence 20815, A
c 993 12.8 71.1 1050 6 US-10-156-761-3473 Sequence 3473, App
c 994 12.8 71.1 1052 7 US-10-439-703-65 Sequence 65, Appl
c 995 12.8 71.1 1052 9 US-10-887-553A-473 Sequence 473, App
c 996 12.8 71.1 1078 8 US-10-425-115-170712 Sequence 170712, A
c 997 12.8 71.1 1084 8 US-10-363-345A-34349 Sequence 34349, A
c 998 12.8 71.1 1084 8 US-10-363-345A-34350 Sequence 34350, A
c 999 12.8 71.1 1084 8 US-10-363-483A-34349 Sequence 34349, A
c1000 12.8 71.1 1084 9 US-10-363-483A-34350 Sequence 34350, A

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## ALIGNMENTS

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RESULT 1
US-09-824-468-60/c
; Sequence 60, Application US/09824468
; Patent No. US20020064515A1
; GENERAL INFORMATION:
; APPLICANT: Kitley, Arthur M.
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods and Products for Stimulating the
; TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
; TITLE OF INVENTION: Cytokines
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/824,468
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/286,098
; PRIOR FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-824-468-60

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Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AGAGGUGCGACGCGGUA 18
DB 18 AGAGGUGCGACGCGGUA 1

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RESULT 2
US-09-888-326-485/c
; Sequence 485, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George

```

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; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AMS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 485
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-485

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Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AGAGGUGCGACGCGGUA 18
DB 18 AGAGGUGCGACGCGGUA 1

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RESULT 3
US-09-776-479-4/c
; Sequence 4, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-4

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```

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AGAGGUGCGACGCGGUA 18
DB 18 AGAGGUGCGACGCGGUA 1

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RESULT 4
US-09-776-479-56/c
; Sequence 56, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouton, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the

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TITLE OF INVENTION: Treatment of Asthma and Allergy  
FILE REFERENCE: C1037/7013 (HCL/MAT)  
CURRENT APPLICATION NUMBER: US/09/776,479  
CURRENT FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: US 60/179,991  
PRIOR FILING DATE: 2000-02-03  
NUMBER OF SEQ ID NOS: 1093  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 56  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-56

Query Match 100.0%; Score 18; DB 3; Length 18;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18  
DB 18 AGAGGTCGACGCGGTA 1

## RESULT 5

US-09-954-987B-67/c  
Sequence 67, Application US/0954987B  
Publication No. US20030104523A1  
GENERAL INFORMATION:  
APPLICANT: Stefan Bauer  
APPLICANT: Grayson B. Lipford  
APPLICANT: Hermann Wagner  
TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF  
FILE REFERENCE: C1041/7016 (AMS)  
CURRENT APPLICATION NUMBER: US/09/954,987B  
CURRENT FILING DATE: 2001-09-17  
PRIOR APPLICATION NUMBER: US 60/233,035  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: US 60/263,657  
PRIOR FILING DATE: 2001-01-23  
PRIOR APPLICATION NUMBER: US 60/291,726  
PRIOR FILING DATE: 2001-05-17  
PRIOR APPLICATION NUMBER: US 60/300,210  
PRIOR FILING DATE: 2001-06-22  
NUMBER OF SEQ ID NOS: 230  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 67  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic oligonucleotide  
US-09-954-987B-67

Query Match 100.0%; Score 18; DB 3; Length 18;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18  
DB 18 AGAGGTCGACGCGGTA 1

## RESULT 6

US-09-776-479-4/c  
Sequence 4, Application US/09776479  
Publication No. US20040067902A9  
GENERAL INFORMATION:  
APPLICANT: Bratzler, Robert L.  
APPLICANT: Petersen, Deanna M.  
APPLICANT: Fourn, Yves

TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
FILE REFERENCE: C1037/7013 (HCL/MAT)  
CURRENT APPLICATION NUMBER: US/09/776,479  
CURRENT FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: US 60/179,991  
PRIOR FILING DATE: 2000-02-03  
NUMBER OF SEQ ID NOS: 1093  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-4

Query Match 100.0%; Score 18; DB 3; Length 18;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18  
DB 18 AGAGGTCGACGCGGTA 1

## RESULT 7

US-09-776-479-56/c  
Sequence 56, Application US/09776479  
Publication No. US20040067902A9  
GENERAL INFORMATION:  
APPLICANT: Bratzler, Robert L.  
APPLICANT: Petersen, Deanna M.  
APPLICANT: Fourn, Yves  
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
FILE REFERENCE: C1037/7013 (HCL/MAT)  
CURRENT APPLICATION NUMBER: US/09/776,479  
CURRENT FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: US 60/179,991  
PRIOR FILING DATE: 2000-02-03  
NUMBER OF SEQ ID NOS: 1093  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 56  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-56

Query Match 100.0%; Score 18; DB 3; Length 18;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18  
DB 18 AGAGGTCGACGCGGTA 1

## RESULT 8

US-10-112-653-4/c  
Sequence 4, Application US/10112653  
Publication No. US20030050268A1  
GENERAL INFORMATION:  
APPLICANT: Krieger, Arthur M.  
APPLICANT: Berg, Daniel J.  
TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES  
FILE REFERENCE: C01039/70060 (AMS)  
CURRENT APPLICATION NUMBER: US/10/112,653  
CURRENT FILING DATE: 2002-03-29  
PRIOR APPLICATION NUMBER: US 60/279,642

;; PRIOR FILING DATE: 2001-03-29  
;; NUMBER OF SEQ ID NOS: 1040  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 4  
;; LENGTH: 18  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-112-653-4

Query Match 100.0%; Score 18; DB 5; Length 18;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGUGCGACGCGGUA 18  
Db 18 AGAGGGTCGACGCGGTA 1

RESULT 9  
US-10-017-995-4/c  
; Sequence 4, Application US/10017995  
; Publication No. US20030055014A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids  
; FILE REFERENCE: C1037/7025 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/10/017,995  
; CURRENT FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: US 60/255,534  
; PRIOR FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-017-995-4

Query Match 100.0%; Score 18; DB 5; Length 18;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGUGCGACGCGGUA 18  
Db 18 AGAGGGTCGACGCGGTA 1

RESULT 10  
US-10-017-995-56/c  
; Sequence 56, Application US/10017995  
; Publication No. US20030055014A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids  
; FILE REFERENCE: C1037/7025 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/10/017,995  
; CURRENT FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: US 60/255,534  
; PRIOR FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 56  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-017-995-56

Query Match 100.0%; Score 18; DB 5; Length 18;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGUGCGACGCGGUA 18  
Db 18 AGAGGGTCGACGCGGTA 1

RESULT 11  
US-10-161-229-54/c  
; Sequence 54, Application US/10161229  
; Publication No. US20030100527A1  
; GENERAL INFORMATION:  
; APPLICANT: Kriegl, Arthur M.  
; APPLICANT: Hartmann, Gunther  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules for  
; FILE REFERENCE: C01039/70061  
; CURRENT APPLICATION NUMBER: US/10/161,229  
; CURRENT FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: US 09/191,170  
; PRIOR FILING DATE: 1998-11-13  
; PRIOR APPLICATION NUMBER: US 08/960,774  
; PRIOR FILING DATE: 1997-10-30  
; PRIOR APPLICATION NUMBER: US 08/738,652  
; PRIOR FILING DATE: 1996-10-30  
; PRIOR APPLICATION NUMBER: US 08/386,063  
; PRIOR FILING DATE: 1995-02-07  
; PRIOR APPLICATION NUMBER: US 08/276,358  
; PRIOR FILING DATE: 1994-07-15  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 54  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-161-229-54

Query Match 100.0%; Score 18; DB 5; Length 18;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGUGCGACGCGGUA 18  
Db 18 AGAGGGTCGACGCGGTA 1

RESULT 12  
US-10-187-264A-60/c  
; Sequence 60, Application US/10187264A  
; Publication No. US20030162734A1  
; GENERAL INFORMATION:  
; APPLICANT: Kriegl, Arthur M.  
; APPLICANT: Klimberg, Dennis  
; APPLICANT: Steinberg, Alfred D.  
; TITLE OF INVENTION: Methods for Treating and Preventing  
; FILE REFERENCE: C01039/70062.US  
; CURRENT APPLICATION NUMBER: US/10/187,264A  
; CURRENT FILING DATE: 2002-06-28  
; PRIOR APPLICATION NUMBER: US 09/630,319  
; PRIOR FILING DATE: 2000-07-31  
; PRIOR APPLICATION NUMBER: US 08/960,774  
; PRIOR FILING DATE: 1997-10-30  
; PRIOR APPLICATION NUMBER: US 08/738,652  
; PRIOR FILING DATE: 1996-10-30  
; PRIOR APPLICATION NUMBER: US 08/386,063  
; PRIOR FILING DATE: 1995-02-07  
; PRIOR APPLICATION NUMBER: US 08/276,358  
; PRIOR FILING DATE: 1994-07-15

NUMBER OF SEQ ID NOS: 124  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 60  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-187-264A-60

Query Match 100.0%; Score 18; DB 6; Length 18;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGTCGACGCGGTA 18  
|||:|||||:  
Db 18 AGAGGTCGACGCGGTA 1

RESULT 13  
US-10-265-072-75/c

Sequence 75; Application US/10265072  
Publication No. US20030166001A1  
GENERAL INFORMATION:  
APPLICANT: Lipford, Grayson  
TITLE OF INVENTION: TOLL-LIKE RECEPTOR 3 SIGNALING AGONISTS AND ANTAGONISTS  
FILE REFERENCE: C01041.70031.US  
CURRENT APPLICATION NUMBER: US/10/265,072  
CURRENT FILING DATE: 2002-10-05  
NUMBER OF SEQ ID NOS: 117  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 75  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Synthetic oligonucleotide  
US-10-265-072-75

Query Match 100.0%; Score 18; DB 6; Length 18;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGTCGACGCGGTA 18  
|||:|||||:  
Db 18 AGAGGTCGACGCGGTA 1

RESULT 14  
US-10-306-522-60/c

Sequence 60; Application US/10306522  
Publication No. US20030191079A1  
GENERAL INFORMATION:  
APPLICANT: Kriegl, Arthur M.  
APPLICANT: Kliman, Dennis  
APPLICANT: Steindberg, Alfred D.  
TITLE OF INVENTION: Methods for Treating and Preventing  
FILE OF INVENTION: Infectious Disease  
FILE REFERENCE: C01039.70062.US  
CURRENT APPLICATION NUMBER: US/10/306,522  
CURRENT FILING DATE: 2002-11-27  
PRIOR APPLICATION NUMBER: US 09/630,319  
PRIOR FILING DATE: 2000-07-31  
PRIOR APPLICATION NUMBER: US 08/960,774  
PRIOR FILING DATE: 1997-10-30  
PRIOR APPLICATION NUMBER: US 08/738,652  
PRIOR FILING DATE: 1996-10-30  
PRIOR APPLICATION NUMBER: US 08/386,063  
PRIOR FILING DATE: 1995-02-07  
PRIOR APPLICATION NUMBER: US 08/276,358  
PRIOR FILING DATE: 1994-07-15  
NUMBER OF SEQ ID NOS: 124  
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 60  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic oligonucleotide  
US-10-306-522-60

Query Match 100.0%; Score 18; DB 6; Length 18;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGTCGACGCGGTA 18  
|||:|||||:  
Db 18 AGAGGTCGACGCGGTA 1

RESULT 15  
US-10-314-578-4/c

Sequence 4; Application US/10314578  
Publication No. US20030212026A1  
GENERAL INFORMATION:  
APPLICANT: Kriegl, Arthur M.  
APPLICANT: Schetter, Christian  
APPLICANT: Vollmer, Jorg  
TITLE OF INVENTION: Immunostimulatory Nucleic Acids  
FILE REFERENCE: C1039/7035 (HCL/MAT)  
CURRENT APPLICATION NUMBER: US/10/314,578  
CURRENT FILING DATE: 2002-12-09  
PRIOR APPLICATION NUMBER: US 60/156,113  
PRIOR FILING DATE: 1999-09-25  
PRIOR APPLICATION NUMBER: US 60/156,135  
PRIOR FILING DATE: 1999-09-27  
PRIOR APPLICATION NUMBER: US 60/227,436  
PRIOR FILING DATE: 2000-08-23  
NUMBER OF SEQ ID NOS: 1145  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Sequence  
US-10-314-578-4

Query Match 100.0%; Score 18; DB 6; Length 18;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGTCGACGCGGTA 18  
|||:|||||:  
Db 18 AGAGGTCGACGCGGTA 1

RESULT 16  
US-10-314-578-56/c

Sequence 56; Application US/10314578  
Publication No. US20030212026A1  
GENERAL INFORMATION:  
APPLICANT: Kriegl, Arthur M.  
APPLICANT: Schetter, Christian  
APPLICANT: Vollmer, Jorg  
TITLE OF INVENTION: Immunostimulatory Nucleic Acids  
FILE REFERENCE: C1039/7035 (HCL/MAT)  
CURRENT APPLICATION NUMBER: US/10/314,578  
CURRENT FILING DATE: 2002-12-09  
PRIOR APPLICATION NUMBER: US 60/156,113  
PRIOR FILING DATE: 1999-09-25  
PRIOR APPLICATION NUMBER: US 60/156,135  
PRIOR FILING DATE: 1999-09-27  
PRIOR APPLICATION NUMBER: US 60/227,436  
PRIOR FILING DATE: 2000-08-23  
NUMBER OF SEQ ID NOS: 1145



SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 56  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Sequence  
US-10-314-578-56

Query Match 100.0%; Score 18; DB 6; Length 18;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGCGCGACGCGGUA 18  
DB 18 AGAGGCGCGACGCGGTA 1

RESULT 17  
US-10-373-381-47/c  
Sequence 47, Application US/10373381  
Publication No. US20040030118A1  
GENERAL INFORMATION:  
APPLICANT: Wagner, Hermann  
APPLICANT: Lipford, Grayson  
TITLE OF INVENTION: Methods for Regulating Hematopoiesis  
FILE REFERENCE: C01041.70035.US  
CURRENT APPLICATION NUMBER: US/10/373,381  
CURRENT FILING DATE: 2003-02-24  
PRIOR APPLICATION NUMBER: US 09/241,653  
PRIOR FILING DATE: 1999-02-02  
PRIOR APPLICATION NUMBER: US 60/085,516  
PRIOR FILING DATE: 1998-05-14  
NUMBER OF SEQ ID NOS: 90  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 47  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic oligonucleotide  
US-10-373-381-47

Query Match 100.0%; Score 18; DB 7; Length 18;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGCGCGACGCGGUA 18  
DB 18 AGAGGCGCGACGCGGTA 1

RESULT 18  
US-10-719-493-60/c  
Sequence 60, Application US/10719493  
Publication No. US20040087538A1  
GENERAL INFORMATION:  
APPLICANT: Krieg, Arthur M.  
TITLE OF INVENTION: Methods of Treating Cancer Using  
FILE REFERENCE: C1039/7021/HCL  
CURRENT APPLICATION NUMBER: US/10/719,493  
CURRENT FILING DATE: 2003-11-21  
PRIOR APPLICATION NUMBER: US 08/960,774  
PRIOR FILING DATE: 1997-10-30  
PRIOR APPLICATION NUMBER: US 08/738,652  
PRIOR FILING DATE: 1996-10-30  
PRIOR APPLICATION NUMBER: US 08/386,063  
PRIOR FILING DATE: 1995-02-07  
PRIOR APPLICATION NUMBER: US 08/276,358  
PRIOR FILING DATE: 1994-07-15  
NUMBER OF SEQ ID NOS: 123

SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 60  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic oligonucleotide  
US-10-719-493-60

Query Match 100.0%; Score 18; DB 7; Length 18;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGCGCGACGCGGUA 18  
DB 18 AGAGGCGCGACGCGGTA 1

RESULT 19  
US-10-627-331-60/c  
Sequence 60, Application US/10627331  
Publication No. US20040106568A1  
GENERAL INFORMATION:  
APPLICANT: Krieg, Arthur M.  
APPLICANT: Kliman, Dennis  
APPLICANT: Steinberg, Alfred D.  
TITLE OF INVENTION: Methods for Treating and Preventing  
FILE REFERENCE: C01039.70062.US  
CURRENT APPLICATION NUMBER: US/10/627,331  
CURRENT FILING DATE: 2003-07-25  
PRIOR APPLICATION NUMBER: US 09/630,319  
PRIOR FILING DATE: 2000-07-31  
PRIOR APPLICATION NUMBER: US 08/960,774  
PRIOR FILING DATE: 1997-10-30  
PRIOR APPLICATION NUMBER: US 08/738,652  
PRIOR FILING DATE: 1996-10-30  
PRIOR APPLICATION NUMBER: US 08/386,063  
PRIOR FILING DATE: 1995-02-07  
PRIOR APPLICATION NUMBER: US 08/276,358  
PRIOR FILING DATE: 1994-07-15  
NUMBER OF SEQ ID NOS: 124  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 60  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic oligonucleotide  
US-10-627-331-60

Query Match 100.0%; Score 18; DB 7; Length 18;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGCGCGACGCGGUA 18  
DB 18 AGAGGCGCGACGCGGTA 1

RESULT 20  
US-10-877-369-47/c  
Sequence 47, Application US/10877369  
Publication No. US20040234512A1  
GENERAL INFORMATION:  
APPLICANT: Wagner, Hermann  
APPLICANT: Lipford, Grayson  
TITLE OF INVENTION: Methods for Regulating Hematopoiesis  
FILE REFERENCE: C1041.70020US01  
CURRENT APPLICATION NUMBER: US/10/877,369  
CURRENT FILING DATE: 2004-06-25  
PRIOR APPLICATION NUMBER: US 09/241,653

PRIOR FILING DATE: 1999-02-02  
PRIOR APPLICATION NUMBER: US 60/085,516  
PRIOR FILING DATE: 1998-05-14  
NUMBER OF SEQ ID NOS: 90  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 47  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic oligonucleotide  
US-10-877-369-47

Query Match 100.0%; Score 18; DB 8; Length 18;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18  
DB 18 AGAGGTCGCGACCGGTA 1

RESULT 21  
US-10-831-778-4/c  
Sequence 4, Application US/10831778  
Publication No. US20040235774A1  
GENERAL INFORMATION:  
APPLICANT: Bratzler, Robert L.  
APPLICANT: Petersen, Deanna M.  
APPLICANT: Fourn, Yves  
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
FILE REFERENCE: C1037/7013 (HCL/MAT)  
CURRENT APPLICATION NUMBER: US/10/831,778  
PRIOR FILING DATE: 2004-04-23  
PRIOR APPLICATION NUMBER: US 60/179,991  
PRIOR FILING DATE: 2000-02-03  
NUMBER OF SEQ ID NOS: 1093  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Sequence  
US-10-831-778-4

Query Match 100.0%; Score 18; DB 8; Length 18;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18  
DB 18 AGAGGTCGCGACCGGTA 1

RESULT 22  
US-10-831-778-56/c  
Sequence 56, Application US/10831778  
Publication No. US20040235774A1  
GENERAL INFORMATION:  
APPLICANT: Bratzler, Robert L.  
APPLICANT: Petersen, Deanna M.  
APPLICANT: Fourn, Yves  
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
FILE REFERENCE: C1037/7013 (HCL/MAT)  
CURRENT APPLICATION NUMBER: US/10/831,778  
PRIOR FILING DATE: 2004-04-23  
PRIOR APPLICATION NUMBER: US 60/179,991  
PRIOR FILING DATE: 2000-02-03  
NUMBER OF SEQ ID NOS: 1093  
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 56  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Sequence  
US-10-831-778-56

Query Match 100.0%; Score 18; DB 8; Length 18;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18  
DB 18 AGAGGTCGCGACCGGTA 1

RESULT 23  
US-10-876-892-47/c  
Sequence 47, Application US/10876892  
Publication No. US20040235777A1  
GENERAL INFORMATION:  
APPLICANT: Wagner, Hermann  
APPLICANT: Lipford, Grayson  
TITLE OF INVENTION: Methods for Regulating Hematopoiesis  
FILE REFERENCE: C1041.700020503  
CURRENT APPLICATION NUMBER: US/10/876,892  
PRIOR FILING DATE: 2004-06-25  
PRIOR APPLICATION NUMBER: US 09/241,653  
PRIOR FILING DATE: 1999-02-02  
PRIOR APPLICATION NUMBER: US 60/085,516  
PRIOR FILING DATE: 1998-05-14  
NUMBER OF SEQ ID NOS: 90  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 47  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic oligonucleotide  
US-10-876-892-47

Query Match 100.0%; Score 18; DB 8; Length 18;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18  
DB 18 AGAGGTCGCGACCGGTA 1

RESULT 24  
US-10-876-965-47/c  
Sequence 47, Application US/10876965  
Publication No. US20040235778A1  
GENERAL INFORMATION:  
APPLICANT: Wagner, Hermann  
APPLICANT: Lipford, Grayson  
TITLE OF INVENTION: Methods for Regulating Hematopoiesis  
FILE REFERENCE: C1041.700020502  
CURRENT APPLICATION NUMBER: US/10/876,965  
PRIOR FILING DATE: 2004-06-25  
PRIOR APPLICATION NUMBER: US 09/241,653  
PRIOR FILING DATE: 1999-02-02  
PRIOR APPLICATION NUMBER: US 60/085,516  
PRIOR FILING DATE: 1998-05-14  
NUMBER OF SEQ ID NOS: 90  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 47  
LENGTH: 18  
TYPE: DNA

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic oligonucleotide  
US-10-876-965-47

Query Match 100.0%; Score 18; DB 8; Length 18;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18  
|||||:|||||:|  
DB 18 AGAGGTCGACGCGGTA 1

RESULT 25  
US-10-800-926-1  
Sequence 1, Application US/10800926  
Publication No. US20050032731A1  
GENERAL INFORMATION:

APPLICANT: MARSHALL, WILLIAM E.  
TITLE OF INVENTION: OLIGORIBONUCLEOTIDES ALERT THE IMMUNE SYSTEM OF ANIMALS  
FILE REFERENCE: P01936US06  
CURRENT APPLICATION NUMBER: US/10/800,926  
CURRENT FILING DATE: 2004-03-15  
PRIOR APPLICATION NUMBER: 09/883,550  
PRIOR FILING DATE: 2001-06-18  
PRIOR APPLICATION NUMBER: 09/193,653  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 08/739,264  
PRIOR FILING DATE: 1996-10-29  
PRIOR APPLICATION NUMBER: 08/517,016  
PRIOR FILING DATE: 1995-08-18  
PRIOR APPLICATION NUMBER: 08/376,175  
PRIOR FILING DATE: 1995-01-20  
PRIOR APPLICATION NUMBER: 08/059,745  
PRIOR FILING DATE: 1993-05-11  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 1  
LENGTH: 18  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-800-926-1

Query Match 100.0%; Score 18; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18  
|||||:|||||:|  
DB 1 AGAGGUGCGACGCGGUA 18

RESULT 26  
US-10-627-413-60/C  
Sequence 60, Application US/10627413  
Publication No. US20050101554A1  
GENERAL INFORMATION:

APPLICANT: Kriegl, Arthur M.  
APPLICANT: Kleinman, Dennis  
APPLICANT: Steinberg, Alfred D.  
TITLE OF INVENTION: Methods for Treating and Preventing  
TITLE OF INVENTION: Infectious Disease  
FILE REFERENCE: C01039, 70062, US  
CURRENT APPLICATION NUMBER: US/10/627,413  
CURRENT FILING DATE: 2003-07-25  
PRIOR APPLICATION NUMBER: US 09/630,319  
PRIOR FILING DATE: 2000-07-31  
PRIOR APPLICATION NUMBER: US 08/960,774

PRIOR FILING DATE: 1997-10-30  
PRIOR APPLICATION NUMBER: US 08/738,652  
PRIOR FILING DATE: 1996-10-30  
PRIOR APPLICATION NUMBER: US 08/386,063  
PRIOR FILING DATE: 1995-02-07  
PRIOR APPLICATION NUMBER: US 08/276,358  
PRIOR FILING DATE: 1994-07-15  
NUMBER OF SEQ ID NOS: 124  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 60  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:

Query Match 100.0%; Score 18; DB 9; Length 18;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18  
|||||:|||||:|  
DB 18 AGAGGTCGACGCGGTA 1

RESULT 27  
US-10-921-086-60/C  
Sequence 60, Application US/10921086  
Publication No. US2005010157A1  
GENERAL INFORMATION:

APPLICANT: Kriegl, Arthur M.  
APPLICANT: Kline, Joel N.  
TITLE OF INVENTION: Methods of Treating Allergic and  
TITLE OF INVENTION: Asthmatic Disorders Using Immunostimulatory Oligonucleotides  
FILE REFERENCE: C1039/7020/HCL  
CURRENT APPLICATION NUMBER: US/10/921,086  
CURRENT FILING DATE: 2004-08-17  
PRIOR APPLICATION NUMBER: US/09/337,584  
PRIOR FILING DATE: 1999-06-21  
PRIOR APPLICATION NUMBER: US 08/960,774  
PRIOR FILING DATE: 1997-10-30  
PRIOR APPLICATION NUMBER: US 08/738,652  
PRIOR FILING DATE: 1996-10-30  
PRIOR APPLICATION NUMBER: US 08/386,063  
PRIOR FILING DATE: 1995-02-07  
PRIOR APPLICATION NUMBER: US 08/276,358  
PRIOR FILING DATE: 1994-07-15  
NUMBER OF SEQ ID NOS: 123  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 60  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:

Query Match 100.0%; Score 18; DB 9; Length 18;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18  
|||||:|||||:|  
DB 18 AGAGGTCGACGCGGTA 1

RESULT 28  
US-11-084-777-67/C  
Sequence 67, Application US/11084777  
Publication No. US20050181422A1  
GENERAL INFORMATION:  
APPLICANT: Stefan Bauer

APPLICANT: Grayson B. Lipford  
APPLICANT: Hermann Wagner  
TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF  
TITLE OF INVENTION: CpG-BASED IMMUNO-AGONIST/ANTAGONIST  
FILE REFERENCE: C1041.70016US02  
CURRENT FILING DATE: 2005-03-18  
PRIOR APPLICATION NUMBER: US 09/954,987  
PRIOR FILING DATE: 2001-09-17  
PRIOR APPLICATION NUMBER: US 60/300,210  
PRIOR FILING DATE: 2001-06-22  
PRIOR APPLICATION NUMBER: US 60/291,726  
PRIOR FILING DATE: 2001-05-17  
PRIOR APPLICATION NUMBER: US 60/263,657  
PRIOR FILING DATE: 2001-01-23  
PRIOR APPLICATION NUMBER: US 60/233,035  
PRIOR FILING DATE: 2000-09-15  
NUMBER OF SEQ ID NOS: 230  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 67  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic oligonucleotide  
US-11-084-777-67

Query Match 100.0%; Score 18; DB 10; Length 18;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18  
DB 18 AGAGGTCGACGCGGTA 1

RESULT 29  
US-11-071-836-60/c  
Sequence 60, Application US/11071836  
Publication No. US20050182017A1  
GENERAL INFORMATION:  
APPLICANT: Kriegl, Arthur M.  
TITLE OF INVENTION: Methods of Redirecting an Immune  
TITLE OF INVENTION: Response Using Immunostimulatory Oligonucleotides  
FILE REFERENCE: C1039/7022/HCL  
CURRENT FILING DATE: 2005-03-03  
CURRENT APPLICATION NUMBER: US/11/071,836  
PRIOR FILING DATE: 1997-10-30  
PRIOR APPLICATION NUMBER: US 08/960,774  
PRIOR FILING DATE: 1996-10-30  
PRIOR APPLICATION NUMBER: US 08/738,652  
PRIOR FILING DATE: 1995-02-07  
PRIOR APPLICATION NUMBER: US 08/386,063  
PRIOR FILING DATE: 1994-07-15  
NUMBER OF SEQ ID NOS: 123  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 60  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide  
US-11-071-836-60

Query Match 100.0%; Score 18; DB 10; Length 18;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18  
DB 18 AGAGGTCGACGCGGTA 1

RESULT 30  
US-11-110-189-60/c  
Sequence 60, Application US/11110189  
Publication No. US20050197314A1  
GENERAL INFORMATION:  
APPLICANT: Weiner, George  
APPLICANT: Kriegl, Arthur M.  
TITLE OF INVENTION: Methods and Products for Stimulating the  
TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and  
FILE REFERENCE: C1039/7026/HCL  
CURRENT FILING DATE: 2005-04-19  
CURRENT APPLICATION NUMBER: US/11/110,189  
PRIOR FILING DATE: 1999-04-02  
PRIOR APPLICATION NUMBER: US/09/286,098  
PRIOR FILING DATE: 1998-04-03  
PRIOR APPLICATION NUMBER: US 60/080,729  
NUMBER OF SEQ ID NOS: 105  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 60  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Sequence  
US-11-110-189-60

Query Match 100.0%; Score 18; DB 10; Length 18;  
Best Local Similarity 88.9%; Pred. No. 13;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18  
DB 18 AGAGGTCGACGCGGTA 1

RESULT 31  
US-10-053-645A-43  
Sequence 43, Application US/10053645A  
Publication No. US20030176376A1  
GENERAL INFORMATION:  
APPLICANT: Robert E. Klem  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A  
TITLE OF INVENTION: CELL-PROLIFERATIVE DISORDER USING CRE DECOY OLIGOMERS, BCL-2  
TITLE OF INVENTION: ANTISENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF  
FILE REFERENCE: 10412-022-999  
CURRENT FILING DATE: 2002-01-22  
CURRENT APPLICATION NUMBER: US/10/053,645A  
PRIOR FILING DATE: 2001-01-22  
PRIOR APPLICATION NUMBER: 60/263,244  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 43  
LENGTH: 57  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of artificial sequence: Synthetic Antisense  
US-10-053-645A-43

Query Match 100.0%; Score 18; DB 6; Length 57;  
Best Local Similarity 88.9%; Pred. No. 11;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGUA 18  
DB 37 AGAGGTCGACGCGGTA 54

RESULT 32  
US-10-053-645A-9/c

```
/ Sequence 9, Application US/10053645A
/ Publication No. US20030176376A1
/ GENERAL INFORMATION:
/ APPLICANT: Robert B. Klam
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A
/ TITLE OF INVENTION: CELL-PROLIFERATIVE DISORDER USING CBE DECOY OLIGOMERS, BCL-2
/ TITLE OF INVENTION: ANTISENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF
/ FILE REFERENCE: 10412-022-999
/ CURRENT APPLICATION NUMBER: US/10/053,645A
/ PRIOR FILING DATE: 2002-01-22
/ PRIOR APPLICATION NUMBER: 60/263,244
/ PRIOR FILING DATE: 2001-01-22
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Description of artificial sequence: Synthetic Antisense
/ OTHER INFORMATION: Oligonucleotide
US-10-053-645A-9
```

```
Query Match 94.4%; Score 17; DB 6; Length 17;
Best Local Similarity 88.2%; Pred. No. 45;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 2 GAGGUGCGACGCGGUA 18
DB 17 GAGGTCGCACGCGGTA 1
```

```
RESULT 33
US-10-822-205-5/c
/ Sequence 5, Application US/10822205
/ Publication No. US20040235773A1
/ GENERAL INFORMATION:
/ APPLICANT: GREENWALD, RICHARD B.
/ APPLICANT: ZHAO, HONG
/ TITLE OF INVENTION: POLYMERIC OLIGONUCLEOTIDE PRODRUGS
/ FILE REFERENCE: 213.1152CIP
/ CURRENT APPLICATION NUMBER: US/10/822,205
/ CURRENT FILING DATE: 2004-04-09
/ PRIOR APPLICATION NUMBER: 60/462,070
/ PRIOR FILING DATE: 2003-04-13
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 5
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: oligonucleotide
US-10-822-205-5
```

```
Query Match 94.4%; Score 17; DB 8; Length 17;
Best Local Similarity 88.2%; Pred. No. 45;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 2 GAGGUGCGACGCGGUA 18
DB 17 GAGGTCGCACGCGGTA 1
```

```
RESULT 34
US-10-961-458-9/c
/ Sequence 9, Application US/10961458
/ Publication No. US20050170377A1
/ GENERAL INFORMATION:
/ APPLICANT: Reed, John C.
/ TITLE OF INVENTION: REGULATION OF BCL-2 GENE EXPRESSION
/ FILE REFERENCE: 04040/1200990-US7
```

```
/ CURRENT APPLICATION NUMBER: US/10/961,458
/ CURRENT FILING DATE: 2004-10-07
/ PRIOR APPLICATION NUMBER: US/10/961,458
/ PRIOR FILING DATE: 2004-10-07
/ PRIOR APPLICATION NUMBER: US 09/375,514
/ PRIOR FILING DATE: 1999-08-17
/ PRIOR APPLICATION NUMBER: US 09/080,285
/ PRIOR FILING DATE: 1998-05-18
/ PRIOR APPLICATION NUMBER: US 08/465,485
/ PRIOR FILING DATE: 1995-06-05
/ PRIOR APPLICATION NUMBER: US 08/124,256
/ PRIOR FILING DATE: 1993-09-20
/ PRIOR APPLICATION NUMBER: US 07/840,716
/ PRIOR FILING DATE: 1992-02-21
/ PRIOR APPLICATION NUMBER: US 07/288,692
/ PRIOR FILING DATE: 1988-12-22
/ NUMBER OF SEQ ID NOS: 29
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 9
/ LENGTH: 17
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-961-458-9
```

```
Query Match 94.4%; Score 17; DB 9; Length 17;
Best Local Similarity 88.2%; Pred. No. 45;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 2 GAGGUGCGACGCGGUA 18
DB 17 GAGGTCGCACGCGGTA 1
```

```
RESULT 35
US-09-781-980-4/c
/ Sequence 4, Application US/09781980
/ Publication No. US20010029035A1
/ GENERAL INFORMATION:
/ APPLICANT: EISENHUT, MICHAEL
/ APPLICANT: MIER, WALTER
/ APPLICANT: ERITJA, RAMON
/ APPLICANT: HABERKORN, UWE
/ TITLE OF INVENTION: OLIGONUCLEOTIDE CONJUGATES
/ FILE REFERENCE: 2502498.991110
/ CURRENT APPLICATION NUMBER: US/09/781,980
/ CURRENT FILING DATE: 2001-02-14
/ PRIOR APPLICATION NUMBER: DE 100 06 572
/ PRIOR FILING DATE: 2000-02-14
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: oligonucleotide
US-09-781-980-4
```

```
Query Match 91.1%; Score 16.4; DB 3; Length 20;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 AGAGGUGCGACGCGGUA 18
DB 18 AGAGGTCGCACGCGGTA 1
```

```
RESULT 36
US-11-021-729-58/c
/ Sequence 58, Application US/11021729
/ Publication No. US20050203042A1
/ GENERAL INFORMATION:
```

```
APPLICANT: FRIEDEN, MIRIAM
APPLICANT: HANSEN, JENS BO
APPLICANT: OROM, HENRIK
APPLICANT: WESTERGARD, MAJKEN
APPLICANT: THRUDE, CHARLOTTE ALBAEK
TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF BCL-2
FILE REFERENCE: 50533-60537
CURRENT APPLICATION NUMBER: US/11/021,729
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/521,594
PRIOR FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: 60/586,340
PRIOR FILING DATE: 2004-07-07
PRIOR APPLICATION NUMBER: 60/558,392
PRIOR FILING DATE: 2004-03-31
PRIOR APPLICATION NUMBER: 60/532,844
PRIOR FILING DATE: 2003-12-23
PRIOR APPLICATION NUMBER: DK PA 2004 01629
PRIOR FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: DK PA 2004 01069
PRIOR FILING DATE: 2004-07-07
PRIOR APPLICATION NUMBER: DK PA 2004 00517
PRIOR FILING DATE: 2004-03-31
PRIOR APPLICATION NUMBER: DK PA 2003 01929
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.3
SEQ ID NO 58
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
FEATURE:
OTHER INFORMATION: oligonucleotide
NAME/KEY: misc_feature
LOCATION: (1)
OTHER INFORMATION: modified LNA nucleotide
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2)
OTHER INFORMATION: 5-methyl cytosine
FEATURE:
NAME/KEY: misc_feature
LOCATION: (15)
OTHER INFORMATION: modified LNA nucleotide
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)-(16)
OTHER INFORMATION: Phosphorothioate linkage
US-11-021-729-58

Query Match      88.9%; Score 16; DB 10; Length 16;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2  GAGGTCGACGCGGCU 17
DB      16  GAGGTCGACGCGGT 1

RESULT 37
US-09-965-116A-79/c
Sequence 79, Application US/09965116A
Patent No. US20020137714A1
GENERAL INFORMATION:
APPLICANT: Kandimala, Ekambar R.
APPLICANT: Zhao, Qiyuan
APPLICANT: Yu, Dong
```

```
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: Modulation of Immunostimulatory Activity of Immunostimulatory
TITLE OF INVENTION: Modified oligodeoxynucleotide phosphorothioate Analogs by
TITLE OF INVENTION: Positional Chemical Changes
FILE REFERENCE: HY2-479CP (47508,577)
CURRENT APPLICATION NUMBER: US/09/965,116A
CURRENT FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: US 09/712,898
PRIOR FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: US 60/235,452
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 60/235,453
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 79
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: modified linkage of oligodeoxynucleotide phosphorothioate
FEATURE:
NAME/KEY: modified_base
LOCATION: 16
OTHER INFORMATION: 3'-3' linkage
US-09-965-116A-80

Query Match      88.9%; Score 16; DB 3; Length 32;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3  AGGTCGACGCGGCUA 18
DB      16  AGGTCGACGCGGTA 1

RESULT 38
US-09-965-116A-80/c
Sequence 80, Application US/09965116A
Patent No. US20020137714A1
GENERAL INFORMATION:
APPLICANT: Kandimala, Ekambar R.
APPLICANT: Zhao, Qiyuan
APPLICANT: Yu, Dong
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: Modulation of Immunostimulatory Activity of Immunostimulatory
TITLE OF INVENTION: Modified oligodeoxynucleotide phosphorothioate Analogs by
FILE REFERENCE: HY2-479CP (47508,577)
CURRENT APPLICATION NUMBER: US/09/965,116A
CURRENT FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: US 09/712,898
PRIOR FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: US 60/235,452
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 60/235,453
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 80
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: modified linkage of oligodeoxynucleotide phosphorothioate
FEATURE:
NAME/KEY: modified_base
LOCATION: 16
OTHER INFORMATION: 3'-3' linkage
US-09-965-116A-80

Query Match      88.9%; Score 16; DB 3; Length 32;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 3 AGGGUGCAGCGCGUA 18  
||||:|||||:  
Db 32 AGGTCGACGCGGTA 17

RESULT 39  
US-10-694-075-79/c  
; Sequence 79, Application US/10694075  
; Publication No. US20040266709A1  
; GENERAL INFORMATION:  
; APPLICANT: Kandimalle, Ekambar R.  
; APPLICANT: Zhao, QiuYan  
; APPLICANT: Yu, Dong  
; APPLICANT: Agrawal, Sudhir  
; TITLE OF INVENTION: Modulation of Immunostimulatory Activity of  
; TITLE OF INVENTION: Immunostimulatory  
; TITLE OF INVENTION: Modified oligodeoxynucleotide phosphorothioate Analogs by  
; FILE REFERENCE: HYZ-479CP (47508.577)  
; CURRENT APPLICATION NUMBER: US/10/694,075  
; PRIOR FILING DATE: 2003-10-27  
; PRIOR APPLICATION NUMBER: US/09/965,116  
; PRIOR FILING DATE: 2002-03-08  
; PRIOR APPLICATION NUMBER: US 60/235,452  
; PRIOR FILING DATE: 2000-11-15  
; PRIOR APPLICATION NUMBER: US 60/235,452  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 60/235,453  
; PRIOR FILING DATE: 2000-09-26  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 79  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: modified linkage of oligodeoxynucleotide  
; OTHER INFORMATION: phosphorothioate  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: 16  
; OTHER INFORMATION: 5'-5' linkage  
US-10-694-075-79  
Query Match 88.9%; Score 16; DB 8; Length 32;  
Best Local Similarity 87.5%; Pred. No. 1.4e+02;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 3 AGGGUGCAGCGCGUA 18  
||||:|||||:  
Db 16 AGGTCGACGCGGTA 1

RESULT 40  
US-10-694-075-80/c  
; Sequence 80, Application US/10694075  
; Publication No. US20040266709A1  
; GENERAL INFORMATION:  
; APPLICANT: Kandimalle, Ekambar R.  
; APPLICANT: Zhao, QiuYan  
; APPLICANT: Yu, Dong  
; APPLICANT: Agrawal, Sudhir  
; TITLE OF INVENTION: Modulation of Immunostimulatory Activity of  
; TITLE OF INVENTION: Immunostimulatory  
; TITLE OF INVENTION: Modified oligodeoxynucleotide phosphorothioate Analogs by  
; FILE REFERENCE: HYZ-479CP (47508.577)  
; CURRENT APPLICATION NUMBER: US/10/694,075  
; PRIOR FILING DATE: 2003-10-27  
; PRIOR APPLICATION NUMBER: US/09/965,116  
; PRIOR FILING DATE: 2002-03-08

; PRIOR APPLICATION NUMBER: US 09/712,898  
; PRIOR FILING DATE: 2000-11-15  
; PRIOR APPLICATION NUMBER: US 60/235,452  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 60/235,453  
; PRIOR FILING DATE: 2000-09-26  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 80  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: modified linkage of oligodeoxynucleotide  
; OTHER INFORMATION: phosphorothioate  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: 16  
; OTHER INFORMATION: 3'-3' linkage  
US-10-694-075-80

Query Match 88.9%; Score 16; DB 8; Length 32;  
Best Local Similarity 87.5%; Pred. No. 1.4e+02;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 3 AGGGUGCAGCGCGUA 18  
||||:|||||:  
Db 32 AGGTCGACGCGGTA 17

RESULT 41  
US-10-694-383-79/c  
; Sequence 79, Application US/10694383  
; Publication No. US20040266710A1  
; GENERAL INFORMATION:  
; APPLICANT: Kandimalle, Ekambar R.  
; APPLICANT: Zhao, QiuYan  
; APPLICANT: Yu, Dong  
; APPLICANT: Agrawal, Sudhir  
; TITLE OF INVENTION: Modulation of Immunostimulatory Activity of  
; TITLE OF INVENTION: Immunostimulatory  
; TITLE OF INVENTION: Modified oligodeoxynucleotide phosphorothioate Analogs by  
; FILE REFERENCE: HYZ-479CP (47508.577)  
; CURRENT APPLICATION NUMBER: US/10/694,383  
; PRIOR FILING DATE: 2003-10-27  
; PRIOR APPLICATION NUMBER: US/09/965,116  
; PRIOR FILING DATE: 2002-03-08  
; PRIOR APPLICATION NUMBER: US 60/235,452  
; PRIOR FILING DATE: 2000-11-15  
; PRIOR APPLICATION NUMBER: US 60/235,452  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 60/235,453  
; PRIOR FILING DATE: 2000-09-26  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 79  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: modified linkage of oligodeoxynucleotide  
; OTHER INFORMATION: phosphorothioate  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: 16  
; OTHER INFORMATION: 5'-5' linkage  
US-10-694-383-79

Query Match 88.9%; Score 16; DB 8; Length 32;  
Best Local Similarity 87.5%; Pred. No. 1.4e+02;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;



QY 3 AGGTCGACGCGGUA 18  
||||:|||||:|  
DB 16 AGGTCGACGCGGTA 1

## RESULT 42

US-10-694-383-80/c  
Sequence 80, Application US/10694383  
Publication No. US20040266710A1  
GENERAL INFORMATION:  
APPLICANT: Kandimala, Ekambar R.  
APPLICANT: Zhao, Qiyuan  
APPLICANT: Yu, Dong  
APPLICANT: Agrawal, Sudhir  
TITLE OF INVENTION: Modulation of Immunostimulatory Activity of  
TITLE OF INVENTION: Immunostimulatory  
TITLE OF INVENTION: Modified oligodeoxynucleotide phosphorothioate Analogs by  
FILE REFERENCE: HYZ-479CP (47508,577)  
CURRENT APPLICATION NUMBER: US/10/694,383  
CURRENT FILING DATE: 2003-10-27  
PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/965,116  
PRIOR FILING DATE: CURRENT FILING DATE: 2002-03-08  
PRIOR APPLICATION NUMBER: US 09/712,898  
PRIOR FILING DATE: 2000-11-15  
PRIOR APPLICATION NUMBER: US 60/235,452  
PRIOR FILING DATE: 2000-09-26  
PRIOR APPLICATION NUMBER: US 60/235,453  
PRIOR FILING DATE: 2000-09-26  
NUMBER OF SEQ ID NOS: 112  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 80  
LENGTH: 32  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: modified linkage of oligodeoxynucleotide  
OTHER INFORMATION: phosphorothioate  
NAME/KEY: modified\_base  
LOCATION: 16  
OTHER INFORMATION: 3'-3' linkage  
US-10-694-383-80

Query Match 88.9%; Score 16; DB 8; Length 32;  
Best Local Similarity 87.5%; Pred. No. 1.4e+02;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

## RESULT 43

US-10-694-418-79/c  
Sequence 79, Application US/10694418  
Publication No. US20050026858A1  
GENERAL INFORMATION:  
APPLICANT: Kandimala, Ekambar R.  
APPLICANT: Zhao, Qiyuan  
APPLICANT: Yu, Dong  
APPLICANT: Agrawal, Sudhir  
TITLE OF INVENTION: Modulation of Immunostimulatory Activity of Immunostimulatory  
TITLE OF INVENTION: Modified oligodeoxynucleotide phosphorothioate Analogs by  
FILE REFERENCE: HYZ-479CP (47508,577)  
CURRENT APPLICATION NUMBER: US/10/694,418  
CURRENT FILING DATE: 2003-10-27  
PRIOR APPLICATION NUMBER: US/09/965,116  
PRIOR FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: US 09/712,898  
PRIOR FILING DATE: 2000-11-15  
PRIOR APPLICATION NUMBER: US 60/235,452

PRIOR FILING DATE: 2000-09-26  
PRIOR APPLICATION NUMBER: US 60/235,453  
PRIOR FILING DATE: 2000-09-26  
NUMBER OF SEQ ID NOS: 112  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 79  
LENGTH: 32  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: modified linkage of oligodeoxynucleotide phosphorothioate  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 16  
OTHER INFORMATION: 5'-5' linkage  
US-10-694-418-79

Query Match 88.9%; Score 16; DB 8; Length 32;  
Best Local Similarity 87.5%; Pred. No. 1.4e+02;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGGTCGACGCGGUA 18  
||||:|||||:|  
DB 16 AGGTCGACGCGGTA 1

## RESULT 44

US-10-694-418-80/c  
Sequence 80, Application US/10694418  
Publication No. US20050026858A1  
GENERAL INFORMATION:  
APPLICANT: Kandimala, Ekambar R.  
APPLICANT: Zhao, Qiyuan  
APPLICANT: Yu, Dong  
APPLICANT: Agrawal, Sudhir  
TITLE OF INVENTION: Modulation of Immunostimulatory Activity of Immunostimulatory  
TITLE OF INVENTION: Modified oligodeoxynucleotide phosphorothioate Analogs by  
FILE REFERENCE: HYZ-479CP (47508,577)  
CURRENT APPLICATION NUMBER: US/10/694,418  
CURRENT FILING DATE: 2003-10-27  
PRIOR APPLICATION NUMBER: US/09/965,116  
PRIOR FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: US 09/712,898  
PRIOR FILING DATE: 2000-11-15  
PRIOR APPLICATION NUMBER: US 60/235,452  
PRIOR FILING DATE: 2000-09-26  
PRIOR APPLICATION NUMBER: US 60/235,453  
PRIOR FILING DATE: 2000-09-26  
NUMBER OF SEQ ID NOS: 112  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 80  
LENGTH: 32  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: modified linkage of oligodeoxynucleotide phosphorothioate  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 16  
OTHER INFORMATION: 3'-3' linkage  
US-10-694-418-80

Query Match 88.9%; Score 16; DB 8; Length 32;  
Best Local Similarity 87.5%; Pred. No. 1.4e+02;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGGTCGACGCGGUA 18  
||||:|||||:|  
DB 32 AGGTCGACGCGGTA 17

## RESULT 45

US-10-053-645A-8/c  
; Sequence 8, Application US/10053645A  
; Publication No. US2003016376A1  
; GENERAL INFORMATION:  
; APPLICANT: Robert E. Klem  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A  
; TITLE OF INVENTION: CRIL-PROLIFERATIVE DISORDER USING CBE DECOY OLIGOMERS, BCL-2  
; TITLE OF INVENTION: ANTISENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF  
; FILE REFERENCE: 10412-022-999  
; CURRENT FILING DATE: 2002-01-22  
; PRIOR FILING DATE: 2001-01-22  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Description of artificial sequence: Synthetic Antisense  
; OTHER INFORMATION: Oligonucleotide  
US-10-053-645A-8

Query Match 83.3%; Score 15; DB 6; Length 17;  
Best Local Similarity 93.3%; Pred. No. 5.2e+02;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCG 15  
|||:|||||  
Db 15 AGAGGTCGACGCG 1

RESULT 46  
US-10-961-458-8/c  
; Sequence 8, Application US/10961458  
; Publication No. US20050170377A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; TITLE OF INVENTION: REGULATION OF BCL-2 GENE EXPRESSION  
; FILE REFERENCE: 04040/1200990-US7  
; CURRENT APPLICATION NUMBER: US/10/961,458  
; CURRENT FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: US/10/961,458  
; PRIOR FILING DATE: 2004-10-07  
; PRIOR FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: US 09/375,514  
; PRIOR FILING DATE: 1999-08-17  
; PRIOR APPLICATION NUMBER: US 09/080,285  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: US 08/465,485  
; PRIOR FILING DATE: 1995-06-05  
; PRIOR APPLICATION NUMBER: US 08/124,256  
; PRIOR FILING DATE: 1993-09-20  
; PRIOR APPLICATION NUMBER: US 07/840,716  
; PRIOR FILING DATE: 1992-02-21  
; PRIOR APPLICATION NUMBER: US 07/288,692  
; PRIOR FILING DATE: 1988-12-22  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-961-458-8

Query Match 83.3%; Score 15; DB 9; Length 17;  
Best Local Similarity 93.3%; Pred. No. 5.2e+02;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCG 15  
|||:|||||  
Db 15 AGAGGTCGACGCG 1

RESULT 47  
US-10-723-860-668  
; Sequence 668, Application US/10723860  
; Publication No. US20040253606A1  
; GENERAL INFORMATION:  
; APPLICANT: Aziz, Natassha  
; APPLICANT: Ginsburg, Wendy M.  
; APPLICANT: Zlocnik, Albert  
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
; FILE REFERENCE: 05882.0193.NPUS01  
; CURRENT APPLICATION NUMBER: US/10/723,860  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 60/429,739  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 8393  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 668  
; LENGTH: 337  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-723-860-668

Query Match 83.3%; Score 15; DB 8; Length 337;  
Best Local Similarity 93.3%; Pred. No. 3.3e+02;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGCG 16  
|||:|||||  
Db 128 GAGGTCGACGCG 142

RESULT 48  
US-10-756-149-689  
; Sequence 689, Application US/10756149  
; Publication No. US20050181375A1  
; GENERAL INFORMATION:  
; APPLICANT: Aziz, Natassha  
; APPLICANT: Zlocnik, Albert  
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER  
; FILE REFERENCE: file  
; CURRENT APPLICATION NUMBER: US/10/756,149  
; CURRENT FILING DATE: 2004-01-12  
; NUMBER OF SEQ ID NOS: 5818  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 689  
; LENGTH: 337  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-10-756-149-689

Query Match 83.3%; Score 15; DB 9; Length 337;  
Best Local Similarity 93.3%; Pred. No. 3.3e+02;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGCG 16  
|||:|||||  
Db 128 GAGGTCGACGCG 142

RESULT 49  
US-10-424-599-126012/c  
; Sequence 126012, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J  
; APPLICANT: Kovalic, David K  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B  
 CURRENT APPLICATION NUMBER: US/10/424,599  
 CURRENT FILING DATE: 2003-04-28  
 NUMBER OF SEQ ID NOS: 285684  
 SEQ ID NO 126012  
 LENGTH: 363  
 TYPE: DNA  
 ORGANISM: Glycine max  
 FEATURE:  
 OTHER INFORMATION: Clone ID: PAT\_MRT3847\_84798C.1  
 US-10-424-599-126012

Query Match 83.3%; Score 15; DB 7; Length 363;  
 Best Local Similarity 93.3%; Pred. No. 3.3e+02;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUCGACGCG 15  
 |||||:|||||  
 DB 19 AGAGGTCGACGCG 5

RESULT 50  
 US-09-918-995-34640  
 Sequence 34640, Application US/09918995  
 Publication No. US20030073623A1  
 GENERAL INFORMATION:  
 APPLICANT: Hyseq, Inc.  
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES  
 FILE REFERENCE: 20411-756  
 CURRENT APPLICATION NUMBER: US/09/918,995  
 CURRENT FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: US/09/235,076  
 PRIOR FILING DATE: 1999-01-20  
 NUMBER OF SEQ ID NOS: 38054  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 34640  
 LENGTH: 381  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-918-995-34640

Query Match 83.3%; Score 15; DB 3; Length 381;  
 Best Local Similarity 93.3%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUCGACGCG 16  
 |||||:|||||  
 DB 20 GAGGTCGACGCG 34

Search completed: March 19, 2006, 07:52:28  
 Job time : 2721.85 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 18:35:23 ; Search time 1694.77 Seconds  
(without alignments)  
496.922 Million cell updates/sec

Title: US-10-800-926-1

Perfect score: 18

Sequence: 1 agaggggacgacgagcggua 18

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

BST:\*

1: gb\_esc1:\*

2: gb\_esc2:\*

3: gb\_esc3:\*

4: gb\_esc4:\*

5: gb\_esc5:\*

6: gb\_esc6:\*

7: gb\_esc7:\*

8: gb\_esc8:\*

9: gb\_esc9:\*

10: gb\_esc10:\*

11: gb\_esc11:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.4	91.1	448	1	AA796833 VP15G04.r
2	16.4	91.1	759	9	AO903738 GSTG0477
3	16.4	91.1	791	10	CG056537 PUTG38TD
4	16.4	91.1	854	10	CG117658 PUFYD77TB
5	16.4	91.1	891	10	CG117700 PUFYD77TD
6	16.4	88.9	730	5	BX765851 BX765851
7	16.4	88.9	841	8	CK774850 UI-EH-HG2
8	15.4	85.6	296	1	BB081347 BB081347
9	15.4	85.6	479	5	BM344647 BM344647
10	15.4	85.6	521	3	BM344647 BM344647
11	15.4	85.6	546	7	BM344647 BM344647
12	15.4	85.6	600	3	BM344647 BM344647
13	15.4	85.6	614	9	BM344647 BM344647
14	15.4	85.6	630	9	BM344647 BM344647
15	15.4	85.6	667	10	BM344647 BM344647
16	15.4	85.6	713	3	BM344647 BM344647
17	15.4	85.6	732	3	BM344647 BM344647
18	15.4	85.6	750	3	BM344647 BM344647
19	15.4	85.6	770	8	BM344647 BM344647
20	15.4	85.6	771	3	BM344647 BM344647
21	15.4	85.6	812	10	BM344647 BM344647
22	15.4	85.6	906	5	BM344647 BM344647

23	15.4	85.6	926	8	CV762975	CV762975
24	15.4	85.6	1101	10	CNS001UI	AT061582 Drosophila
25	15.4	85.6	1204	10	AG038447	AG038447 Pan trogl
26	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
27	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
28	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
29	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
30	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
31	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
32	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
33	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
34	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
35	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
36	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
37	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
38	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
39	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
40	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
41	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
42	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
43	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
44	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
45	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
46	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
47	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
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49	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
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51	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
52	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
53	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
54	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
55	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
56	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
57	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
58	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
59	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
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62	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
63	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
64	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
65	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
66	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
67	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
68	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
69	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
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71	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
72	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
73	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
74	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
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76	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
77	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
78	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
79	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
80	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
81	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
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83	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
84	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
85	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
86	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
87	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
88	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
89	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
90	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
91	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
92	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
93	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
94	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl
95	15.4	85.6	1310	10	AG038547	AG038547 Pan trogl

96	15	83.3	900	5	BU601342	BU601342	AGENCOURT	C 169	14.8	82.2	788	10	CG830999	CG830999	ZMREB0325
97	15	83.3	908	3	BI597901	BI597901	603245386	C 170	14.8	82.2	809	9	CC373466	CC373466	PUNNN387D
98	15	83.3	992	1	AL530375	AL530375		C 171	14.8	82.2	812	9	CC373465	CC373465	PUNNN387B
99	15	83.3	999	1	AL545950	AL545950		C 172	14.8	82.2	814	9	CC517338	CC517338	CH240_363
100	15	83.3	999	7	CO648029	CO648029	ILLIUMGEN	C 173	14.8	82.2	814	10	CG284685	CG284685	OG2M64TH
101	15	83.3	1001	5	BU960184	BU960184	AGENCOURT	C 174	14.8	82.2	838	8	DR028792	DR028792	BD8010061
102	15	83.3	1003	3	BM459984	BM459984	AGENCOURT	C 175	14.8	82.2	839	2	BF624069	BF624069	HVSMXA000
103	15	83.3	1098	10	AG071030	AG071030	Pan txcg1	C 176	14.8	82.2	847	10	AG106838	AG106838	Pan txcg1
104	15	83.3	1136	4	BM455062	BM455062	AGENCOURT	C 177	14.8	82.2	855	9	BH478909	BH478909	BOGYX7ATR
105	15	83.3	1136	4	BC029815	BC029815	Homo sap1	C 178	14.8	82.2	871	10	CL503217	CL503217	SAIL_721
106	15	83.3	1253	10	BG855194	BG855194	1024042A0	C 179	14.8	82.2	879	2	BQ333527	BQ333527	602460185
107	15	83.3	1428	10	AG0588872	AG0588872	Pan txcg1	C 180	14.8	82.2	881	8	CX113905	CX113905	RI084L16
108	15	83.3	1470	4	CR617172	CR617172	full-1eng	C 181	14.8	82.2	890	10	CZ220092	CZ220092	AlAA-aa6
109	15	83.3	1798	4	CR611959	CR611959	full-1eng	C 182	14.8	82.2	899	2	BG696181	BG696181	602659304
110	15	83.3	1872	4	CR621535	CR621535	full-1eng	C 183	14.8	82.2	905	10	AG071019	AG071019	Pan txcg1
111	15	83.3	1878	4	CR603240	CR603240	full-1eng	C 184	14.8	82.2	907	10	AG849952	AG849952	Oryza sat
112	15	83.3	1909	4	CR592676	CR592676	full-1eng	C 185	14.8	82.2	909	10	CL097307	CL097307	ISB1-29K1
113	14.8	82.2	257	7	CF844844	CF844844	PAHB030Xr	C 186	14.8	82.2	920	10	AG895708	AG895708	Oryza sat
114	14.8	82.2	267	7	BH036493	BH036493	RPCI-24-2	C 187	14.8	82.2	930	10	CG123667	CG123667	PUPFN63TD
115	14.8	82.2	273	7	CF839902	CF839902	PAHB004XG	C 188	14.8	82.2	968	10	BO956997	BO956997	Tetradon
116	14.8	82.2	285	7	CF852423	CF852423	PAMC005XG	C 189	14.8	82.2	982	5	BO708608	BO708608	AGENCOURT
117	14.8	82.2	335	3	BQ341778	BQ341778	NR3-NN12	C 190	14.8	82.2	1005	5	BH853111	BH853111	AGENCOURT
118	14.8	82.2	340	9	AO379902	AO379902	RPCI11-16	C 191	14.8	82.2	1008	5	BH853111	BH853111	AGENCOURT
119	14.8	82.2	356	3	BI530687	BI530687	1024108A0	C 192	14.8	82.2	1040	10	CZ363738	CZ363738	AGENCOURT
120	14.8	82.2	372	7	CF843232	CF843232	PAHB024Xr	C 193	14.8	82.2	1052	10	AG523727	AG523727	Mus muscu
121	14.8	82.2	387	7	CF847397	CF847397	PAHB043XG	C 194	14.8	82.2	1143	5	BU903516	BU903516	AGENCOURT
122	14.8	82.2	397	7	CF844825	CF844825	PAHB030XG	C 195	14.8	82.2	1143	5	CG267604	CG267604	CH261-BM1
123	14.8	82.2	387	7	CF852737	CF852737	PAMC006Xr	C 196	14.8	82.2	1146	3	BM544423	BM544423	AGENCOURT
124	14.8	82.2	400	11	CR081703	CR081703	Reverse 8	C 197	14.8	82.2	1251	3	BM911470	BM911470	AGENCOURT
125	14.8	82.2	404	7	CF842396	CF842396	PAHB019Xr	C 198	14.8	82.2	1335	9	CC192277	CC192277	CH261-129
126	14.8	82.2	410	7	CF843050	CF843050	PAHB023X1	C 199	14.8	82.2	1535	2	BG767840	BG767840	602741325
127	14.8	82.2	420	9	AO436228	AO436228	HS_5049_B	C 200	14.8	82.2	1947	10	CG756482	CG756482	P051-3-H0
128	14.8	82.2	421	7	CF847037	CF847037	PAHB041Xr	C 201	14.4	80.0	228	9	AC938337	AC938337	NLI-BH10R
129	14.8	82.2	433	7	CF841367	CF841367	PAHB014XG	C 202	14.4	80.0	260	3	BI789554	BI789554	IC96C01_Y
130	14.8	82.2	427	7	CF847954	CF847954	PMAA003Xr	C 203	14.4	80.0	275	3	BI791199	BI791199	10013406_Y
131	14.8	82.2	439	7	CF850103	CF850103	PMAA012Xr	C 204	14.4	80.0	291	6	CA405547	CA405547	1001696_H
132	14.8	82.2	438	10	CL416283	CL416283	ZMREB043	C 205	14.4	80.0	292	5	BQ817613	BQ817613	103006580
133	14.8	82.2	448	9	BG937526	BG937526	1b00020G7	C 206	14.4	80.0	302	1	AA795306	AA795306	VV33907_X
134	14.8	82.2	455	2	AZ919143	AZ919143	1006014B0	C 207	14.4	80.0	302	5	BO810016	BO810016	1030014G0
135	14.8	82.2	478	2	BG242401	BG242401	602354183	C 208	14.4	80.0	309	1	AI466683	AI466683	mg88604_Y
136	14.8	82.2	497	9	AO402168	AO402168	HS_5069_A	C 209	14.4	80.0	312	1	AV392647	AV392647	AV392647
137	14.8	82.2	522	10	CG047096	CG047096	PURCR587B	C 210	14.4	80.0	322	1	AM123892	AM123892	UI-M-BH2
138	14.8	82.2	538	7	CF844249	CF844249	PAHB027X5	C 211	14.4	80.0	332	9	AO849231	AO849231	LMALFV1_1
139	14.8	82.2	551	1	AV391666	AV391666	AV391666	C 212	14.4	80.0	334	6	CF155176	CF155176	B0621H11_1
140	14.8	82.2	565	8	CF779520	CF779520	UI-BH-HG2	C 213	14.4	80.0	334	6	CF155799	CF155799	B0629D06-
141	14.8	82.2	570	3	BP875603	BP875603	BP875603	C 214	14.4	80.0	334	6	CF157155	CF157155	B0645C06-
142	14.8	82.2	584	9	BH067296	BH067296	RPCI-24-3	C 215	14.4	80.0	346	3	BUS39130	BUS39130	BT539130
143	14.8	82.2	586	10	CG059973	CG059973	PURFPA4TD	C 216	14.4	80.0	362	2	BG278523	BG278523	ASC01mp_X
144	14.8	82.2	588	7	CN827677	CN827677	EL2452F_B	C 217	14.4	80.0	377	1	AA016343	AA016343	mg88604_X
145	14.8	82.2	590	10	CG059971	CG059971	PURFPA4TB	C 218	14.4	80.0	385	1	AV641375	AV641375	AV641375
146	14.8	82.2	597	7	CN579901	CN579901	MDfW20361	C 219	14.4	80.0	391	3	BP089197	BP089197	BP089197
147	14.8	82.2	653	2	BG858515	BG858515	1024058B0	C 220	14.4	80.0	393	1	AV638911	AV638911	AV638911
148	14.8	82.2	673	6	CD819990	CD819990	BM20_050M	C 221	14.4	80.0	393	5	AV623725	AV623725	AV623725
149	14.8	82.2	683	8	DR103401	DR103401	UHU033A03	C 222	14.4	80.0	395	1	AV623725	AV623725	AV623725
150	14.8	82.2	686	2	BE705043	BE705043	SC02_06eU	C 223	14.4	80.0	395	1	AV631701	AV631701	AV631701
151	14.8	82.2	688	2	CN826207	CN826207	EL1365F_B	C 224	14.4	80.0	396	1	AV621233	AV621233	AV621233
152	14.8	82.2	689	2	BE704739	BE704739	SC02_01eU	C 225	14.4	80.0	397	9	BZ802657	BZ802657	BZ802657
153	14.8	82.2	691	2	BE705258	BE705258	SC02_10C0	C 226	14.4	80.0	397	11	CR162053	CR162053	Reverse 8
154	14.8	82.2	693	10	BE704809	BE704809	SC02_02G0	C 227	14.4	80.0	399	1	AA503031	AA503031	rh56810_8
155	14.8	82.2	693	2	CG850054	CG850054	ZMREB033	C 228	14.4	80.0	402	1	AV632574	AV632574	AV632574
156	14.8	82.2	705	7	CV096863	CV096863	FAMU_USDA	C 229	14.4	80.0	403	1	AV619735	AV619735	AV619735
157	14.8	82.2	716	10	AG271951	AG271951	Cyanid108	C 230	14.4	80.0	407	3	BP086426	BP086426	BP086426
158	14.8	82.2	727	9	CC912925	CC912925	1074e24ba	C 231	14.4	80.0	408	3	BP089039	BP089039	BP089039
159	14.8	82.2	727	10	AG175950	AG175950	Pan txcg1	C 232	14.4	80.0	411	1	AA855806	AA855806	AV75802_X
160	14.8	82.2	728	9	BH898666	BH898666	MB61P9H9	C 233	14.4	80.0	412	1	AV388383	AV388383	AV388383
161	14.8	82.2	731	8	DN764944	DN764944	AGENCOURT	C 234	14.4	80.0	412	5	BI642312	BI642312	BI642312
162	14.8	82.2	738	10	AG334318	AG334318	Mus muscu	C 235	14.4	80.0	413	3	BB790234	BB790234	BB790234
163	14.8	82.2	740	7	CK782694	CK782694	UI-D-GC1_	C 236	14.4	80.0	416	1	AV387145	AV387145	AV387145
164	14.8	82.2	757	10	BI96271	BI96271	Danio rer	C 237	14.4	80.0	419	2	AV624670	AV624670	AV624670
165	14.8	82.2	768	10	AG468797	AG468797	Mus muscu	C 238	14.4	80.0	419	2	BB783406	BB783406	BB783406
166	14.8	82.2	780	8	DN875872	DN875872	nae02d08_	C 239	14.4	80.0	420	1	AI1449643	AI1449643	mr4C011_X
167	14.8	82.2	782	8	CO423708	CO423708	GGEZHT100	C 240	14.4	80.0	421	6	CF583452	CF583452	AGENCOURT
168	14.8	82.2	782	8	CX881930	CX881930	JGI_CNAL2	C 241	14.4	80.0	422	1	AV388436	AV388436	AV388436

C 242	14.4	80.0	423	9	AZ157089	AZ157089 SP 0044 A	C 315	14.4	80.0	530	1	AV392089	AV392089
C 243	14.4	80.0	424	5	BY444280	BY444280	C 316	14.4	80.0	530	10	BO813994	BO813994
C 244	14.4	80.0	424	5	AO852000	AO852000 LMAJFV1.1	C 317	14.4	80.0	532	5	CM811018	CM811018
C 245	14.4	80.0	425	1	AV389207	AV389207	C 318	14.4	80.0	533	5	BO8223290	BO8223290
C 246	14.4	80.0	427	1	AV625996	AV625996	C 319	14.4	80.0	534	7	CJ016207	CJ016207
C 247	14.4	80.0	428	7	CF937680	CF937680 NCEST3e34	C 320	14.4	80.0	536	5	BO821116	BO821116
C 248	14.4	80.0	429	2	BB790488	BB790488	C 321	14.4	80.0	537	7	AM661465	AM661465
C 249	14.4	80.0	430	1	AV639238	AV639238	C 322	14.4	80.0	537	7	CK300941	CK300941
C 250	14.4	80.0	431	6	W65581	W65581 me10f05.r1	C 323	14.4	80.0	539	3	BI844975	BI844975
C 251	14.4	80.0	432	3	BI428417	BI428417 f83f08.y	C 324	14.4	80.0	539	3	BO186412	BO186412
C 252	14.4	80.0	437	3	AV635435	AV635435	C 325	14.4	80.0	542	2	BF288038	BF288038
C 253	14.4	80.0	438	1	AV627289	AV627289	C 326	14.4	80.0	542	5	BO813972	BO813972
C 254	14.4	80.0	445	1	AV636351	AV636351	C 327	14.4	80.0	542	5	BO818492	BO818492
C 255	14.4	80.0	445	2	BE227811	BE227811 894035D02	C 328	14.4	80.0	543	1	AV390403	AV390403
C 256	14.4	80.0	446	1	AV387026	AV387026	C 329	14.4	80.0	545	2	BO847357	BO847357
C 257	14.4	80.0	447	2	BE337229	BE337229 894044F08	C 330	14.4	80.0	546	1	AM280812	AM280812
C 258	14.4	80.0	449	8	DN351971	DN351971 L1B3580-0	C 331	14.4	80.0	548	5	BU650717	BU650717
C 259	14.4	80.0	452	1	AV634611	AV634611	C 332	14.4	80.0	549	1	AV389928	AV389928
C 260	14.4	80.0	455	2	BF510481	BF510481 UI-H-B14-	C 333	14.4	80.0	553	1	AV389454	AV389454
C 261	14.4	80.0	465	2	BE129110	BE129110 894020C04	C 334	14.4	80.0	558	1	AV391820	AV391820
C 262	14.4	80.0	466	2	BP511101	BP511101 UI-H-B14-	C 335	14.4	80.0	558	3	BM342592	BM342592
C 263	14.4	80.0	467	3	BI721329	BI721329 103105EC1	C 336	14.4	80.0	562	1	AV387895	AV387895
C 264	14.4	80.0	467	3	BM000829	BM000829 1031091D1	C 337	14.4	80.0	562	3	BI720351	BI720351
C 265	14.4	80.0	469	2	BE452249	BE452249 894062E06	C 338	14.4	80.0	562	6	CF558608	CF558608
C 266	14.4	80.0	472	1	AV387898	AV387898	C 339	14.4	80.0	564	5	BO814494	BO814494
C 267	14.4	80.0	473	1	AV622823	AV622823	C 340	14.4	80.0	568	1	BI728922	BI728922
C 268	14.4	80.0	473	7	CV001518	CV001518 aam01-10m	C 341	14.4	80.0	569	1	AV387517	AV387517
C 269	14.4	80.0	473	10	CM174301	CM174301 104_586_1	C 342	14.4	80.0	572	1	AV390312	AV390312
C 270	14.4	80.0	474	8	DN395863	DN395863 L1B3935-0	C 343	14.4	80.0	572	3	BI874831	BI874831
C 271	14.4	80.0	476	1	AA030414	AA030414 m126e08.r	C 344	14.4	80.0	574	6	CF559337	CF559337
C 272	14.4	80.0	476	1	AV396518	AV396518	C 345	14.4	80.0	575	3	BI533713	BI533713
C 273	14.4	80.0	478	1	AV624162	AV624162	C 346	14.4	80.0	577	1	AM289118	AM289118
C 274	14.4	80.0	479	1	AV619750	AV619750	C 347	14.4	80.0	578	1	AW819934	AW819934
C 275	14.4	80.0	480	1	AV639460	AV639460	C 348	14.4	80.0	578	2	BE726705	BE726705
C 276	14.4	80.0	481	3	BI716621	BI716621 1031011D1	C 349	14.4	80.0	580	3	BI839754	BI839754
C 277	14.4	80.0	483	5	BO820556	BO820556 1030085F0	C 350	14.4	80.0	583	1	AV387548	AV387548
C 278	14.4	80.0	483	5	BM947987	BM947987	C 351	14.4	80.0	583	6	CF556640	CF556640
C 279	14.4	80.0	484	2	BE337245	BE337245 894044G04	C 352	14.4	80.0	584	6	CF562005	CF562005
C 280	14.4	80.0	484	9	BH500430	BH500430 BCGD015TF	C 353	14.4	80.0	584	3	BI994878	BI994878
C 281	14.4	80.0	486	5	BY414092	BY414092	C 354	14.4	80.0	584	5	BU654410	BU654410
C 282	14.4	80.0	486	10	CL183093	CL183093 104_395_1	C 355	14.4	80.0	584	10	EX994698	EX994698
C 283	14.4	80.0	488	3	BI719681	BI719681 1031045B0	C 356	14.4	80.0	589	1	AM147019	AM147019
C 284	14.4	80.0	489	1	AV637127	AV637127	C 357	14.4	80.0	591	2	BE452216	BE452216
C 285	14.4	80.0	492	3	BI723824	BI723824 1031067H0	C 358	14.4	80.0	593	1	BI999363	BI999363
C 286	14.4	80.0	492	3	BI723825	BI723825 1031067H0	C 359	14.4	80.0	594	1	AV392430	AV392430
C 287	14.4	80.0	492	3	BM035169	BM035169	C 360	14.4	80.0	594	2	BE452445	BE452445
C 288	14.4	80.0	492	5	BO823794	BO823794 1030112G1	C 361	14.4	80.0	594	3	BM002587	BM002587
C 289	14.4	80.0	493	5	BU651725	BU651725 1112095B1	C 362	14.4	80.0	594	6	CF555790	CF555790
C 290	14.4	80.0	495	1	AI673626	AI673626 w676e12.x	C 363	14.4	80.0	595	3	BI725071	BI725071
C 291	14.4	80.0	495	2	BE212384	BE212384 894029F06	C 364	14.4	80.0	597	1	BI530841	BI530841
C 292	14.4	80.0	496	2	BE212384	BE212384 894029F06	C 365	14.4	80.0	602	1	AV391482	AV391482
C 293	14.4	80.0	496	5	BO824069	BO824069 1030115B0	C 366	14.4	80.0	602	9	BH878231	BH878231
C 294	14.4	80.0	497	3	BM001866	BM001866 1031098H0	C 367	14.4	80.0	604	3	BI725154	BI725154
C 295	14.4	80.0	500	3	BI725073	BI725073 1031077A0	C 368	14.4	80.0	606	2	BE726689	BE726689
C 296	14.4	80.0	501	1	AI326861	AI326861 m350c04.x	C 369	14.4	80.0	607	3	BI718195	BI718195
C 297	14.4	80.0	507	1	AM077570	AM077570 f335h04.y	C 370	14.4	80.0	608	3	BI878379	BI878379
C 298	14.4	80.0	510	1	AI481050	AI481050 v331D06.x	C 371	14.4	80.0	609	3	BI725072	BI725072
C 299	14.4	80.0	511	1	AV389838	AV389838	C 372	14.4	80.0	611	2	BE112088	BE112088
C 300	14.4	80.0	512	3	BM070729	BM070729 f198f03.y	C 373	14.4	80.0	612	6	CF569451	CF569451
C 301	14.4	80.0	513	2	BE129075	BE129075 894021D10	C 374	14.4	80.0	615	5	BU651902	BU651902
C 302	14.4	80.0	516	3	BI350743	BI350743 f38a08.y	C 375	14.4	80.0	616	2	BG985593	BG985593
C 303	14.4	80.0	516	5	BO814406	BO814406 1030043C0	C 376	14.4	80.0	617	6	CF556647	CF556647
C 304	14.4	80.0	518	8	DN354231	DN354231 L1B3581-0	C 377	14.4	80.0	618	3	BM002874	BM002874
C 305	14.4	80.0	520	3	BI874673	BI874673 963117C02	C 378	14.4	80.0	624	5	BO818261	BO818261
C 306	14.4	80.0	520	8	DN343897	DN343897 L1B3550-0	C 379	14.4	80.0	624	5	BU655144	BU655144
C 307	14.4	80.0	520	8	DN343897	DN343897 L1B3550-0	C 380	14.4	80.0	625	3	BI718807	BI718807
C 308	14.4	80.0	522	3	BI725155	BI725155 1031077B1	C 381	14.4	80.0	626	3	BI717556	BI717556
C 309	14.4	80.0	524	1	AI326834	AI326834 m339c09.x	C 382	14.4	80.0	626	9	CE147586	CE147586
C 310	14.4	80.0	524	3	BE452858	BE452858 894066C10	C 383	14.4	80.0	628	5	BU650727	BU650727
C 311	14.4	80.0	524	3	BI725699	BI725699 1031080F0	C 384	14.4	80.0	630	3	BI997343	BI997343
C 312	14.4	80.0	525	1	AV390935	AV390935	C 385	14.4	80.0	632	3	BI718055	BI718055
C 313	14.4	80.0	528	6	CF564027	CF564027 1115088G0	C 386	14.4	80.0	632	7	CK750246	CK750246
C 314	14.4	80.0	528	9	BH667076	BH667076 BOWLB90TF	C 387	14.4	80.0	634	3	BI874089	BI874089
C 315	14.4	80.0	530	1	AV392089	AV392089	C 316	14.4	80.0	530	1	BO813994	BO813994
C 316	14.4	80.0	532	5	CM811018	CM811018	C 317	14.4	80.0	532	5	BO8223290	BO8223290
C 317	14.4	80.0	533	5	BO8223290	BO8223290	C 318	14.4	80.0	534	7	AM661465	AM661465
C 318	14.4	80.0	534	7	AM661465	AM661465	C 319	14.4	80.0	536	5	BO821116	BO821116
C 319	14.4	80.0	536	5	BO821116	BO821116	C 320	14.4	80.0	537	7	CK300941	CK300941
C 320	14.4	80.0	537	7	CK300941	CK300941	C 321	14.4	80.0	537	7	BI844975	BI844975
C 321	14.4	80.0	537	7	BI844975	BI844975	C 322	14.4	80.0	539	3	BO186412	BO186412
C 322	14.4	80.0	539	3	BO186412	BO186412	C 323	14.4	80.0	542	2	BF288038	BF288038
C 323	14.4	80.0	542	2	BF288038	BF288038	C 324	14.4	80.0	542	5	BO813972	BO813972
C 324	14.4	80.0	542	5	BO813972	BO813972	C 325	14.4	80.0	542	5	BO818492	BO818492
C 325	14.4	80.0	542	5	BO818492	BO818492	C 326	14.4	80.0	543	1	AV390403	AV390403
C 326	14.4	80.0	543	1	AV390403	AV390403	C 327	14.4	80.0	545	2	BO847357	BO847357
C 327	14.4	80.0	545	2	BO847357	BO847357	C 328	14.4	80.0	546	1	AM280812	AM280812
C 328	14.4	80.0	546	1	AM280812	AM280812	C 329	14.4	80.0	548	5	BU650717	BU650717
C 329</													



C 388	14.4	80.0	636	1	AL544385	AL544385	C 461	14.4	80.0	795	8	DR880929	DR880929 JGI_CABK3
C 389	14.4	80.0	636	3	BI873610	BI873610	C 462	14.4	80.0	795	3	CA427685	CA427685 PUHL771TB
C 390	14.4	80.0	640	3	BI722730	BI722730	C 463	14.4	80.0	807	3	BP441510	BP441510 BP441510
C 391	14.4	80.0	642	3	BI998181	BI998181	C 464	14.4	80.0	807	6	CD752768	CD752768 AGENCOURT
C 392	14.4	80.0	643	9	BZ624291	BZ624291	C 465	14.4	80.0	809	9	BZ438504	BZ438504 BOND65TF
C 393	14.4	80.0	645	3	BI716796	BI716796	C 466	14.4	80.0	814	8	DR658311	DR658311 JGI_CABK3
C 394	14.4	80.0	650	10	CM140157	CM140157	C 467	14.4	80.0	820	8	DR853874	DR853874 JGI_CABK1
C 395	14.4	80.0	652	3	BI890967	BI890967	C 468	14.4	80.0	824	8	DR853874	DR853874 JGI_CABK1
C 396	14.4	80.0	653	3	BM000617	BM000617	C 469	14.4	80.0	825	8	CX982444	CX982444 JGI_CABP1
C 397	14.4	80.0	654	3	BM002586	BM002586	C 470	14.4	80.0	825	8	BZ574669	BZ574669 mnh2_3777
C 398	14.4	80.0	655	5	BU655143	BU655143	C 471	14.4	80.0	828	3	BI728466	BI728466 BP172846
C 399	14.4	80.0	656	3	BI720039	BI720039	C 472	14.4	80.0	831	9	BZ441366	BZ441366 BONT894TF
C 400	14.4	80.0	657	6	CF523157	CF523157	C 473	14.4	80.0	836	9	BH527007	BH527007 BOG6035TR
C 401	14.4	80.0	658	3	BI875056	BI875056	C 474	14.4	80.0	846	8	CX980553	CX980553 JGI_CABP1
C 402	14.4	80.0	660	3	BOJ08589	BOJ08589	C 475	14.4	80.0	847	8	CX982411	CX982411 JGI_CABP1
C 403	14.4	80.0	660	5	BOJ81385	BOJ81385	C 476	14.4	80.0	848	2	BH541751	BH541751 601063709
C 404	14.4	80.0	663	3	BI723823	BI723823	C 477	14.4	80.0	854	8	BH644752	BH644752 BOGUC54TF
C 405	14.4	80.0	663	5	BOJ814337	BOJ814337	C 478	14.4	80.0	862	8	CX965094	CX965094 JGI_CABP7
C 406	14.4	80.0	668	3	BM002754	BM002754	C 479	14.4	80.0	868	8	CX971846	CX971846 JGI_CABP7
C 407	14.4	80.0	669	3	BI725153	BI725153	C 480	14.4	80.0	868	8	DR881181	DR881181 JGI_CABK5
C 408	14.4	80.0	669	3	BI874072	BI874072	C 481	14.4	80.0	869	8	CX982267	CX982267 JGI_CABP1
C 409	14.4	80.0	671	6	CF524855	CF524855	C 482	14.4	80.0	869	9	BZ898809	BZ898809 FUGDX35TD
C 410	14.4	80.0	673	5	BU653297	BU653297	C 483	14.4	80.0	873	7	CR412086	CR412086 CR412086
C 411	14.4	80.0	675	10	CM140156	CM140156	C 484	14.4	80.0	874	2	BE784921	BE784921 601479147
C 412	14.4	80.0	676	10	BK209207	BK209207	C 485	14.4	80.0	874	6	CF374256	CF374256 AGENCOURT
C 413	14.4	80.0	678	5	BU651853	BU651853	C 486	14.4	80.0	877	8	DR856773	DR856773 JGI_CABK3
C 414	14.4	80.0	680	10	CZ742904	CZ742904	C 487	14.4	80.0	880	8	DR855331	DR855331 JGI_CABK2
C 415	14.4	80.0	681	6	CF524540	CF524540	C 488	14.4	80.0	882	8	DR871563	DR871563 JGI_CABG1
C 416	14.4	80.0	685	5	BOJ824313	BOJ824313	C 489	14.4	80.0	887	3	BP442568	BP442568 BP442568
C 417	14.4	80.0	685	6	CF523487	CF523487	C 490	14.4	80.0	891	8	DR859790	DR859790 JGI_CABK4
C 418	14.4	80.0	687	5	BU646523	BU646523	C 491	14.4	80.0	893	8	DR881562	DR881562 JGI_CABK7
C 419	14.4	80.0	688	5	BY755058	BY755058	C 492	14.4	80.0	896	8	DR856424	DR856424 JGI_CABK2
C 420	14.4	80.0	688	10	CL183094	CL183094	C 493	14.4	80.0	897	8	DR859955	DR859955 JGI_CABK4
C 421	14.4	80.0	689	10	BZ996309	BZ996309	C 494	14.4	80.0	903	3	BM801577	BM801577 AGENCOURT
C 422	14.4	80.0	691	9	CC168063	CC168063	C 495	14.4	80.0	909	6	CD051213	CD051213 AGENCOURT
C 423	14.4	80.0	696	2	BH223101	BH223101	C 496	14.4	80.0	917	2	BG542857	BG542857 602572055
C 424	14.4	80.0	698	6	CA079874	CA079874	C 497	14.4	80.0	922	9	CC418065	CC418065 PUHRG79TD
C 425	14.4	80.0	698	6	CF343579	CF343579	C 498	14.4	80.0	933	2	BE541926	BE541926 601064220
C 426	14.4	80.0	699	5	BK670047	BK670047	C 499	14.4	80.0	934	10	CG234739	CG234739 AGENCOURT
C 427	14.4	80.0	700	2	BF662542	BF662542	C 500	14.4	80.0	936	2	BG343536	BG343536 HVSMBG000
C 428	14.4	80.0	701	9	CC424127	CC424127	C 501	14.4	80.0	947	5	BO674530	BO674530 AGENCOURT
C 429	14.4	80.0	702	5	BU627645	BU627645	C 502	14.4	80.0	968	10	CL485192	CL485192 SAIL_410
C 430	14.4	80.0	702	9	BZ411889	BZ411889	C 503	14.4	80.0	971	10	CZ277322	CZ277322 ZMBMF0061
C 431	14.4	80.0	707	3	BP138731	BP138731	C 504	14.4	80.0	981	6	CB193781	CB193781 AGENCOURT
C 432	14.4	80.0	712	6	CF522881	CF522881	C 505	14.4	80.0	990	6	CA183543	CA183543 SCQGST315
C 433	14.4	80.0	714	3	BP451176	BP451176	C 506	14.4	80.0	991	5	BU939617	BU939617 AGENCOURT
C 434	14.4	80.0	718	7	BZ411886	BZ411886	C 507	14.4	80.0	998	5	BO709351	BO709351 AGENCOURT
C 435	14.4	80.0	718	7	CU001409	CU001409	C 508	14.4	80.0	1029	10	CL251528	CL251528 ZMBMBD060
C 436	14.4	80.0	722	6	CF525122	CF525122	C 509	14.4	80.0	1037	1	AL696502	AL696502 AL696502
C 437	14.4	80.0	723	6	CF524239	CF524239	C 510	14.4	80.0	1038	3	BM470002	BM470002 AGENCOURT
C 438	14.4	80.0	724	6	CF525075	CF525075	C 511	14.4	80.0	1060	7	CK631807	CK631807 AMO-AL001
C 439	14.4	80.0	724	2	BF662255	BF662255	C 512	14.4	80.0	1071	5	BO961067	BO961067 AGENCOURT
C 440	14.4	80.0	725	8	DN423379	DN423379	C 513	14.4	80.0	1073	5	BO931293	BO931293 AGENCOURT
C 441	14.4	80.0	726	10	CZ914920	CZ914920	C 514	14.4	80.0	1146	2	BI253887	BI253887 602974672
C 442	14.4	80.0	742	2	BF683083	BF683083	C 515	14.4	80.0	1146	5	BO654223	BO654223 AGENCOURT
C 443	14.4	80.0	745	6	DR816669	DR816669	C 516	14.4	80.0	1217	3	BM555241	BM555241 AGENCOURT
C 444	14.4	80.0	745	6	CD778766	CD778766	C 517	14.4	80.0	1337	10	AG041848	AG041848 Pan tciog1
C 445	14.4	80.0	753	7	CK448135	CK448135	C 518	14.4	80.0	1365	5	BO935014	BO935014 AGENCOURT
C 446	14.4	80.0	755	6	CF523991	CF523991	C 519	14.4	80.0	1380	5	BU482492	BU482492 603472595
C 447	14.4	80.0	757	6	CF374578	CF374578	C 520	14.4	80.0	1383	10	AG072071	AG072071 Pan tciog1
C 448	14.4	80.0	758	2	BG753604	BG753604	C 521	14.4	80.0	1476	4	CN80FO00	CN80FO00 Tetratodon
C 449	14.4	80.0	759	10	CG686994	CG686994	C 522	14.4	80.0	1514	10	AG533701	AG533701 Mus muscu
C 450	14.4	80.0	764	3	CK146963	CK146963	C 523	14.4	80.0	1574	8	DN656309	DN656309 CEC22-DO5
C 451	14.4	80.0	770	9	BZ469393	BZ469393	C 524	14.4	80.0	1631	10	AG176417	AG176417 Pan tciog1
C 452	14.4	80.0	771	6	CF374494	CF374494	C 525	14.4	80.0	1631	10	AG543066	AG543066 Mus muscu
C 453	14.4	80.0	776	10	CG297277	CG297277	C 526	14.4	80.0	1798	1	AW727718	AW727718 GA_Ba001
C 454	14.4	80.0	777	6	CF524758	CF524758	C 527	14.4	80.0	1808	10	AG565996	AG565996 Mus muscu
C 455	14.4	80.0	783	3	CX981871	CX981871	C 528	14.4	80.0	2213	1	AW730161	AW730161 GA_Ba000
C 456	14.4	80.0	784	6	CF132436	CF132436	C 529	14.4	80.0	2217	4	AK041073	AK041073 Mus muscu
C 457	14.4	80.0	784	10	CZ275722	CZ275722	C 530	14.4	80.0	2607	10	CL506397	CL506397 SATL_766
C 458	14.4	80.0	789	6	CB899989	CB899989	C 531	14	77.8	269	8	FO5367	FO5367 HSC08D041 n
C 459	14.4	80.0	790	8	CX772547	CX772547	C 532	14	77.8	339	8	DN351798	DN351798 LIB3580-0
C 460	14.4	80.0	794	10	CM005217	CM005217	C 533	14	77.8	343	5	BY118452	BY118452 BY118452

C 534	14	77.8	384	2	BF511904	UI-H-B14-	607	14	77.8	1039	9	CC270828	CC270828	CH261-37H
C 535	14	77.8	388	3	BP429210	BP429210	C 608	14	77.8	1060	10	CL985679	CL985679	CL985679 ZMMBB000
C 536	14	77.8	393	1	AA31898	EST5906	C 609	14	77.8	1105	5	BU160090	BU160090	BU160090 AGENCOURT
C 537	14	77.8	394	7	CO319101	EC276241.	C 610	14	77.8	1126	5	BU119676	BU119676	BU119676 603143459
C 538	14	77.8	396	7	CO319102	EC276242.	C 611	14	77.8	1437	5	BO896991	BO896991	BO896991 AGENCOURT
C 539	14	77.8	416	1	AM256108	687062C09	C 612	14	77.8	1465	3	BM551325	BM551325	BM551325 AGENCOURT
C 540	14	77.8	429	3	BM432445	1JEB486.a	C 613	14	77.8	1470	9	BZ576488	BZ576488	meb2 4956
C 541	14	77.8	436	7	CP653469	DEMCO08X.a	C 614	13.8	76.7	68	9	CC200396	CC200396	CC200396 RRB089 Ba
C 542	14	77.8	442	2	BI277229	UI-R-CY0-	C 615	13.8	76.7	97	10	CL302980	CL302980	CL302980 P012C03 G
C 543	14	77.8	451	1	AI025850	OM12C06.8	C 616	13.8	76.7	97	11	CL610276	CL610276	EY10262-5
C 544	14	77.8	464	3	BM676857	UI-E-E01-	C 617	13.8	76.7	122	8	H45582	H45582	HA5582 y97a06.r1
C 545	14	77.8	474	8	DN392149	LIB3934-0	C 618	13.8	76.7	125	7	CM468089	CM468089	CB 01 VR
C 546	14	77.8	485	2	BE429978	TAS005.G0	C 619	13.8	76.7	139	2	BM651305	BM651305	BM651305 PM4-BN021
C 547	14	77.8	516	3	BM953580	952064A03	C 620	13.8	76.7	164	2	BM659237	BM659237	BM659237 TGE8TZY98
C 548	14	77.8	523	8	DN389358	LI8396-0	C 621	13.8	76.7	183	1	AI121496	AI121496	AI121496 qm31d06.x
C 549	14	77.8	527	3	BN293067	LI70006001	C 622	13.8	76.7	189	1	AM481842	AM481842	AM481842 38720 MAR
C 550	14	77.8	533	7	BM566449	AGENCOURT	C 623	13.8	76.7	196	2	BM558529	BM558529	BM558529 RH122 56
C 551	14	77.8	535	3	BM556449	AGENCOURT	C 624	13.8	76.7	198	6	CB392244	CB392244	CB392244 OSTR06D6
C 552	14	77.8	537	3	BM556449	AGENCOURT	C 625	13.8	76.7	207	1	AA352367	AA352367	AA352367 EST60355
C 553	14	77.8	537	3	BM556449	AGENCOURT	C 626	13.8	76.7	215	10	CE565034	CE565034	CE565034 t1gr-g88-
C 554	14	77.8	561	6	CB286736	CMD45.A10	C 627	13.8	76.7	216	1	AN233272	AN233272	AN233272 AV233272
C 555	14	77.8	579	7	CO049082	DBA06B02.	C 628	13.8	76.7	217	8	DN339826	DN339826	DN339826 LIB3523-0
C 556	14	77.8	587	6	CA211604	SCRLAD110	C 629	13.8	76.7	224	8	N33784	N33784	N33784 yx72a06.r1
C 557	14	77.8	601	4	AY108569	Zea.mays	C 630	13.8	76.7	232	2	BM660027	BM660027	BM660027 TGE8TZY90
C 558	14	77.8	604	2	BR392116	601307759	C 631	13.8	76.7	232	6	CA775341	CA775341	CA775341 1088C04.x
C 559	14	77.8	605	6	CA732967	wJpIC.pK0	C 632	13.8	76.7	233	10	CL632140	CL632140	CL632140 EY03570 D
C 560	14	77.8	614	8	CL190473	65-E01937	C 633	13.8	76.7	234	2	BM659692	BM659692	BM659692 TGE8TZY94
C 561	14	77.8	637	6	CF722835	H09.LKFO0	C 634	13.8	76.7	234	9	BH818236	BH818236	BH818236 BACP10-H
C 562	14	77.8	652	10	CL403525	CG329360	C 635	13.8	76.7	237	1	AA014751	AA014751	AA014751 mh18C03.r
C 563	14	77.8	657	2	BG746906	602703457	C 636	13.8	76.7	237	3	CB220026	CB220026	CB220026 1AB014G06
C 564	14	77.8	680	8	DR113115	1436067 M	C 637	13.8	76.7	239	6	CR191581	CR191581	CR191581 t1gr-g88-
C 565	14	77.8	680	9	CC962086	BOIDP20TF	C 638	13.8	76.7	241	9	AA023329	AA023329	mh69E02.r
C 566	14	77.8	699	7	CN790525	4125124 B	C 639	13.8	76.7	256	10	CB724817	CB724817	CB724817 t1gr-g88-
C 567	14	77.8	707	10	CG329360	CG5AG40TC	C 640	13.8	76.7	260	10	CG885413	CG885413	CG885413 ZMMBB0049
C 568	14	77.8	719	3	BM728592	UI-E-EJ0-	C 641	13.8	76.7	261	3	BP945147	BP945147	BP945147
C 569	14	77.8	746	7	CO202435	Qa.sp1bn	C 642	13.8	76.7	262	3	BJ518693	BJ518693	BJ518693
C 570	14	77.8	749	2	BE868991	601444764	C 643	13.8	76.7	266	7	CK728932	CK728932	CK728932 UMC-bend
C 571	14	77.8	756	10	CG363400	CGM7208TH	C 644	13.8	76.7	274	10	AA641952	AA641952	AA641952 n818d02.r
C 572	14	77.8	758	2	BE305923	CG363400	C 645	13.8	76.7	279	10	CG423942	CG423942	CG423942 ZMMBB004
C 573	14	77.8	761	9	CC701277	OOMDHA9TV	C 646	13.8	76.7	280	5	BU948369	BU948369	BU948369
C 574	14	77.8	761	10	CG125255	PUPFOF20TD	C 647	13.8	76.7	282	5	BU966622	BU966622	BU966622 tca-1107
C 575	14	77.8	780	10	CG194120	PUII63TH	C 648	13.8	76.7	285	3	AIU178408	AIU178408	AIU178408
C 576	14	77.8	788	10	CG193441	PUIGB31TH	C 649	13.8	76.7	286	1	AV206513	AV206513	AV206513
C 577	14	77.8	798	10	CG288497	CG3AC06TH	C 650	13.8	76.7	286	5	BU097038	BU097038	BU097038 tca-1523
C 578	14	77.8	818	2	BG747323	602704988	C 651	13.8	76.7	286	5	BU097038	BU097038	BU097038 tca-1523
C 579	14	77.8	824	8	DR829812	2M.BP007	C 652	13.8	76.7	287	7	CO053358	CO053358	CO053358 TGE8TZY99
C 580	14	77.8	824	10	CG31889	CGXBC93TH	C 653	13.8	76.7	290	7	BB192219	BB192219	BB192219
C 581	14	77.8	827	10	CG331897	CG331897	C 654	13.8	76.7	291	1	BM239128	BM239128	BM239128
C 582	14	77.8	831	2	BF211674	601812189	C 655	13.8	76.7	292	2	CN314950	CN314950	CN314950 170004177
C 583	14	77.8	833	2	BF130408	601818704	C 656	13.8	76.7	292	7	BM636308	BM636308	BM636308 h07C03.Y
C 584	14	77.8	837	9	CC618856	OCUJ226TV	C 657	13.8	76.7	296	5	BU097133	BU097133	BU097133 tca-1618
C 585	14	77.8	842	10	CL415904	ZMMBB042	C 658	13.8	76.7	297	5	BM517219	BM517219	BM517219
C 586	14	77.8	847	9	BZ744170	OCFAO54TM	C 659	13.8	76.7	297	2	BU095836	BU095836	BU095836 tca-321 C
C 587	14	77.8	847	9	CC698388	OCMEBA93TH	C 660	13.8	76.7	297	5	BM517219	BM517219	BM517219
C 588	14	77.8	863	6	CD753105	AGENCOURT	C 661	13.8	76.7	297	7	CN196010	CN196010	CN196010 TGE8TZY19
C 589	14	77.8	864	9	BZ744165	OCFAO54TC	C 662	13.8	76.7	301	1	AV024980	AV024980	AV024980
C 590	14	77.8	873	10	CG314205	CG5DL94TC	C 663	13.8	76.7	303	9	AQ094853	AQ094853	AQ094853 GSSTC0801
C 591	14	77.8	887	6	CD754915	AGENCOURT	C 664	13.8	76.7	303	3	BZ307589	BZ307589	BZ307589 hX59H07.b
C 592	14	77.8	887	7	CO065619	eat.k.bre	C 665	13.8	76.7	306	3	AO764656	AO764656	AO764656 HS.3131.B
C 593	14	77.8	897	9	CC396599	PUIHBC2TD	C 666	13.8	76.7	306	9	BJ532643	BJ532643	BJ532643
C 594	14	77.8	914	10	CG178629	PUIHBC4TD	C 667	13.8	76.7	310	5	BU096149	BU096149	BU096149 tca-6134 C
C 595	14	77.8	925	10	CG454601	PUIK667TD	C 668	13.8	76.7	314	5	BG014380	BG014380	BG014380 PM3-GN030
C 596	14	77.8	931	8	DN478494	altt010Xa	C 669	13.8	76.7	315	5	BY183524	BY183524	BY183524
C 597	14	77.8	936	10	CG288509	CG3AC06TV	C 670	13.8	76.7	320	3	BM147989	BM147989	BM147989 tCAAP1Q15
C 598	14	77.8	944	10	CG377887	OGYCH59TV	C 671	13.8	76.7	323	1	AA023781	AA023781	AA023781 mh05B03.r
C 599	14	77.8	946	10	CG182658	PUKOJ67TH	C 672	13.8	76.7	327	1	AU243309	AU243309	AU243309
C 600	14	77.8	953	9	CC396595	PUIHBC2TB	C 673	13.8	76.7	327	7	CO830393	CO830393	CO830393 LM.GB5.01
C 601	14	77.8	964	7	AG112767	Fan.tEO91	C 674	13.8	76.7	329	5	BU096124	BU096124	BU096124 tca-605 C
C 602	14	77.8	966	7	CK409304	altt010Xa	C 675	13.8	76.7	330	6	CD637451	CD637451	CD637451
C 603	14	77.8	978	10	CG454556	PUIK667TH	C 676	13.8	76.7	333	8	TS5917	TS5917	ydb2f02.r1
C 604	14	77.8	987	10	CG377878	OGYCH59TH	C 677	13.8	76.7	335	8	DM1550	DM1550	DM1550 HDM416H08B
C 605	14	77.8	1004	10	CG103711	PUIHBC7TH	C 678	13.8	76.7	337	7	CO343845	CO343845	CO343845 BP18219.3
C 606	14	77.8	1011	10	CL429027	ZMMBB044	C 679	13.8	76.7	337	7	CO343845	CO343845	CO343845 BP18219.3

C 680	13.8	76.7	339	5	BU096315	lca-800.t	753	13.8	76.7	417	2	BG937520	BG937520
681	13.8	76.7	340	1	AV669207		C 754	13.8	76.7	418	7	CO742901	CO742901
682	13.8	76.7	340	6	CB694226	AMGNNUC:C	C 755	13.8	76.7	419	6	CB368445	CB368445
683	13.8	76.7	341	10	CZ770873	OC_Ba012	C 756	13.8	76.7	420	7	CN195234	CN195234
684	13.8	76.7	345	1	AV124058	AV124058	C 757	13.8	76.7	420	6	CD568054	CD568054
685	13.8	76.7	347	2	BG938269	lbo14F09	C 758	13.8	76.7	421	9	AQ059931	AQ059931
C 686	13.8	76.7	351	5	BU096817	lca-1302	759	13.8	76.7	422	9	CC605478	CC605478
687	13.8	76.7	353	1	AA016872	ml36h10.r	760	13.8	76.7	422	10	CG432841	CG432841
C 688	13.8	76.7	354	1	AI214675	qm32d06.x	761	13.8	76.7	423	3	BJ531099	BJ531099
689	13.8	76.7	355	3	BJ520061	AI131609	762	13.8	76.7	424	2	BG373462	BG373462
690	13.8	76.7	356	1	AI143609	mb25e05.x	763	13.8	76.7	426	1	AV710934	AV710934
691	13.8	76.7	356	1	BG938341	lbo15H05	C 764	13.8	76.7	429	6	CB220801	CB220801
C 692	13.8	76.7	358	6	CF641641	D2_B12.F	C 765	13.8	76.7	431	10	CM031801	CM031801
C 693	13.8	76.7	359	3	BM708196	UI-E-C11-	C 766	13.8	76.7	432	6	CB027739	CB027739
694	13.8	76.7	359	9	B2188729	CH230-436	C 767	13.8	76.7	433	2	BG382922	BG382922
695	13.8	76.7	360	5	BY190337	BY190337	C 768	13.8	76.7	434	1	AI297710	AI297710
C 696	13.8	76.7	363	8	H74328	YU56G09.r1	769	13.8	76.7	434	3	BP254612	BP254612
C 697	13.8	76.7	364	5	BY310605	BY310605	C 770	13.8	76.7	435	2	BG937524	BG937524
C 698	13.8	76.7	365	8	DN277485	lbo14B06	C 771	13.8	76.7	435	3	BI964714	BI964714
C 699	13.8	76.7	368	8	H70540	Yr90e08.r1	C 772	13.8	76.7	435	6	CB721848	CB721848
C 700	13.8	76.7	368	8	H70540	Yr90e08.r1	C 773	13.8	76.7	437	3	CO316060	CO316060
C 701	13.8	76.7	369	3	BJ508920	BJ508920	C 774	13.8	76.7	437	3	BI476983	BI476983
C 702	13.8	76.7	373	3	AO909877	G8STC0835	C 775	13.8	76.7	439	1	AA236757	AA236757
C 703	13.8	76.7	373	10	CM444438	feb0001f1	C 776	13.8	76.7	439	2	BG937520	BG937520
C 704	13.8	76.7	374	5	BU097022	lca-1507	C 777	13.8	76.7	439	8	CV919901	CV919901
C 705	13.8	76.7	375	2	BF833758	RC1-H708	C 778	13.8	76.7	441	9	AZ217796	AZ217796
C 706	13.8	76.7	375	2	BG938005	lbo00805	C 779	13.8	76.7	443	2	BF552216	BF552216
C 707	13.8	76.7	376	7	CO722082	TG8Tzyq2	C 780	13.8	76.7	444	2	BG556574	BG556574
C 708	13.8	76.7	377	2	BG938067	lbo12H05	781	13.8	76.7	444	9	AO731504	AO731504
C 709	13.8	76.7	377	5	BU095881	lca-366.t	C 782	13.8	76.7	446	1	AV619833	AV619833
C 710	13.8	76.7	377	8	H74327	YU56G09.r1	C 783	13.8	76.7	446	3	BM482983	BM482983
C 711	13.8	76.7	378	1	AV429392	AV429392	C 784	13.8	76.7	449	1	AU066252	AU066252
C 712	13.8	76.7	382	1	BG937610	lbo003H5	C 785	13.8	76.7	451	7	BI614933	BI614933
C 713	13.8	76.7	382	3	BJ495366	BJ495366	C 786	13.8	76.7	451	7	CN122681	CN122681
C 714	13.8	76.7	382	10	AG930914	Drogeoph11	C 787	13.8	76.7	451	9	CC372505	CC372505
C 715	13.8	76.7	384	2	BG937688	lbo005B03	C 788	13.8	76.7	451	9	AO641782	AO641782
C 716	13.8	76.7	384	5	BY609376	BY609376	C 789	13.8	76.7	452	2	BE700000	BE700000
C 717	13.8	76.7	385	2	BF927866	CM1-NT024	C 790	13.8	76.7	452	2	CV551352	CV551352
C 718	13.8	76.7	385	2	BG937547	lbo003B9	C 791	13.8	76.7	453	2	BG659832	BG659832
C 719	13.8	76.7	386	8	R84301	YP89G04.r1	C 792	13.8	76.7	453	9	AO913442	AO913442
C 720	13.8	76.7	386	1	AM480976	34023.MAR	C 793	13.8	76.7	455	1	AV632664	AV632664
C 721	13.8	76.7	388	3	BP432198	BP432198	C 794	13.8	76.7	455	3	BM073808	BM073808
C 722	13.8	76.7	388	3	BM026874	fl10g09.y	C 795	13.8	76.7	456	1	AI376359	AI376359
C 723	13.8	76.7	390	3	AA446742	zw89a06.r	C 796	13.8	76.7	456	1	AM277316	AM277316
C 724	13.8	76.7	391	3	BJ551231	BJ551231	C 797	13.8	76.7	457	1	AV622258	AV622258
C 725	13.8	76.7	394	2	BG937669	lbo004G04	C 798	13.8	76.7	457	2	BR334956	BR334956
C 726	13.8	76.7	395	5	BY287433	BY287433	799	13.8	76.7	457	10	CZ795913	CZ795913
C 727	13.8	76.7	395	6	CB773640	AMGNNUC:N	C 800	13.8	76.7	458	2	BG378022	BG378022
C 728	13.8	76.7	396	8	T80723	Yd23G08.r1	C 801	13.8	76.7	458	6	CB024483	CB024483
C 729	13.8	76.7	396	9	CC443938	POHGN75TD	C 802	13.8	76.7	459	9	BH758470	BH758470
C 730	13.8	76.7	396	10	CG809889	FSAN77TF	C 803	13.8	76.7	459	9	CC833156	CC833156
C 731	13.8	76.7	402	5	BU095825	lca-310.t	C 804	13.8	76.7	460	7	CN197418	CN197418
C 732	13.8	76.7	402	7	CO186111	EX015937	C 805	13.8	76.7	461	4	CN8068MU	CN8068MU
C 733	13.8	76.7	403	3	BO159787	WHE0969.E	C 806	13.8	76.7	462	1	AJ735529	AJ735529
C 734	13.8	76.7	405	2	BG938247	lbo14D09	C 807	13.8	76.7	462	2	BF603101	BF603101
C 735	13.8	76.7	406	2	BJ963669	BJ963669	C 808	13.8	76.7	462	3	BM311997	BM311997
C 736	13.8	76.7	406	3	BF348390	602022450	C 809	13.8	76.7	462	6	CB220079	CB220079
C 737	13.8	76.7	408	2	BG937846	lbo007H08	C 810	13.8	76.7	462	7	CN199957	CN199957
C 738	13.8	76.7	408	7	CN780145	TG8Tzyr5	C 811	13.8	76.7	463	2	BG938076	BG938076
C 739	13.8	76.7	408	7	CO748571	SHE8TBd4	C 812	13.8	76.7	464	2	CO515882	CO515882
C 740	13.8	76.7	409	5	BQ820787	l030087C1	C 813	13.8	76.7	465	7	CV703283	CV703283
C 741	13.8	76.7	410	6	CA618606	w11n.pk00	C 814	13.8	76.7	466	2	BG937447	BG937447
C 742	13.8	76.7	412	2	BG938379	lbo016B06	C 815	13.8	76.7	466	6	CF247518	CF247518
C 743	13.8	76.7	412	2	BE847761	uw35G09.y	C 816	13.8	76.7	467	1	AM654571	AM654571
C 744	13.8	76.7	414	1	AA017860	ml44E09.r	C 817	13.8	76.7	467	2	BG938367	BG938367
C 745	13.8	76.7	414	1	BP743883	BP743883	C 818	13.8	76.7	467	3	BM425561	BM425561
C 746	13.8	76.7	414	5	BO642527	mcmk012x1	C 819	13.8	76.7	467	11	DE022290	DE022290
C 747	13.8	76.7	414	5	CO343145	BP16163.3	C 820	13.8	76.7	468	3	BP417559	BP417559
C 748	13.8	76.7	414	8	N83037	TG8Tzy59a1	C 821	13.8	76.7	468	6	CB030861	CB030861
C 749	13.8	76.7	415	1	AV390213	AV390213	C 822	13.8	76.7	468	7	CN7880035	CN7880035
C 750	13.8	76.7	416	7	CK930392	bsa1ga003	C 823	13.8	76.7	469	10	CI9551321	CI9551321
C 751	13.8	76.7					C 824	13.8	76.7		2	BG658062	BG658062
C 752	13.8	76.7					C 825	13.8	76.7				

826	13.8	76.7	469	2	BG938083	BG938083	1Ab011A04	899	13.8	76.7	509	1	AU178852	AU178852
827	13.8	76.7	469	2	BG938356	BG938356	1Ab016B02	900	13.8	76.7	509	5	B08082E0	B08082E0
828	13.8	76.7	470	1	AI659450	AI659450	wd72A06.x	901	13.8	76.7	510	2	BG937412	BG937412
829	13.8	76.7	470	1	AJ457417	AJ457417		902	13.8	76.7	510	3	BT793278	BT793278
830	13.8	76.7	470	3	BU531571	BU531571		903	13.8	76.7	513	3	BM591238	BM591238
831	13.8	76.7	470	3	BM446881	BM446881	DSA004D11	904	13.8	76.7	514	1	AA428906	AA428906
832	13.8	76.7	471	3	BM507361	BM507361	1h27R02.Y	905	13.8	76.7	515	1	AW702514	AW702514
833	13.8	76.7	472	2	BG938038	BG938038	1Ab012E03	906	13.8	76.7	516	2	BG420790	BG420790
834	13.8	76.7	472	2	BR465079	BR465079	hw74F05.X	907	13.8	76.7	516	2	BR377347	BR377347
835	13.8	76.7	472	2	BM447985	BM447985	DSA021A11	908	13.8	76.7	517	3	BM622315	BM622315
836	13.8	76.7	472	6	CF645331	CF645331	K55.B12.F	909	13.8	76.7	518	6	CB329513	CB329513
837	13.8	76.7	472	8	H42278	H42278	yo63C06.x1	910	13.8	76.7	519	1	AO143729	AO143729
838	13.8	76.7	473	1	AV637170	AV637170	AV637170	911	13.8	76.7	519	1	AV634074	AV634074
839	13.8	76.7	473	2	BG937802	BG937802	1Ab007C01	912	13.8	76.7	519	7	CN196662	CN196662
840	13.8	76.7	473	2	BG937844	BG937844	1Ab007R06	913	13.8	76.7	520	2	BG019038	BG019038
841	13.8	76.7	473	5	BY711646	BY711646		914	13.8	76.7	521	7	CO190377	CO190377
842	13.8	76.7	473	6	CF004035	CF004035	OBH26A02.	915	13.8	76.7	522	3	BM635281	BM635281
843	13.8	76.7	473	7	CN196774	CN196774	TGSTRZYM0	916	13.8	76.7	522	7	CN658039	CN658039
844	13.8	76.7	474	4	AK019237	AK019237	Mus.muscu	917	13.8	76.7	522	8	CK899149	CK899149
845	13.8	76.7	475	3	BM354158	BM354158	1f31B07.Y	918	13.8	76.7	523	1	AV620318	AV620318
846	13.8	76.7	475	4	AK012519	AK012519	Mus.muscu	919	13.8	76.7	524	3	BI450205	BI450205
847	13.8	76.7	477	2	BE674978	BE674978	7f11E01.X	920	13.8	76.7	525	2	BE722730	BE722730
848	13.8	76.7	478	3	BI960954	BI960954	MONO1.3.B	921	13.8	76.7	525	2	BE852897	BE852897
849	13.8	76.7	478	6	CA691256	CA691256	w1m96.pK0	922	13.8	76.7	525	6	CB010036	CB010036
850	13.8	76.7	479	2	BG937508	BG937508	1Ab002G03	923	13.8	76.7	525	9	BZ894763	BZ894763
851	13.8	76.7	481	2	BG938275	BG938275	1Ab008C09	924	13.8	76.7	527	1	AI060232	AI060232
852	13.8	76.7	481	6	CB220341	CB220341	1Ab020D08	925	13.8	76.7	527	2	BI251247	BI251247
853	13.8	76.7	482	2	BE335157	BE335157	u893F08.Y	926	13.8	76.7	527	10	AG935111	AG935111
854	13.8	76.7	482	3	BM000305	BM000305	1031087A0	927	13.8	76.7	528	1	AV624321	AV624321
855	13.8	76.7	483	6	CD668778	CD668778	geec1c.pK0	928	13.8	76.7	529	1	AV621078	AV621078
856	13.8	76.7	484	1	AL798728	AL798728		929	13.8	76.7	529	2	BG937751	BG937751
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859	13.8	76.7	487	5	BU070194	BU070194	1m19402.Y	932	13.8	76.7	529	9	CB686062	CB686062
860	13.8	76.7	487	6	CB028580	CB028580	TGSTRZy47	933	13.8	76.7	529	6	BT747830	BT747830
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862	13.8	76.7	488	3	BI528050	BI528050	1024087A0	935	13.8	76.7	530	9	AC063222	AC063222
863	13.8	76.7	488	5	BY711778	BY711778		936	13.8	76.7	530	10	AG945018	AG945018
864	13.8	76.7	489	3	BI728606	BI728606	1031100C1	937	13.8	76.7	532	1	AU081835	AU081835
865	13.8	76.7	489	6	CB239035	CB239035	TGSTRZyF5	938	13.8	76.7	532	9	AO651812	AO651812
866	13.8	76.7	490	3	BU183425	BU183425		939	13.8	76.7	534	1	AM163316	AM163316
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868	13.8	76.7	492	7	CN197740	CN197740	TGSTRZy15	941	13.8	76.7	534	3	BM718258	BM718258
869	13.8	76.7	493	2	BG938351	BG938351	1Ab016B10	942	13.8	76.7	534	3	BM930554	BM930554
870	13.8	76.7	493	3	BZ323558	BZ323558	1a79G03.G	943	13.8	76.7	534	3	BM930668	BM930668
871	13.8	76.7	493	9	AO659162	AO659162	Sheared.D	944	13.8	76.7	534	3	AO186198	AO186198
872	13.8	76.7	493	10	CZ602116	CZ602116	OM_Ba012	945	13.8	76.7	535	1	AV392772	AV392772
873	13.8	76.7	494	3	BI362167	BI362167	RE4661.5	946	13.8	76.7	535	5	AV392772	AV392772
874	13.8	76.7	495	7	CN197447	CN197447	TGSTRZy13	947	13.8	76.7	535	5	BO811887	BO811887
875	13.8	76.7	496	3	BI356280	BI356280	RE42394.5	948	13.8	76.7	536	5	EX115048	EX115048
876	13.8	76.7	496	3	BM352149	BM352149	1983B07.Y	949	13.8	76.7	536	10	CM464036	CM464036
877	13.8	76.7	496	6	CF790095	CF790095	867440.MA	950	13.8	76.7	538	3	BI161675	BI161675
878	13.8	76.7	496	6	CN197470	CN197470	TGSTRZy13	951	13.8	76.7	538	6	CF754546	CF754546
879	13.8	76.7	497	2	BG937701	BG937701	1Ab005F04	952	13.8	76.7	538	8	CK945169	CK945169
880	13.8	76.7	499	1	AU180619	AU180619		953	13.8	76.7	539	8	AI908586	AI908586
881	13.8	76.7	499	7	CO742909	CO742909	TGSTRZy4	954	13.8	76.7	539	1	AL915673	AL915673
882	13.8	76.7	500	1	AV637702	AV637702	UI-E-DW1	955	13.8	76.7	539	1	AL918570	AL918570
883	13.8	76.7	500	3	BM712143	BM712143	UI-E-DW1	956	13.8	76.7	539	3	BO184736	BO184736
884	13.8	76.7	500	6	CB250225	CB250225	Ga630069	957	13.8	76.7	539	5	BT743307	BT743307
885	13.8	76.7	500	11	TA172B020	TA172B020		958	13.8	76.7	541	5	AV395663	AV395663
886	13.8	76.7	501	1	AI390821	AI390821	mb25E05.Y	959	13.8	76.7	541	3	BI964206	BI964206
887	13.8	76.7	501	7	CN198115	CN198115	TGSTRZy13	960	13.8	76.7	541	6	CA181224	CA181224
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889	13.8	76.7	502	9	CG821340	CG821340	MBSPID3.U	962	13.8	76.7	542	3	BI721028	BI721028
890	13.8	76.7	502	2	BG937770	BG937770	1Ab006B11	963	13.8	76.7	543	7	CN242738	CN242738
891	13.8	76.7	504	2	BR809730	BR809730	215469.MA	964	13.8	76.7	544	3	AA476807	AA476807
892	13.8	76.7	504	3	BM272752	BM272752	1998A10.Y	965	13.8	76.7	544	3	BI3247279	BI3247279
893	13.8	76.7	504	6	CB220411	CB220411	1Ab021D01	966	13.8	76.7	548	3	BM176130	BM176130
894	13.8	76.7	507	3	BU900468	BU900468		967	13.8	76.7	549	3	BO524991	BO524991
895	13.8	76.7	508	3	BM447347	BM447347	DSA009B04	968	13.8	76.7	550	10	CM143033	CM143033
896	13.8	76.7	508	5	BO564466	BO564466	g117B12.Y	969	13.8	76.7	551	6	CB614463	CB614463
897	13.8	76.7	508	8	W72564	W72564	zdg5f09.g1	970	13.8	76.7	551	7	CN122367	CN122367
898	13.8	76.7	508	8	W72564	W72564	zdg5f09.g1	971	13.8	76.7	551	7	CN122367	CN122367

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972 13.8 76.7 552 9 AZ335078 1M0064B15
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980 13.8 76.7 555 7 CN780155
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984 13.8 76.7 558 11 DE121380
985 13.8 76.7 559 3 BU886423
986 13.8 76.7 560 3 BM176786
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989 13.8 76.7 561 3 BM189038
990 13.8 76.7 561 3 BM694591
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992 13.8 76.7 562 3 BM828073
993 13.8 76.7 563 3 BM354128
994 13.8 76.7 565 3 BJ184512
995 13.8 76.7 565 3 BM002095
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999 13.8 76.7 567 7 COS11329
1000 13.8 76.7 568 7 CV461090

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## ALIGNMENTS

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RESULT 1
AA796833 448 bp mRNA linear EST 09-FEB-1998
LOCUS VPI5904.r1 Soares_mammary_gland_NBMWG Mus musculus cDNA clone
DEFINITION IMAGB:1068726 5', mRNA sequence.
ACCESSION AA796833
VERSION AA796833.1 GI:2859788
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

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REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 448)
Marte, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisler, S., Kucaba, T., Lacey, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

```

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TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Maira W/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LIND, contact the
IMAG Consortium (info@image.lind.gov) for further information.
MGI:591086

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FEATURES
source
Seq primer: -28m13 rev2 ET from Amerisham
High quality sequence stop: 388.
Location/Qualifiers
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/organism="Mus musculus"
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## ORIGIN

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Query Match 91.1%; Score 16.4; DB 1; Length 448;
Best Local Similarity 88.9%; Pred. No. 5.9e+02;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 AGAGGCGCGACGCGGUA 18
DB 9 AGAGGCGCGACGCGGUA 26

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RESULT 2
AQ903738/c 759 bp DNA linear GSS 09-JAN-2001
LOCUS GSS04779 Trypanosoma cruzi random genomic library Trypanosoma
DEFINITION cruzi genomic clone G24D14, genomic survey sequence.
ACCESSION AQ903738
VERSION AQ903738.2 GI:9378045
KEYWORDS GSS.
SOURCE Trypanosoma cruzi
ORGANISM Trypanosoma cruzi
Eukaryota; Euzoenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
1 (bases 1 to 759)
Aguero, F., Verdun, R., Frasch, A.C.C. and Sanchez, D.O.
A random sequencing approach for the analysis of the trypanosoma
cruzi genome: general structure, large gene and repetitive DNA
families, and gene discovery
Genome Res. 10 (12), 1996-2005 (2000)
1116094
COMMENT On Jul 21, 2000 this sequence version replaced gi:6484020.
Contact: Sanchez D.O.
Instituto de Investigaciones Biologicas (Univ. Nac. de Gral
San Martin)
Av. Gral Paz S/N, INTI, Edificio 24, B 1650 KNA, San Martin, Buenos
Aires, Argentina
Tel: (54-11) 4580/7255/7
Fax: (54-11) 4752-9639
Email: dsanchez@lib.unsam.edu.ar
Seq primer: 17
Class: shotgun.

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FEATURES
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Location/Qualifiers
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/cell_type="epimastigote"
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/note="Vector: pBS(-) (Stratagene); T. cruzi DNA was
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was gel purified and cloned into the dephosphorylated
HincII site of the vector."

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## ORIGIN

Query Match 91.1%; Score 16.4; DB 9; Length 759;  
 Best Local Similarity 83.3%; Pred. No. 5.8e+02;  
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUGCCACCGCGUA 18  
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 665 AGAGGCTCCACCGCTTA 648

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 CG056737/c PUFYD77TB\_ZM\_0.6\_1.0\_KB\_Zea\_mays genomic clone ZM5910,  
 DEFINITION genomic survey sequence.  
 ACCESSION CG056737 GI:33928917  
 VERSION CG056737.1  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 791)  
 Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
 Bennetzen,J.  
 WhiteIaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
 WhiteIaw,C.A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
 Bennetzen,J.  
 Maize Genomics Consortium  
 Unpublished (2003)  
 Contact: Cathy WhiteIaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whiteIaw@tigr.org  
 Seg primer: TF  
 Class: sheared ends.

FEATURES  
 source Location/Qualifiers  
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ORIGIN  
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 Best Local Similarity 83.3%; Pred. No. 5.8e+02;  
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUGCCACCGCGUA 18  
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RESULT 4  
 CG117698 854 bp DNA linear GSS 20-AUG-2003  
 CG117698/c PUFYD77TB\_ZM\_0.6\_1.0\_KB\_Zea\_mays genomic clone ZM5910,  
 DEFINITION genomic survey sequence.  
 ACCESSION CG117698 GI:34001135  
 VERSION CG117698.1  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 854)  
 Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and

Bennetzen,J.  
 Maize Genomics Consortium  
 Unpublished (2003)  
 Other\_GSSs: PUFYD77TB  
 Contact: Cathy WhiteIaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whiteIaw@tigr.org  
 Seg primer: TF  
 Class: sheared ends.

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 Cot selected genomic DNA library"

ORIGIN  
 Query Match 91.1%; Score 16.4; DB 10; Length 854;  
 Best Local Similarity 83.3%; Pred. No. 5.8e+02;  
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUGCCACCGCGUA 18  
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 365 AGAGGCTCCACCGCTTA 382

RESULT 5  
 CG117700 891 bp DNA linear GSS 20-AUG-2003  
 CG117700/c PUFYD77TB\_ZM\_0.6\_1.0\_KB\_Zea\_mays genomic clone ZM5910,  
 DEFINITION genomic survey sequence.  
 ACCESSION CG117700 GI:34001137  
 VERSION CG117700.1  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 891)  
 Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
 Bennetzen,J.  
 WhiteIaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
 WhiteIaw,C.A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
 Bennetzen,J.  
 Maize Genomics Consortium  
 Unpublished (2003)  
 Other\_GSSs: PUFYD77TB  
 Contact: Cathy WhiteIaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whiteIaw@tigr.org  
 Seg primer: TF  
 Class: sheared ends.

FEATURES  
 source Location/Qualifiers  
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 Cot selected genomic DNA library"

ORIGIN



Query Match 91.1%; Score 16.4; DB 10; Length 891;  
 Best Local Similarity 83.3%; Pred. No. 5.8e+02;  
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGGUCCACGCGGUA 18  
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 Db 725 AGAGGGTCGACACGGTA 708

RESULT 6  
 BX765851 730 bp mRNA linear EST 10-DEC-2003  
 LOCUS BX765851 Normalized Anopheles Fat Body (NAFB) Library Anopheles  
 DEFINITION gambiæe cDNA clone AGCCU12TR, mRNA sequence.  
 ACCESSION BX765851  
 VERSION BX765851  
 KEYWORDS GI:39673060  
 SOURCE EST.  
 ORGANISM Anopheles gambiæe (African malaria mosquito)  
 Anopheles gambiæe  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
 Culicidae; Anophelinae; Anopheles.  
 1 (bases 1 to 730)  
 Lobo, N.L., Gardner, M., Romans, P. and Collins, F.H.  
 Anopheles gambiæe EST, Center for Tropical Disease Research and  
 Training  
 Unpublished (2003)  
 Contact: Frank H. Collins  
 Center for Tropical Disease Research and Training  
 University of Notre Dame  
 Notre Dame, IN 46556, USA  
 Tel: 574-631-9245  
 Fax: 574-631-3996  
 Email: frank.h.collins.75@nd.edu.

FEATURES  
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 /clone\_1lb="Normalized Anopheles Fat Body (NAFB) Library"  
 /note="vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: EcoRI (5' end); Site 2: NotI (3' end); a  
 directionally cloned and normalized, oligo-T primed cDNA  
 library constructed from equal numbers of 24 and 40 hr  
 post Plasmodium imul infection, 4arr and 135 strain adult  
 female mosquito abdomens (omitting ovaries and midguts):  
 Bonaldo, Lennon & Soares (1996): Normalization and  
 Subtraction: Two Approaches to Facilitate Gene Discovery,  
 Genome Research 6, 791-806. ESTs sequenced from the M13  
 reverse priming site reading from the 5' ends of the cDNAs  
 are indicated by 'R' in the clone name."

ORIGIN  
 Query Match 88.3%; Score 16; DB 5; Length 730;  
 Best Local Similarity 87.5%; Pred. No. 9.5e+02;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGUCCACGCGGU 17  
 |||||:|||||:|||||:  
 Db 8 GAGGGTCGACGCGGT 23

RESULT 7  
 CX774850 841 bp mRNA linear EST 25-JAN-2005  
 LOCUS CX774850  
 DEFINITION UI-EH-HG2-aap-c-17-0-UI.s1 UI-EH-HG2 Emiliaenia huxleyi cDNA clone  
 CX774850  
 ACCESSION CX774850  
 VERSION CX774850.1 GI:58185203  
 KEYWORDS EST.  
 SOURCE Emiliaenia huxleyi

ORGANISM Emiliaenia huxleyi  
 Eukaryota; Haptophyceae; Isochrysidales; Emiliaenia.  
 1 (bases 1 to 841)  
 Bonaldo, M.F., Lennon, G. and Soares, M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 Genome Res. 6 (9), 791-806 (1996)

JOURNAL PUBMED  
 8889548  
 COMMENT Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@uiowa.edu  
 Tissue Procurement: Provasoli-Gulliard National Center for Culture  
 of Marine Phytoplankton (CCMP)  
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/diioflagellate.html>  
 The following repetitive elements were found in this cDNA  
 sequence: 1-30, >AT-rich#Low\_complexity (matched complement)  
 277-322, >GC-rich#Low\_complexity  
 Seq primer: M13 FORWARD  
 POLYA=yes.

FEATURES  
 source Location/Qualifiers  
 1..841  
 /organism="Emiliaenia huxleyi"  
 /mol\_type="mRNA"  
 /strain="CCMP 371"  
 /db\_xref="taxon:2903"  
 /clone="UI-EH-HG2-aap-c-17-0-UI"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_1lb="UI-EH-HG2"  
 /note="vector: pT73-Pac (Pharmacia) with a modified  
 polylinker; Site 1: EcoRI; Site 2: NotI; UI-EH-HG2 is a  
 normalized library derived from UI-EH-HG1. The library was  
 constructed and normalized according to Bonaldo, Lennon  
 and Soares, Genome Research, 6:791-806, 1996. First strand  
 cDNA synthesis was primed with an oligo-dT primer  
 containing a Not I site. Double stranded cDNA was ligated  
 to an EcoRI adaptor, digested with Not I, and cloned  
 directionally into pT73-Pac vector. The oligonucleotide  
 used to prime the synthesis of first-strand cDNA contains  
 a library tag sequence that is located between the Not I  
 site and the (dT)18 tail. The sequence tag for this  
 library is GAGGCTAGT. Tissue was obtained from the  
 Provasoli-Gulliard National Center for Culture of Marine  
 Phytoplankton (CCMP).  
 TAG TISSUE=Emiliaenia huxleyi coccolithophorid  
 TAG LIB=UI-EH-HG2  
 TAG\_SEQ=GAGGCTAGT"

ORIGIN  
 Query Match 88.9%; Score 16; DB 8; Length 841;  
 Best Local Similarity 93.8%; Pred. No. 9.5e+02;  
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGGUCCACGCGG 16  
 |||||:|||||:|||||:  
 Db 726 AGAGGGTCGACGCGG 741

RESULT 8  
 BB081347 296 bp mRNA linear EST 27-JUN-2000  
 LOCUS BB081347  
 DEFINITION BB081347 RIKEN full-length enriched, adult male diencephalon Mus  
 musculus cDNA clone 9330168K08 3' similar to L07924 Mus musculus  
 guanine nucleotide dissociation stimulator for a ras-related GTPase  
 mRNA, mRNA sequence.  
 ACCESSION BB081347





LOCUS BM344647 521 bp mRNA linear EST 23-JAN-2002

DEFINITION r757e03.y1 Globodera rostochiensis J2 pCDNAL1 Smart v1 Globodera  
rostochiensis cDNA 5' similar to SWHGD\_MOUSE C09173 HOMOGENTISATE  
1,2-DIOXYGENASE, mRNA sequence.

ACCESSION BM344647

VERSION BM344647.1 GI:18081562

KEYWORDS EST.

SOURCE Globodera rostochiensis

ORGANISM Globodera rostochiensis

REFERENCE Bukaryota Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
Tylenchidae; Heterodidae; Heteroderinae; Globodera.

AUTHORS 1 (bases 1 to 521)  
McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,  
Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theisling,B.,  
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,  
Tasgareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,  
Underwood,K., Steptoe,M., Allen,M., Person,B., Swiller,T.,  
Harvey,N., Schurt,R., Kohn,S., Shih,T., Jackson,Y., Cardenas,M.,  
McCamu,R., Waterston,R. and Wilson,R.

TITLE The Washington Univ. Nematode EST Project, 1999

JOURNAL Unpublished (1999)

COMMENT Contact: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
The library was contributed by Dr. Geert Smant of the Laboratory of  
Nematology at Wageningen University, Wageningen,  
Netherlands (geert.sman@emema.dpw.wau.nl). DNA Sequencing by:  
Washington University Genome Sequencing Center  
Seq primer: -40RP from Glbco  
High quality sequence stop: 480.  
Location/Qualifiers  
1..521  
/organism="Globodera rostochiensis"  
/mol\_type="mRNA"  
/db\_xref="taxon:31243"  
/dev\_stage="J2"  
/lab\_host="DH10B"  
/clone\_lib="Globodera rostochiensis J2 pCDNAL1 Smart v1"  
/note="Vector: pCDNAL1 (Invitrogen); Site\_1: BeckX1;  
Site\_2: BcoRI; The library was donated for sequencing by  
Geert Smant from Wageningen University, Laboratory of  
Nematology, The Netherlands."

ORIGIN

Query Match 85.6%; Score 15.4; DB 3; Length 521;  
Best Local Similarity 88.2%; Fred. No. 2e+03;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGGGUCGACGCGGUA 18  
|||||  
Db 268 GAGGGGACCGACCGCTA 252

RESULT 11

LOCUS CN122209 546 bp mRNA linear EST 01-APR-2004

DEFINITION TGSSTGY121e08.y1 TGYEG118 Tachyzoite cDNA Library-2 Toxoplasma  
gondii cDNA clone TGSSTzy121e08.y1 5' mRNA sequence.

ACCESSION CN122209

VERSION CN122209.1 GI:45943781

KEYWORDS EST.

SOURCE Toxoplasma gondii

ORGANISM Toxoplasma gondii

REFERENCE Bukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
Sarcocystidae; Toxoplasma.  
1 (bases 1 to 546)  
Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajioke,J.A., White,M.,  
Clifton,S., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M.,

```

TITLE
JOURNAL
COMMENT
Hiller,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M.,
Ritter,B., Bennett,J., Franklin,C., Tsagaratshvili,R., Ronko,I.,
Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.
Toxoplasma EST Project
Unpublished (2001)
Contact: Clifton, S.
Toxoplasma EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: toxow@wateron.wustl.edu
Contact David Sibley (toxoes@borcim.wustl.edu) for further
information relating to organisms, libraries, or clone availability.
Seq primer: -40UP from gcgc
High quality sequence sbpc 546.
Location/Qualifiers
1. 546
/organism="Toxoplasma gondii"
/mol_type="mRNA"
/strain="VEG"
/db_xref="taxon:5811"
/clone="TGESTry121e08.y1"
/dev_stage="tachyzoite"
/lib_host="GC10"
/clone_id="TGVEG118 Tachyzoite CDNA Library-2"
/note="Vector: Bluescript SK; Site 1: EcoRI; Site 2:
XhoI; The library was constructed by Kellang Tang, Robert
Cole and L. David Sibley at Washington University. cDNAs
were synthesized from poly(A)+ RNAsy oligo d(T) priming,
site-selected and directionally cloned into the Uni-ZAP XR
lambda vector (Stratagene). The primary library was mass
excised as phagemids and rescued in SOLR cells. The
plasmid library was recovered from the SOLR cells and
transformed in mass into GC10 cells for sequencing.
WARNING: the library may contain a small percentage
contaminants from human fibroblast cells."

ORIGIN
Query Match 85.6%; Score 15.4; DB 7; Length 546;
Best Local Similarity 82.4%; Pred. No. 2e+03;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 2 GAGGCTCCGACGCGGUA 18
|||||:|||||
Db 349 GAGGCTCGCGCGCGGTA 365

RESULT 12
BM355249/c 600 bp mRNA linear EST 23-JAN-2002
LOCUS
BM355249/c
DEFINITION
rx22f03.y1 Globodera rostochiensis J2 pCDNAII smant v1 globodera
rostochiensis cDNA 5' similar to SW:HGDI_MOUSE 009173 HOMOGENTISATE
1,2-DIOXYGENASE ; mRNA sequence.
BM355249
BM355249.1 GI:18089880
EST.
Accession
BM355249 Globodera rostochiensis
VERSION Globodera rostochiensis
KEYWORDS
ORGANISM Globodera rostochiensis
SOURCE
Bukaryot; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heterodoridae; Heterodorinae; Globodera.
REFERENCE
1 (bases 1 to 600)
McCarter,J., Clifton,S., Chippelli,B., Pape,D., Martin,J.,
Wyle,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,
Tsagaratshvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
Underwood,K., Stepien,M., Allen,M., Person,B., Swallier,T.,
Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
COMMENT
The Washington Univ. Nematode EST Project, 1999

```

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estewatson.wustl.edu  
The library was contributed by Dr. Geert Smant of the Laboratory of  
Nematology at Wageningen University, Wageningen,  
Netherlands (geert.smant@wur.nl). DNA Sequencing by:  
Washington University Genome Sequencing Center  
Seq primer: -40RP from G1bco  
High quality sequence stop: 481.  
Location/Qualifiers  
1. 600  
/organism="Globodera rostochiensis"  
/mol\_type="mRNA"  
/db\_xref="taxon:31243"  
/dev\_stage="J2"  
/lab\_host="DH10B"  
/clone\_lib="Globodera rostochiensis J2 pCDNA11 Smant v1"  
/note="Vector: pCDNA11 (Invitrogen); Site\_1: Becki;  
Site\_2: EcoRI; The library was donated for sequencing by  
Geert Smant from Wageningen University, Laboratory of  
Nematology, The Netherlands."

## ORIGIN

Query Match 85.6%; Score 15.4; DB 3; Length 600;  
Best Local Similarity 88.2%; Pred. No. 2e+03;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGGUA 18  
|||||  
DB 293 GAGGGACGACGCGGTA 277

RESULT 13 614 bp DNA linear GSS 27-JAN-2000  
LOCUS AQ946516  
DEFINITION Sheared DNA-49A17.TF Sheared DNA Trypanosoma brucei genomic clone  
ACCESSION AQ946516  
VERSION Sheared DNA-49A17, genomic survey sequence.  
KEYWORDS  
SOURCE GS.  
ORGANISM Trypanosoma brucei  
Trypanosoma brucei  
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.  
1 (bases 1 to 614)  
El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Sub, E., Malek, J., Fujii, C.,  
Gerrard, C., Leech, V., de Jong, P., Ullrich, E., Melville, S.,  
Donelson, J., Frazer, C. and Adams, M.  
Determination of clone end sequences from Trypanosoma brucei GUTat  
10.1 sheared DNA library  
Unpublished (1999)  
Other GSSs: Sheared DNA-49A17.TR  
Contact: Najib M. El-Sayed  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: nelsayed@tigr.org  
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared  
DNA library constructed at TIGR. Clones will be available for  
distribution through ATCC. Sheared DNA end sequences search page:  
<http://www.tigr.org/cdb/mdb/cbdb/>.  
Seq primer: M13-Forward  
Class: shotgun.  
Location/Qualifiers  
1. 614  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TRBU927/4 GUTat 10.1"  
/db\_xref="taxon:5691"

FEATURES  
source  
Location/Qualifiers  
1. 614

## ORIGIN

Query Match 85.6%; Score 15.4; DB 9; Length 614;  
Best Local Similarity 82.4%; Pred. No. 2e+03;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGGUA 18  
|||||  
DB 76 GAGGGTCCGACGCGGTA 92

/clone="Sheared DNA-49A17"  
/clone\_lib="Sheared DNA"  
/note="Vector: pUC18; Site\_1: SmaI; Constructed at The  
Institute for Genomic Research (TIGR), Rockville, MD.  
Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TRBU927/4 GUTat 10.1) was mechanically  
sheared to give a tight size distribution (approx 2 kb).  
The v + i method used for the library construction is  
described in detail in Smith, H.O. and Venter, J.C.  
(Making small insert libraries for whole genome shotgun  
sequencing projects. In Genome Sequencing: A Practical  
Approach, eds. M. Vaudin and B. Barrell, Oxford University  
Press, 1999)."

RESULT 14 630 bp DNA linear GSS 27-JAN-2000  
LOCUS AQ953132  
DEFINITION Sheared DNA-43M6.TF Sheared DNA Trypanosoma brucei genomic clone  
ACCESSION AQ953132  
VERSION Sheared DNA-43M6, genomic survey sequence.  
KEYWORDS  
SOURCE GS.  
ORGANISM Trypanosoma brucei  
Trypanosoma brucei  
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.  
1 (bases 1 to 630)  
El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Sub, E., Malek, J., Fujii, C.,  
Gerrard, C., Leech, V., de Jong, P., Ullrich, E., Melville, S.,  
Donelson, J., Frazer, C. and Adams, M.  
Determination of clone end sequences from Trypanosoma brucei GUTat  
10.1 sheared DNA library  
Unpublished (1999)  
Other GSSs: Sheared DNA-43M6.TR  
Contact: Najib M. El-Sayed  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: nelsayed@tigr.org  
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared  
DNA library constructed at TIGR. Clones will be available for  
distribution through ATCC. Sheared DNA end sequences search page:  
<http://www.tigr.org/cdb/mdb/cbdb/>.  
Seq primer: M13-Forward  
Class: shotgun.  
Location/Qualifiers  
1. 630  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TRBU927/4 GUTat 10.1"  
/db\_xref="taxon:5691"  
/clone="Sheared DNA-43M6"  
/clone\_lib="Sheared DNA"  
/note="Vector: pUC18; Site\_1: SmaI; Constructed at The  
Institute for Genomic Research (TIGR), Rockville, MD.  
Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TRBU927/4 GUTat 10.1) was mechanically  
sheared to give a tight size distribution (approx 2 kb).  
The v + i method used for the library construction is  
described in detail in Smith, H.O. and Venter, J.C.  
(Making small insert libraries for whole genome shotgun

FEATURES  
source  
Location/Qualifiers  
1. 630  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TRBU927/4 GUTat 10.1"  
/db\_xref="taxon:5691"  
/clone="Sheared DNA-43M6"  
/clone\_lib="Sheared DNA"  
/note="Vector: pUC18; Site\_1: SmaI; Constructed at The  
Institute for Genomic Research (TIGR), Rockville, MD.  
Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TRBU927/4 GUTat 10.1) was mechanically  
sheared to give a tight size distribution (approx 2 kb).  
The v + i method used for the library construction is  
described in detail in Smith, H.O. and Venter, J.C.  
(Making small insert libraries for whole genome shotgun

sequencing projects. In *Genome Sequencing: A Practical Approach*, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999). \*

Query Match	85.6%;	Score 15.4;	DB 9;	length 630;
Best Local Similarity	82.4%;	Pred. NO. 2e+03;		
Matches	14;	Conservative	2;	Mismatches 1;
				Indels 0;
				Gaps 0;
QY	2	GAGGGUGCGACGCGGUA	18	
		:     :		
Db	397	GAGGATCGACGCGGTA	413	

RESULT	15
AG083294	
LOCUS	AC083294
DEFINITION	Pan troglodytes DNA, clone: PTB-080L03.R, genomic survey sequence.
ACCESSION	AC083294
VERSION	AC083294.1 GI:16635096
KEYWORDS	GSS.
SOURCE	Pan troglodytes (chimpanzee)
ORGANISM	Pan troglodytes

REFERENCE AUTHORS	TITLE	JOURNAL	REFERENCE AUTHORS
1	Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.	BAC end sequences of library PTB	
	Unpublished		
	2 (bases 1 to 667)		
	Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.		

```

Sequencing: M13Rev
LIBRARY
Vector      : pKS145
R.Site 1    : SacI
R.Site 2    : SacI.

```

```

/clone_lib="PTB Chimpanzee Male BAC Library"

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RESULT 16	LOCUS	DEFINITION
BU650743/c	713 bp	mRNA
BU650743		linear
BU650743	<i>Epiratretus burgeri</i> adult	<i>Epiratretus burgeri</i> cDNA clone
		EST 07-OCT-2004

ACCESSION	hg121h06 5', mRNA sequence.
VERSION	B0650743
KEYWORDS	B0650743.1 GI:53865604
SOURCE	EST.
ORGANISM	<i>Eptatretus burgeri</i> (Inshore hagfish)
	<i>Eptatretus burgeri</i>

**REFERENCES**  
1 (bases 1 to 713)  
Suzuki, T., Shin-I, T., Kohara, Y. and Kasahara, M.  
Transcriptome analysis of haффish leukocytes: a framework for  
understanding the immune system of jawless fishes  
Dev. Comp. Immunol. 28 (10), 993-1003 (2004)  
**JOURNAL**  
PUBLISHED  
15236930  
Contact: Tadaseu Shin-i  
Tadaseu Shin-i, T. Shin-I, Y. Kohara, M. Kasahara  
Transcriptome analysis of haффish leukocytes: a framework for  
understanding the immune system of jawless fishes  
Dev. Comp. Immunol. 28 (10), 993-1003 (2004)

**ORIGIN**

[illegible]

RESULT 17	LOCUS	DEFINITION
BJ662705	752 bp	mRNA linear EST 07-OCT-200
		Bu662705 <i>Epiratrectus burgeri</i> adult <i>Epiratrectus burgeri</i> cDNA clone
		hg121h06 3', mRNA sequence.

SOURCE ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
<i>Eptatretus burgeri</i> (Inshore hagfish)				
<i>Eptatretus burgeri</i>				
Eukaryotes; Metazoa; Chordata; Craniata; Hyperoartri; Myxiniiformes; Myxiniidae; Eptatrelinae; Eptatretus.				
1 (bases 1 to 752)				
Suzuki, T., Shih, T., Kohara, Y. and Kasahara, M.				
Transcriptome analysis of hagfish leukocytes: a framework for understanding the immune system of jawless fishes				
Dev. Comp. Immunol. 28 (10), 993-1003 (2004)				

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FEATURES
    source
    location/Qualifiers
    1. 752
    /organism="Epistretus burgeri"
    /mol_type="mRNA"
    /db_xref="taxon:7764"
    /clone="hg12inh06"
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ORIGIN

Query Match 85.6%; Score 15.4; DB 3; Length 752;  
Best Local Similarity 88.2%; Pred. No. 2e+03;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Y 1 AGAGGUGCCAGCGCGU 17  
|||||  
567 AGAGGAGCCAGCGCGT 583

RESULT 18  
BP684217 760 bp mRNA linear EST 27-JUL-2004  
LOCUS BP684217 Osada Taira anterior neuroectoderm (ANE) PCS105 cDNA  
DEFINITION library Xenopus laevis cDNA clone XL445e24ex 5', mRNA sequence.  
ACCESSION BP684217 GI:46032172  
VERSION BP684217  
KEYWORDS EST.  
SOURCE Xenopus laevis (African clawed frog)  
ORGANISM Xenopus laevis

REFERENCE  
AUTHORS Osada, S., Kitayama, A., Ueno, N. and Taira, M.  
TITLE Expression analysis of genes which are expressed in the anterior neuroectoderm of Xenopus embryos  
JOURNAL Unpublished (2004)  
COMMENT Department of Biological Sciences  
Graduate School of Science, University of Tokyo; CREST, Japan  
Science and Technology Corporation, Japan  
7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan  
Tel: 81-03-5841-4434  
Fax: 81-03-5841-4434  
Email: m.taira@biol.s.u-tokyo.ac.jp,  
URL: http://www.shigen.nig.ac.jp/nbrp/xenopus/est/  
Location/Qualifiers  
1..760  
/organism="Xenopus laevis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8355"  
/clone="XL445e24ex"  
/tissue\_type="anterior neuroectoderm"  
/dev\_stage="late gastrula (stage 12.5)"  
/clone\_1lb="Osada Taira anterior neuroectoderm (ANE) PCS105 cDNA library"

ORIGIN

Query Match 85.6%; Score 15.4; DB 3; Length 760;  
Best Local Similarity 88.2%; Pred. No. 2e+03;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Y 2 GAGGUGCCAGCGCGUA 18  
|||||  
454 GAGGCGCCAGCGCGTA 438

RESULT 19  
DR729209 770 bp mRNA linear EST 15-JUL-2005  
LOCUS DR729209/c AGENCYCOURT 55139068 NICHD XGC Emb9 Xenopus laevis cDNA clone  
DEFINITION IMAGE:7978626 5', mRNA sequence.  
ACCESSION DR729209 GI:70903321  
VERSION DR729209  
KEYWORDS EST.  
SOURCE Xenopus laevis (African clawed frog)  
ORGANISM Xenopus laevis

REFERENCE  
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics / NIH  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: csapbs-remail.nih.gov  
Tissue Procurement: Dr. Igor David  
cDNA Library Preparation: Express Genomics  
DNA Sequencing by: The I.M.A.G.E. Consortium (LIML)  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:  
http://image.llnl.gov  
Plate: LIML7106 row: 1 column: 16  
High quality sequence stop: 538.  
Location/Qualifiers  
1..770  
/organism="Xenopus laevis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8355"  
/clone="IMAGE:7978626"  
/tissue\_type="Embryonic stage 17/19"  
/lab\_host="DH10B TONa"  
/clone\_1lb="NICHD XGC Emb9"  
/note="Organ: embryo; Vector: pExpress-1; Site 1: ScoreV; Site 2: NotCl; cDNA was primed using oligo-dT primer: 5'-GACATGTTCTGATCGGAGCGCGCCCTT)25-3' and cloned into the ScoreV/NotI sites of pExpress-1. Size selection 1.4kb resulted in an average insert size of 2.1kb. This is a non-normalized primary library (normalized library is NICHD XGC Emb10) and was constructed by Express Genomics (Frederick, MD). Note: this is a Xenopus Gene Collection (http://xgc.ncl.nih.gov/) library."

ORIGIN

Query Match 85.6%; Score 15.4; DB 8; Length 770;  
Best Local Similarity 88.2%; Pred. No. 2e+03;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Y 2 GAGGUGCCAGCGCGUA 18  
|||||  
451 GAGGCGCCAGCGCGTA 435

RESULT 20  
BP692517 771 bp mRNA linear EST 27-JUL-2004  
LOCUS BP692517 Osada Taira anterior neuroectoderm (ANE) PCS105 cDNA  
DEFINITION library Xenopus laevis cDNA clone XL468m17ex 5', mRNA sequence.  
ACCESSION BP692517  
VERSION BP692517 GI:46040472  
KEYWORDS EST.  
SOURCE Xenopus laevis (African clawed frog)  
ORGANISM Xenopus laevis

REFERENCE  
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics / NIH  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: csapbs-remail.nih.gov  
Tissue Procurement: Dr. Igor David  
cDNA Library Preparation: Express Genomics  
DNA Sequencing by: The I.M.A.G.E. Consortium (LIML)  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:  
http://image.llnl.gov  
Plate: LIML7106 row: 1 column: 16  
High quality sequence stop: 538.  
Location/Qualifiers  
1..770  
/organism="Xenopus laevis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8355"  
/clone="IMAGE:7978626"  
/tissue\_type="Embryonic stage 17/19"  
/lab\_host="DH10B TONa"  
/clone\_1lb="NICHD XGC Emb9"  
/note="Organ: embryo; Vector: pExpress-1; Site 1: ScoreV; Site 2: NotCl; cDNA was primed using oligo-dT primer: 5'-GACATGTTCTGATCGGAGCGCGCCCTT)25-3' and cloned into the ScoreV/NotI sites of pExpress-1. Size selection 1.4kb resulted in an average insert size of 2.1kb. This is a non-normalized primary library (normalized library is NICHD XGC Emb10) and was constructed by Express Genomics (Frederick, MD). Note: this is a Xenopus Gene Collection (http://xgc.ncl.nih.gov/) library."

Tel: 81-03-5841-4434  
 Fax: 81-03-5841-4434  
 Email: m.fair@biol.s.u-tokyo.ac.jp,  
 URL: http://www.shigen.nig.ac.jp/nbrp/xenopus/est/.

## FEATURES

source

1..771  
 /organism="Xenopus laevis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8355"  
 /clone="X1468ml7ex"  
 /issue\_type="anterior neuroectoderm"  
 /dev\_stage="late gastrula (stage 12.5)"  
 /clone\_1lb="osada faira anterior neuroectoderm (ANE)  
 pS105 cDNA library"

## ORIGIN

Query Match 85.6%; Score 15.4; DB 3; Length 771;  
 Best Local Similarity 88.2%; Pred. No. 2e+03; 1; Indels 0; Gaps 0;  
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGGUCCACGCGGUA 18  
 |||||  
 Db 314 GAGGGCCGACGCGGTA 298

## RESULT 21

CZ195323

LOCUS A1AA-aad31k01.g1 Ancylostoma caninum whole genome shotgun library  
 DEFINITION (A1AGSS 001) Ancylostoma caninum genomic, genomic survey sequence.

ACCESSION CZ195323  
 VERSION CZ195323.1 GI:59179408  
 KEYWORDS GSS.

SOURCE Ancylostoma caninum (dog hookworm)  
 ORGANISM Ancylostoma caninum

Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;  
 Ancylostomatidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma.

REFERENCE 1 (bases 1 to 812)  
 Miltreva,M., McCarter,J.P., Page,D., Ritter,E., Tsagarashvili,R.,  
 Ronko,I., Martin,J., Wylie,T., Dante,M., Meyer,R., Messine,D.,  
 Waterson,R.H., Clifton,S.W. and Wilson,R.  
 TITLE Genome Survey sequences from the parasitic nematode Ancylostoma  
 caninum

## JOURNAL

COMMENT

Unpublished (2004)  
 Contact: Miltreva M  
 Washington University in St. Louis  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: nematode@watson.wustl.edu  
 Genomic DNA provided by John Hawdon (mtmjhg@wumc.edu) DNA  
 sequenced by Washington University Genome Sequencing Center  
 Class: shotgun.

## FEATURES

source

Location/Qualifiers  
 1..812  
 /organism="Ancylostoma caninum"  
 /mol\_type="genomic DNA"  
 /strain="Baltimore"  
 /db\_xref="taxon:29170"  
 /dev\_stage="Adult"  
 /lab\_host="GS10"  
 /clone\_1lb="Ancylostoma caninum whole genome shotgun  
 library (A1AGSS 001)"  
 /note="Vector: pOTW13; Site 1: BstXI; Site 2: BstXI;  
 Ancylostoma caninum genomic DNA was randomly sheared,  
 end-repaired and size fractionated to enrich for 2-4 kb  
 fragments. Genomic DNA was provided by John Hawdon  
 (mtmjhg@wumc.edu) at George Washington University.  
 Sequencing by Washington University Genome Sequencing  
 Center, St. Louis, MO."

## ORIGIN

Query Match 85.6%; Score 15.4; DB 10; Length 812;  
 Best Local Similarity 82.4%; Pred. No. 2e+03;  
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUGCCACGCGGU 17  
 |||||  
 Db 274 AGAGGTCGACGCGGT 290

## RESULT 22

BU908733/C

LOCUS BU908733/C 906 bp mRNA EST 17-OCT-2002  
 DEFINITION AGENCOURT\_10487935 NICHD\_XGC\_Emb1 Xenopus laevis cDNA clone  
 IMAGE:6634258 5', mRNA sequence.

ACCESSION BU908733  
 VERSION BU908733.1 GI:24090647  
 KEYWORDS EST

SOURCE Xenopus laevis (African clawed frog)  
 ORGANISM Xenopus laevis

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 Xenopodinae; Xenopus; Xenopus.  
 1 (bases 1 to 906)  
 NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

## JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cga@bcr-remail.nih.gov  
 Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILML)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: NCI-CCGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ILML at:  
 http://image.llnl.gov  
 Plate: LAM14206 row: 1 column: 10  
 High quality sequence stop: 615.

## FEATURES

source

Location/Qualifiers  
 1..906  
 /organism="Xenopus laevis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8355"  
 /clone="IMAGE:6634258"  
 /issue\_type="embryo (stage 10)"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_1lb="NICHD\_XGC\_Emb1"  
 /note="Vector: pCMV-SFORT6; Site 1: NotI; Site 2: SalI;  
 cloned unidirectionally. Primer: Oligo dt. Average insert  
 size 1.55 kb. Constructed by Life Technologies. Note: This  
 is a Xenopus Gene Collection (XGC) library."

## ORIGIN

Query Match 85.6%; Score 15.4; DB 5; Length 906;  
 Best Local Similarity 88.2%; Pred. No. 2e+03;  
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGGUCCACGCGGUA 18  
 |||||  
 Db 392 GAGGGCCGACGCGGTA 376

## RESULT 23

CV762975/C

LOCUS CV762975/C 926 bp mRNA EST 09-NOV-2004  
 DEFINITION FGA8057364 Triticum aestivum FGAS: Library 2 Gate 3 Triticum  
 aestivum cDNA, mRNA sequence.

ACCESSION CV762975  
 VERSION CV762975.1 GI:55604086  
 KEYWORDS EST  
 SOURCE Triticum aestivum (bread wheat)  
 ORGANISM Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Triticum.  
 1 (bases 1 to 926)  
 Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,  
 Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,  
 Link, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,  
 Peniket, C., Roach, J.L., and Sarhan, F.  
 Functional Genomics of Abiotic Stress in Wheat and Canola Crops  
 Unpublished (2003)  
 TITLE  
 JOURNAL  
 COMMENT  
 Contact: Wm L Crosby  
 Bioinformatics  
 University of Saskatchewan, Department of Computer Science  
 1C101 Engineering Building, 57 Campus Drive, Saskatoon,  
 Saskatchewan, S7N 5A9, Canada  
 Tel: 306 966 1769  
 Fax: 306 966 2033  
 Email: fgas\_est@cs.usask.ca

This sequence is the direct result of the base calling software  
 Phred (default parameters). It is the raw base calls. To aid in the  
 identification of the high quality insert the software Lucy  
 (default parameters) has been run on this sequence. Lucy identified  
 the region [79,333].  
 Plate: WEF032 row: C column: 03.

## FEATURES

source

1.926  
 Location/Qualifiers  
 /organism="Triticum aestivum"  
 /mol\_type="RNA"  
 /db\_xref="taxon:4565"  
 /clone\_lib="Triticum aestivum FGAS: Library 2 Gate 3"  
 /note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Aerial  
 parts (crown and leaf) of wheat cultivar Norstar from  
 control and long exposure times to low temperature. 4 mRNA  
 populations were combined before constructing the library;  
 7 days non-acclimated plants and 1, 23, and 53 days  
 cold-acclimated at 4C. Non-acclimated and cold-acclimated  
 plants were grown in vermiculite. This is the only library  
 that was done according to the Invitrogen manual, and  
 therefore, a percentage of clones will not have the 3  
 prime end because of NotI digestion within the cDNA."

## ORIGIN

Query Match 85.6%; Score 15.4; DB 8; Length 926;  
 Best Local Similarity 82.4%; Pred. No. 2e+03;  
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGGGCGCAGCGCGU 17  
 |||||:|||||:  
 Db 447 AGAGGGGCGCAGCGCGT 431

RESULT 24  
 CNS00101  
 LOCUS  
 DEFINITION  
 Drosophila melanogaster genome survey sequence TET3 end of BAC #  
 BACR05D14 of RPCI-98 library from Drosophila melanogaster (fruit  
 fly), genomic survey sequence.  
 AL061582  
 AL061582.1 GI:4939944  
 GSS.  
 Drosophila melanogaster (fruit fly)  
 Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Ephydroidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 1101)  
 Genoscope.  
 Direct Submission  
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
 BP 191 91006 Evry cedex - FRANCE (E-mail: seqref@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 Determination of this BAC-end sequence was carried out as part of a  
 collaboration with the Berkeley Drosophila Genome Project (BDGP).  
 The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information  
 please see <http://www.fruitfly.org> The BDGP Drosophila  
 melanogaster BAC library was prepared by Kazuo Osoegawa, and  
 Aaron Mammot in Peter de Jong's laboratory in the Department of  
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
 NY. The library is named RPCI-98 and was constructed by partial  
 EcoRI digestion of Drosophila DNA provided by the BDGP from the  
 isogenic strain Y2; cn bw sp, the same strain used for the BDGP's  
 P1 and EST libraries. A more detailed description of the library  
 and how to order individual BAC clones, the entire library, or  
 filters for hybridization from the BACPAC Resource Center can be  
 found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

source

1.1101  
 Location/Qualifiers  
 /organism="Drosophila melanogaster"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7227"  
 /clone\_lib="BACR05D14"  
 /clone\_lib="RPCI-98"  
 /note="end : TET3"

## ORIGIN

Query Match 85.6%; Score 15.4; DB 10; Length 1101;  
 Best Local Similarity 88.2%; Pred. No. 2e+03;  
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGGGCGCAGCGCGU 18  
 |||||:|||||:  
 Db 604 GAGGGGCGCAGCGCGTA 620

RESULT 25  
 AG034417 1204 bp DNA linear GSS 01-NOV-2001  
 LOCUS  
 DEFINITION  
 Pan troglodytes DNA, clone: PTB-009M03.F, genomic survey sequence.  
 AG034417  
 AG034417.1 GI:16561290  
 GSS.  
 Pan troglodytes (chimpanzee)  
 Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Pan.  
 1  
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
 Totoki, Y., Watanabe, H., and Sakaki, Y.  
 BAC end sequences of Library PTB  
 Unpublished  
 2 (bases 1 to 1204)  
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
 Totoki, Y., Watanabe, H., and Sakaki, Y.  
 Direct Submission  
 Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC),  
 1-7-22 Suehiro-chou, Tsukuba, Ibaraki, Japan, Kanagawa 230-0045, Japan  
 (E-mail: chimpesgsc.riken.go.jp, URL: <http://hgp.gsc.riken.go.jp/>,  
 Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
 Clones are derived from the chimpanzee BAC library PTB This BAC end  
 was generated during the R&D process and may have higher chance of  
 clone tracking errors.  
 PRIMERS  
 Sequencing: -2M13  
 LIBRARY  
 Vector : pKS145  
 R.site 1 : SacI  
 R.site 2 : SacI  
 Location/Qualifiers  
 1.1204  
 /organism="Pan troglodytes"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9598"  
 /clone="PTB-009M03.F"  
 /sex="male"

## FEATURES

source



```

ORIGIN
    /cell_type="lymphoblast"
    /clone_lib="PTB Chimpanzee Male BAC Library"

Query Match      85.6%; Score 15.4; DB 10; Length 1204;
Best Local Similarity 82.4%; Pred. No. 2e+03;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 GAGGAGCGACGCGGUA 18
      |||:|||||:|
      496 GAGGAGCGACGCGGUA 512

RESULT 26
AG038547      1310 bp      DNA      linear      GSS 01-NOV-2001
LOCUS      Pan troglodytes DNA, clone: PTB-015G04.F, genomic survey sequence.
ACCESSION      AG038547
VERSION      AG038547.1 GI:16567272
KEYWORDS      GSS.
SOURCE      Pan troglodytes (chimpanzee)
ORGANISM      Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Pan.

REFERENCE
AUTHORS      Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
            Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE      BAC end sequences of library PTB
JOURNAL      Unpublished
AUTHORS      2 (bases 1 to 1310)
            Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
            Totoki, Y., Watanabe, H. and Sakaki, Y.
DIRECT SUBMISSION
            Submitted (02-NOV-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suenro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hsp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
            Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the Rad process and may have higher chance of
            clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : PKS145
R.Site 1 : SacI
R.Site 2 : SacI
Location/Qualifiers
1. 1310
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-015G04.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match      85.6%; Score 15.4; DB 10; Length 1310;
Best Local Similarity 82.4%; Pred. No. 1.9e+03;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 GAGGAGCGACGCGGUA 18
      |||:|||||:|
      1136 GAGGAGCGACGCGGUA 1152

RESULT 27
BE958176      99 bp      mRNA      linear      EST 04-OCT-2000
LOCUS      BE958176
DEFINITION      601644634F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3529792 5',
            mRNA sequence.

```

```

ACCESSION      BE958176
VERSION      BE958176.1 GI:10568881
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
REFERENCE
AUTHORS      NIH-MGC http://mgs.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
CONTACT      Robert Strausberg, Ph.D.
            Email: cga@bbs-rmmail.nih.gov
            Tissue Procurement: ATCC
CDNA LIBRARY PREPARATION: CLONTECH Laboratories, Inc.
DNA SEQUENCING BY: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: L16C763 row: c column: 09
High quality sequence stop: 99.
Location/Qualifiers
1. 99
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3929792"
/tissue_type="primitive neuroectoderm"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 56"
note="Organ: brain; Vector: pNMR-h1B (Clontech); Site_1:
SfiI (ggcgccatcgcc); Site_2: SfiI (ggcgccatcgcc);
double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCATATGACC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGGCGGCGACATG-dT(30)BN-3'
(where B = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

ORIGIN
Query Match      83.3%; Score 15; DB 2; Length 99;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 GAGGAGCGACGCGG 16
      |||:|||||:|
      8 GAGGAGCGACGCGG 22

RESULT 28
BG942250      108 bp      mRNA      linear      EST 15-JAN-2003
LOCUS      BG942250
DEFINITION      ax22h10.x1 Hembase; Erythroid Progenitor Cells (LCP:ax library)
ACCESSION      BG942250
VERSION      BG942250.1 GI:14341622
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
REFERENCE
AUTHORS      Gubin, A.N., Mjoroge, J.M., Bouffard, G.G. and Miller, J.L.
TITLE      Gene expression in proliferating human erythroid cells
JOURNAL      Genomics 59 (2), 168-177 (1999)
PUBMED      10409428
CONTACT      Jeffery L. Miller

```



```

/1ab host="DH10B (TI phage-resistant)"
/clone lib="NIH_MGC_55"
/notes="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggcgccctcgcc); Site 2: SfiI
(ggcctatggcc); Double-stranded cDNA was prepared from
cell line RNA. 5' and 3' adaptors were used in cloning as
follows: 5' adaptor sequence: 5'-CACGGCATTATGCCC-3' and
3' adaptor sequence:
5'-ATTCTAGAGCGCGAGCGCGCAGCATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.65 kb (range 0.9-4.0 kb). 14/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."
```

Query Match 83.3%; Score 15; DB 2; Length 149;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGG 16  
|||||  
38 GAGGGTCGCGACGCGG 52

Db 38 GAGGGTCGCGACGCGG 52

RESULT 31  
BG613515 153 bp mRNA linear EST 18-APR-2001  
LOCUS 602641444F1 NIH\_MGC\_61 Homo sapiens cDNA clone IMAGE:4772411 5',  
DEFINITION mRNA sequence.  
ACCESSION BG613515  
VERSION BG613515.1 GI:13664886  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
1 (bases 1 to 153)  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cga@pds-femail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LNCM1642 row: h column: 12  
High quality sequence stop: 153.  
Location/Qualifiers  
1. 153  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4772411"  
/tissue\_type="embryonal carcinoma"  
/1ab host="DH10B (TI phage-resistant)"  
/clone lib="NIH\_MGC\_61"  
/notes="Organ: testis; Vector: pDNR-LIB (Clontech); Site 1:  
SfiI (ggcgccctcgcc); Site 2: SfiI (ggcctatggcc);  
Double-stranded cDNA was prepared from cell line RNA. 5'  
and 3' adaptors were used in cloning as follows: 5'  
adaptor sequence: 5'-CACGGCATTATGCCC-3' and 3' adaptor  
sequence: 5'-ATTCTAGAGCGCGAGCGCGCAGCATG-dT(30)BN-3'  
(where B = A, C, or G and N = A, C, G, or T). Average  
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies  
contained inserts by PCR. This library was enriched for  
full-length clones and was constructed by Clontech  
Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC

```

Library."
```

Query Match 83.3%; Score 15; DB 2; Length 153;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGG 16  
|||||  
38 GAGGGTCGCGACGCGG 52

Db 38 GAGGGTCGCGACGCGG 52

RESULT 32  
BG941945 197 bp mRNA linear EST 15-JAN-2003  
LOCUS ax19c04.x1 Hembase; Erythroid Progenitor Cells (LCB:ax library)  
DEFINITION Homo sapiens cDNA clone ax19c04 random, mRNA sequence.  
ACCESSION BG941945  
VERSION BG941945.1 GI:14341317  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
1 (bases 1 to 197)  
REFERENCE Gubin,A.N., Njoroge,J.M., Bouffard,G.G. and Miller,J.L.  
AUTHORS Gene expression in proliferating human erythroid cells  
TITLE Genomics 59 (2), 168-177 (1999)  
JOURNAL 10409428  
COMMENT Contact: Jeffery L. Miller  
Laboratory of Chemical Biology  
National Institute of Diabetes and Digestive and Kidney Diseases  
Building 10, Room 9B17, National Institutes of Health, Bethesda, MD  
20892, USA  
Tel: 301 402 2373  
Fax: 301 435 5148  
Email: jfm@nih.gov  
DNA Sequencing and analyses by National Institutes of Health  
Intramural Sequencing Center (NISC).  
Plate: 19 row: c column: 04  
Seq primer: 21M3 forward primer (ABI).  
Location/Qualifiers  
1. 197  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="ax19c04"  
/sex="unknown"  
/tissue\_type="blood"  
/cell\_type="Erythroid Cells"  
/cell\_line="Primary Culture of Peripheral Blood  
Mononuclear Cells"  
/dev\_stage="Progenitor; EPO responsive CD71++++"  
/1ab host="SOLR"  
/clone lib="Hembase; Erythroid Progenitor Cells (LCB:ax  
library)"  
/notes="Organ: blood; Vector: Lambda ZAP II; Site 1: EcoRI;  
Site 2: EcoRI. 65,000 proliferating erythroid cells from  
the buffy coat of a blood donation were obtained by flow  
cytometric separation after a 5-day culture period in the  
presence of erythropoietin. Total RNA was purified from  
the sorted cell population using RNeasy reagent. RNA (0.3  
ug) was converted into double stranded cDNA using  
Clontech's CapTrinder cDNA library Construction Kit  
(Clontech) according to the manufacturer's protocol and  
cloned into EcoRI digested Lambda Zap II vector  
(Stratagene). The phage library was amplified once prior  
to in vivo excision in SOLR cells. Individual colonies  
were grown, and the cDNA inserts were sequenced in high  
throughput (NISC Intramural sequencing center  
http://www.nisc.nih.gov/)."

Query Match 83.3%; Score 15; DB 2; Length 197;  
 Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGCGG 16  
 |||||:|||||  
 31 GAGGTCGACGCGG 45

RESULT 33  
 AUI00090 300 bp mRNA linear EST 23-JAN-2004  
 LOCUS AUI00090 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
 DEFINITION LNC6538 similar to Human mitochondrial transcription factor 1  
 mRNA, mRNA sequence.

ACCESSION AUI00090  
 VERSION AUI00090.1 GI:13551219  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Suzuki, Y., Tsunoda, T., Sese, J., Taira, H., Mizushima-Sugano, J.,  
 Hata, H., Oca, T., Isogai, T., Tanaka, T., Nakamura, Y., Suyama, A.,  
 Sakaki, Y., Morishita, S., Okubo, K. and Sugano, S.  
 Identification and characterization of the potential promoter  
 regions of 1031 kinds of human genes  
 Genome Res. 11 (5), 677-684 (2001)  
 11337467

COMMENT  
 Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: yusuzuki@ims.u-tokyo.ac.jp  
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and  
 Sugano, S. Construction and characterization of a full  
 length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
 149-156 (1997).

FEATURES  
 source  
 1..300  
 /location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="LNC6538"  
 /clone\_lib="Sugano Homo sapiens cDNA library"

ORIGIN  
 Query Match 83.3%; Score 15; DB 1; Length 300;  
 Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGCGG 16  
 |||||:|||||  
 40 GAGGTCGACGCGG 54

RESULT 34  
 BX115113 314 bp mRNA linear EST 07-FEB-2003  
 LOCUS BX115113 Soares testis NHT Homo sapiens cDNA clone IMAGE98F081786  
 DEFINITION ; IMAGE:728071, mRNA sequence.

ACCESSION BX115113  
 VERSION BX115113.1 GI:27879949  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 1 (bases 1 to 314)

COMMENT

AUTHORS Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,  
 Radloff, U., Schneider, D. and Korn, B.  
 Human Unigeneset - RZPD3  
 Unpublished (2003)

TITLE JOURNAL  
 COMMENT

CONTACT: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
 RZPD: IMAGP98F081786.  
 RZPDLIB: I.M.A.G.B. cDNA Clone Collection;  
 Human Unigeneset - RZPD3 (RZPDLIB No. 972)  
 http://www.rzpd.de/CloneCards/cgi-  
 bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Neuenheimer Weg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 101  
 Fax: +49 30 32639 111  
 www.rzpd.de

This clone is available royalty-free from RZPD;  
 contact RZPD (clone@rzpd.de) for further information. Seq primer:  
 M13r. Primer sequence: TTTCACACAGGAACACTATGAC.

FEATURES  
 source  
 1..314  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGP98F081786 ; IMAGE:728071"  
 /sex="male"  
 /lab\_host="DH10B"  
 /clone\_lib="Soares testis NHT"  
 /notes="Vector: pRTT3D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
 was prepared from mRNA obtained from Clontech  
 laboratories, Inc., and primed with a Not I - oligo (dT)  
 primer [5',  
 TGTTCATCATCTGAAGTGGAGCGCGCCCAATTTTTTTTTTTT 3']  
 Double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pRTT3 vector. Library  
 went through one round of normalization to Cot5, and was  
 constructed by Bento Soares and W. Fatima Bonaudo."

ORIGIN  
 Query Match 83.3%; Score 15; DB 5; Length 314;  
 Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGCGG 16  
 |||||:|||||  
 128 GAGGTCGACGCGG 142

RESULT 35  
 AA393273 337 bp mRNA linear EST 12-AUG-1997  
 LOCUS AA393273  
 DEFINITION zt74d04.r1 Soares testis NHT Hom sapiens cDNA clone IMAGE:728071  
 5' similar to gb:M62810 MITOCHONDRIAL TRANSCRIPTION FACTOR 1  
 PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION AA393273  
 VERSION AA393273.1 GI:2046241  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 1 (bases 1 to 337)  
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,  
 Kucaba, T., Lacey, M., Le, N., Lennon, G., Martin, J.,  
 Moore, B., Schellendberg, K., Steptoe, M., Tan, F., Theising, B.,  
 White, Y., Wylie, T., Waterston, R. and Wilson, R.  
 WashU-Merck EST Project 1997  
 Unpublished (1997)  
 Contact: Wilson RK

TITLE JOURNAL  
 COMMENT

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
This clone is available royalty-free through LML / contact the  
IMAGS Consortium (info@image.lml.gov) for further information.  
Insert Length: 1084 Std Error: 0.00  
Seq primer: -28m13 rev2 ET from Amersham  
High quality sequence stop: 163.

## FEATURES

source

```
1..337
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:728071"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares, testis_NHT"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5'
TGTTACCAATCTGAGTGGAGCGCGCCCAATTTTCTTTTCTTTT 3']
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization to Cos5, and was
constructed by Bento Soares and M. Fatima Bonaldo."
```

## ORIGIN

Query Match 83.3%; Score 15; DB 1; Length 337;  
Best Local Similarity 93.3%; Pred. No. 3.2e+03;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGTCCGACGCGG 16  
|||||:|||||  
Db 128 GAGGGTCCGACGCGG 142

RESULT 36  
BM851628 349 bp mRNA linear EST 06-MAR-2002  
LOCUS K-EST0132545 S13KMS5 Homo sapiens cDNA clone S13KMS5-44-D04 5',  
DEFINITION mRNA sequence.  
ACCESSION BM851628 GI:19208027  
VERSION EST.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Eumarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
1 (bases 1 to 349)  
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,  
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, D.M., Park, H.S., Kim, S. and  
Kim, Y.S.  
21C Frontier Korean EST Project 2001  
Unpublished (2002)  
CONTACT: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Beon-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 44 row: D column: 04  
High quality sequence stop: 349.  
Location/Qualifiers  
1..349  
/organism="Homo sapiens"

## ORIGIN

Query Match 83.3%; Score 15; DB 3; Length 349;  
Best Local Similarity 93.3%; Pred. No. 3.2e+03;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGTCCGACGCGG 16  
|||||:|||||  
Db 40 GAGGGTCCGACGCGG 54

```
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S13KMS5-44-D04"
/tissue_type="myeloma"
/cell_line="KMS-5"
/lab_host="Top10F"
/clone_lib="S13KMS5"
/notes="Vector: pCNS; Site 1: EcoRI; Site 2: NotI; The poly
(A) + RNA was dephosphorylated with bacterial alkaline
phosphatase (BAP) and then dephosphorylated with tobacco acid
pyrophosphatase (TAP). The dephosphorylated intact mRNA was
ligated with DNA-RNA linker including EcoRI site by
treatment of T4 RNA ligase and the first strand cDNA was
synthesized from oligo dT-selected mRNA by priming with
dT-tailed vector. The dT-tailed vector was adjucted to
have about 60nt. The cDNA vector was circularized with E.
coli DNA ligase after digestion of EcoRI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
Top10F by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
library."
```

RESULT 37  
CW842063/c 376 bp DNA linear GSS 26-NOV-2004  
LOCUS ET11920.Ds3.04.14.2003.jw95.376 Arabidopsis thaliana Landsberg Ds  
DEFINITION insertion lines Arabidopsis thaliana genomic clone ET11920, genomic  
survey sequence.  
ACCESSION CW842063  
VERSION GSS.  
KEYWORDS Arabidopsis thaliana (thale cress)  
SOURCE Arabidopsis thaliana  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
1 (bases 1 to 376)  
May, B.P., Simorowski, J., Arroyo, J.-M., Vaughn, M.W., Shen, R.,  
McCombie, W.R. and Martienssen, R.A.  
Arabidopsis genomic sequences flanking Ds enhancer and gene traps  
in transgenic lines  
Unpublished (2004)  
CONTACT: Martienssen RA  
Cold Spring Harbor Laboratory  
1 Bungtown Rd., Cold Spring Harbor, NY 11724, USA  
Tel: 516 367 8322  
Fax: 516 367 8369  
Email: martiens@cshl.org  
This sequence flanks a Ds transposon carrying an enhancer trap in  
line ET11920. The transposon is located upstream of Atlg72290.  
Nucleotides 1..32 are derived from Zea mays transposon Ds.  
Class: transposon-tagged.  
Location/Qualifiers  
1..376  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Landsberg erecta"  
/db\_xref="taxon:3702"  
/clone="ET11920"  
/clone\_lib="Arabidopsis thaliana Landsberg Ds insertion  
lines"

/note="Lines of Arabidopsis thaliana were generated which each contain a Ds transposon carrying a glucuronidase reporter gene. Genomic DNA flanking the transposon insertion in each line was amplified by PCR and directly sequenced. More information is available at <http://genetrap.cshl.edu>."

## ORIGIN

Query Match 83.3%; Score 15; DB 10; Length 376;  
Best Local Similarity 86.7%; Pred. No. 3.2e+03;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGGCGCGACGCGG 17  
|||||  
96 AGGTCGCGACGCGT 82

## RESULT 38

CB929313/c 396 bp mRNA linear EST 28-APR-2003  
LOCUS AB41\_41\_H09\_g1\_A012 Abscisic acid-treated seedlings Sorghum bicolor

## DEFINITION

CDNA clone AB41\_41\_H09\_A012 5', mRNA sequence.

## ACCESSION

CB929313

## VERSION

CB929313.1 GI:30165584

## KEYWORDS

EST.

## SOURCE

Sorghum bicolor (sorghum)

## ORGANISM

Sorghum bicolor

## REFERENCE

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

## AUTHORS

1 (bases 1 to 396)  
Cordonnier-Pratt, M.-M., Wentzel, V., Suzuki, Y., Sugano, S., Klein, R.K., Liang, C., Sun, F., Sullivan, R., Shan, M., Buchanan, C.D., Baskman, A. and Pratt, L.H.

## TITLE

An EST database from Sorghum: AB41-treated seedlings

## JOURNAL

Unpublished (2003)

## COMMENT

Other ESTs: AB41\_41\_H09\_b1\_A012

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in

the Human Genome Center, University of Tokyo Institute of Medical

Science; plant material and RNA prepared at Texas A & M University;

sequencing done in the laboratory for Genomics and Bioinformatics,

University of Georgia. Sequence ends have been trimmed to exclude

vector and regions below phred quality 16. Three-prime sequences

are presented as their reverse complement and have been trimmed to

exclude polyA.

Seq primer: Sug5 (CTTCTGCTTAAAGCTGCG).

Location/Qualifiers

1..396

/organism="Sorghum bicolor"

/mol\_type="mRNA"

/cultivar="IS3620C"

/db\_xref="taxon:4558"

/clone="AB41\_41\_H09\_A012"

/lab\_host="DH10B-T1 phage-resistant E. coli"

/clone\_lib="Abscisic acid-treated seedlings"

/note="Vector: pM185-FL3; Site 1: XhoI; Site 2: XhoI; The

library was prepared from polyA+ RNA from seedlings grown

in hydroponic culture. After 12 days, medium was

supplemented with 1 mM abscisic acid (ABA), while leaves

were misted with a solution of 1 mM ABA. Roots and leaves

were harvested after 3, 6, 12, and 24 hr and material from

all time points was combined prior to RNA isolation.

Double-stranded cDNA was cloned unidirectionally into

different DraIII sites of the pM185-FL3 vector (5'-prime

DraIII site is CACTGTGG, 3'-prime DraIII site is

CCCATGTG). XhoI excises the cDNA insert."

## ORIGIN

Query Match 83.3%; Score 15; DB 6; Length 396;  
Best Local Similarity 93.3%; Pred. No. 3.2e+03;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGCGCGACGCGG 16  
|||||  
28 GAGGTCGCGACGCGG 14

## RESULT 39

BE045111

LOCUS

DEFINITION

BE045111 412 bp mRNA linear EST 08-JUN-2000  
hm28f08.x1 NCI CGAP Thy7 Homo sapiens CDNA clone IMAGE:3023463 3',  
similar to gb:M62810 MITOCHONDRIAL TRANSCRIPTION FACTOR 1 PRECURSOR  
(HUMAN); mRNA sequence.

ACCESSION

BE045111

VERSION

BE045111.1 GI:8362164

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 412)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strussberg, Ph.D.

Email: cgapb-remail.nih.gov

Tissue procurement: Klaus Kaeser M.D., Bruno Niederle M.D., Mike

Emmert-Buck M.D. Ph.D., Vlado Knezevic M.D.

CDNA Library Preparation: Krizman Laboratory

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LMD, send email to:

info@image.lnl.gov

Possible reversed clone: polyT not found

Seq primer: -40UP from Gibco

High quality sequence atp: 319.

Location/Qualifiers

1..412

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3023463"

/tissue\_type="follicular adenoma (benign lesion)"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP Thy7"

/note="Organ: thyroid; Vector: pAMP10; mRNA made from

thyroid adenoma (benign), cDNA made by oligo-dT priming.

Non-directionally cloned into UDG sites. Size-selected on

agarose gel, average insert size 500 bp. Primary library.

CDNA Library Preparation: David B. Krizman, Ph.D.

REFERENCE: Krizman et al. (1996) Cancer Research

56:5380-5383."

## ORIGIN

Query Match 83.3%; Score 15; DB 2; Length 412;  
Best Local Similarity 93.3%; Pred. No. 3.2e+03;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGCGCGACGCGG 16  
|||||  
20 GAGGTCGCGACGCGG 34

## RESULT 40

BC018628

LOCUS

BC018628

413 bp mRNA linear HTC 06-DEC-2001

DEFINITION Homo sapiens, Similar to transcription factor A, mitochondrial, clone IMAGE:4552415, mRNA.

ACCESSION BC018628

VERSION BC018628.1 GI:17391377

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

AUTHORS 1 (bases 1 to 413)

TITLE Strausberg, R.

JOURNAL Direct Submission

Submitted (03-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Genome Sequence Centre,

BC Cancer Agency, Vancouver, BC, Canada

Info@cgsc.bc.ca

Steven Jones, Jennifer Amano, Ian Bosdet, Yaron Butterfield, Susana Chan, Readman Chiu, Chris Fjell, Erin Garland, Lee Guin, Leticia Hsiao, Martin Krzywnicki, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeary, Steven Ness, Pawan Pandoh, Anna-Lisa Prabh, Parvaneh Saeedi, Jacqueline Schein, Duane Smalish, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranda Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://limage.lnl.gov>

Series: IRL Plate: 40 Row: d Column: 1

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4507400

This clone has the following problem: frame shifted.

FEATURES

source

1..413

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4552415"

/issue\_type="uterus, leiomyosarcoma"

/clone\_lib="NIH\_MGC\_46"

/lab\_host="DH10B-R"

/note="Vector: pOTB7"

ORIGIN

Query Match 83.3%; Score 15; DB 4; Length 413;

Best Local Similarity 93.3%; Pred. No. 3.2e+03;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGCCG 16

|||||:|||||

16 GAGGTCGCCACGCCG 30

RESULT 41

BC337115 414 bp mRNA linear EST 27-FEB-2001

LOCUS 60234393F1 NIH\_MGC\_46 Homo sapiens cDNA clone IMAGE:4552415 5',

DEFINITION mRNA sequence.

ACCESSION BC337115

VERSION BC337115.1 GI:13143553

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 414)

REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

<http://limage.lnl.gov>

Plate: LNCM1248 row: 1 column: 24

High quality sequence start: 4

High quality sequence stop: 413.

FEATURES

source

1..414

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4552415"

/issue\_type="leiomyosarcoma cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_46"

/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGGCGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC library."

ORIGIN

Query Match 83.3%; Score 15; DB 2; Length 414;

Best Local Similarity 93.3%; Pred. No. 3.2e+03;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGCCG 16

|||||:|||||

17 GAGGTCGCCACGCCG 31

RESULT 42

R09557 426 bp mRNA linear EST 05-APR-1995

LOCUS yf27904.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone

DEFINITION IMAGE:128118 3', mRNA sequence.

ACCESSION R09557

VERSION R09557.1 GI:761480

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 426)

REFERENCE Hillier, L., Clark, N., Dubugue, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaastis, B., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

AUTHORS The WashU-Merck EST Project

TITLE Unpublished (1995)

JOURNAL Contact: Wilson RK

COMMENT Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810



Email: est@watson.wustl.edu

Insert Size: 817

High quality sequence stops: 404 Source: IMAGE Consortium, LNLN. This clone is available royalty-free through LNLN; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

Insert Length: 817 Std Error: 0.00

Seq primer: -21m13

High quality sequence stop: 404.

Location/Qualifiers

#### FEATURES

source

1. .426

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:480279"

/db\_xref="taxon:9606"

/clone="IMAGE:128118"

/sex="male"

/dev\_stage="20 week-post conception fetus"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares fetal liver spleen LNLN"

/note="Organ: Liver and Spleen; Vector: pRTT3D (Pharmacia)

with a modified polylinker; Site\_1: Pac I; Site\_2: Eco RI;

1st strand cDNA was primed with a Pac I - oligo(dT) primer

[5' AACTGAGAGATTATTAAGATCTTTTCTTTTCTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Pac I and cloned into the Pac I

and Eco RI sites of the modified pRTT3 vector. Library

went through one round of normalization. Library

constructed by Bento Soares and M.Fatima Bonaldo."

#### ORIGIN

Query Match 83.3%; Score 15; DB 8; Length 426;

Best Local Similarity 86.7%; Pred. No. 3.2e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGGGGCGCAGCGCGU 17

|||||:|||||:

Db 318 AGGGTCCGACGCCGT 332

#### RESULT 43

CA453513

LOCUS AGENCOURT 10578892 NIH\_MGC\_127 Homo sapiens cDNA clone

DEFINITION IMAGE:6717438 5', mRNA sequence.

CA453513

CA453513.1 GI:24902339

EST.

ORGANISM Homo sapiens (human)

SOURCE Homo sapiens

BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.

1 (bases 1 to 429)

NIH-MGC http://mgs.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: c9apbs-r@mail.nih.gov

Tissue Procurement: NCI

cDNA Library Preparation: Michael Brownstein Laboratory

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNLN at:

http://image.lnl.gov

Plate: LNCM3034 row: c column: 06

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

#### FEATURES

source

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6717438"

High quality sequence stop: 409.

Location/Qualifiers

1. .429

/organism="Homo sapiens"

RESULT 45  
LOCUS CD698611  
DEFINITION BBT13134 human nasopharynx Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD698611  
VERSION CD698611.1 GI:32227094  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens (human)  
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.  
AUTHORS 1 (bases 1 to 487)  
Ilu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.  
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx  
JOURNAL Unpublished (2003)  
COMMENT Contact: Yixin Zeng  
Cancer Center  
Sun Yat-sen University  
651 Dongfeng Road East, Guangzhou 510060, China  
Tel: 86-1380-9770-743  
Fax: 86-20-8775-4506  
Email: yxzeng@zsuns.edu.cn  
Location/Qualifiers  
1..487  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/issue\_type="normal nasopharynx"  
/clone\_idb="human nasopharynx"  
/notes="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN  
Query Match 83.3%; Score 15; DB 6; Length 487;  
Best Local Similarity 93.3%; Pred. No. 3.2e+03;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGTCGACGCGG 16  
|||||:|||||  
Db 61 GAGGTCGACGCGG 75

RESULT 46  
LOCUS BU660456  
DEFINITION BU660456.21 Hembase; Erythroid Precursor Cells (LCB:c1 library) Homo sapiens cDNA clone c160c06 5', mRNA sequence.  
ACCESSION BU660456  
VERSION BU660456.1 GI:23372638  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens (human)  
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.  
AUTHORS 1 (bases 1 to 492)  
Gubin,A.N., Lee,Y.T., Bouffard,G.G. and Miller,J.L.  
TITLE Gene Expression in Human Erythroid Precursor Cells  
JOURNAL Unpublished (2002)  
COMMENT Contact: Jeffery L. Miller  
Laboratory of Chemical Biology  
National Institute of Diabetes and Digestive and Kidney Diseases  
Building 10, Room 9B17, National Institutes of Health, Bethesda, MD 20892, USA  
Tel: 301 402 2373  
Fax: 301 435 5148  
Email: jlm7femh.gov  
The c1 library was constructed by Alexander Gubin, Ph.D. in the Laboratory of Chemical Biology, NIDDK, NIH. DNA Sequencing and/or

FEATURES  
source  
1..492  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="c160c06"  
/sex="unknown"  
/issue\_type="blood"  
/cell\_line="Erythroid Precursor Cells"  
/cell\_line="Primary Culture of Peripheral Blood Mononuclear Cells"  
/dev\_stage="Precursor erythroblasts, GPA++"  
/lab\_host="DH5alpha"  
/clone\_idb="Hembase; Erythroid Precursor Cells (LCB:c1 library)"  
/note="Organ: blood; Vector: pTriplEx2; Site 1: SfiI; Site 2: SfiI; A complementary DNA (cDNA) library from human erythroid precursor cells was constructed using SMART PCR (polymerase chain reaction) cDNA library Construction Kit (Clontech, Palo Alto, CA) according to the manufacturer's directions, but with slight modifications. Briefly, reverse transcription was performed in the presence of 1 umol/L peptide nucleic acid (PNA) oligos (N-terminal)-biotin-GTC-CAC-CCG-AAG-CCT-G-(C-terminal) and (N-terminal)-biotin-C(T/C)T-GAA-GTC-CTC-AGG-A-(C-terminal). Synthesized cDNA was digested with SfiI and size-selected on a 1% agarose gel (>800bp). Large-scale sequencing of the library was performed by the NIH Intramural Sequencing Center (NISC; Http://www.nisc.nih.gov/)."

ORIGIN  
Query Match 83.3%; Score 15; DB 5; Length 492;  
Best Local Similarity 93.3%; Pred. No. 3.2e+03;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGTCGACGCGG 16  
|||||:|||||  
Db 28 GAGGTCGACGCGG 42

RESULT 47  
LOCUS CR736151  
DEFINITION CR736151 Soares testis NHT Homo sapiens cDNA clone IMAGE998B164415  
ACCESSION CR736151  
VERSION CR736151.1 GI:51586228  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens (human)  
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.  
AUTHORS 1 (bases 1 to 493)  
Ebert,L., Heil,O., Hennig,S., Korn,B., Neubert,P., Partsch,B., Peters,M., Radloff,U. and Schneider,D.  
TITLE I.M.A.G.E. cDNA Clone Collection  
JOURNAL Unpublished (2004)  
COMMENT Contact: Inge Axlart  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany  
Email: www.rzpd.de  
RZPD: IMAGE998B164415.  
RZPDLIB: I.M.A.G.E. cDNA Clone Collection;  
Contact: Inge Axlart  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 100  
Fax: +49 30 32639 111  
www.rzpd.de

This clone is available royalty-free from RZPD;  
contact RZPD (clone@rzpd.de) for further information. Seq primer:  
M13r, Primer sequence: TTTTCACACAGGAAACAGCTATGAC.

# FEATURES

## source

1. 493

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAG998B1C4415 ; IMAGB:1737519"

/sex="male"

/lab\_host="DH10B"

/clone\_lib="Soares\_tectis\_NHT"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

laboratories, Inc., and primed with a Not I - oligo(dT)

primer [5'

TGTTACCAATCTGAAGTGGAGCGCGCCCAATTTTTTTTTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT7T3 vector. Library

went through one round of normalization to Cot5, and was

constructed by Bento Soares and M. Fatima Bonaldo. "

## ORIGIN

Query Match 83.3%; Score 15; DB 7; Length 493;

Best Local Similarity 93.3%; Pred. No. 3.2e+03; Indels 0; Gaps 0;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGGCGCAGCGCG 16

DB 299 GAGGGTCCGACGCGG 313

Db

RESULT 48 530 bp DNA linear GSS 02-NOV-2004  
CWA52151  
LOCUS fbb001f192120f0 Sorghum methylation filtered library (libid: 104)  
DEFINITION Sorghum bicolor genomic clone fbb001f192120, genomic survey  
sequence.

ACCESSION CWA52151 GI:55200112

VERSION GSS.

KEYWORDS Sorghum bicolor (sorghum)

SOURCE Sorghum bicolor

ORGANISM Sorghum bicolor

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Sorghum.  
1 (bases 1 to 530)

REFERENCE Bedell J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,  
Jones, J., Plick, E., Rohlfing, T., Fries, J., Bradford, K.,  
McMenamy, J., Smith, M., Holman, H., Roe, B.A., Wiley, G., Korf, I. F.,  
Rabinowicz, P.D., Lakey, N., McComb, W.R., Jeddeloh, J.A. and  
Martensen, R.A.

AUTHORS

Sorghum genome sequencing by methylation filtration  
PLoS Biol. 3 (1), e13 (2005)

TITLE

JOURNAL

PUBMED

COMMENT

CONTACT

CONTACT

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CONTACT

/organism="Sorghum bicolor"  
/mol\_type="genomic DNA"  
/cultivar="RTx623"  
/db\_xref="taxon:4558"  
/clone="fbb001f192120"  
/clone\_lib="Sorghum methylation filtered library (libid:  
104)"  
/note="Organ: leaf; Vector: pBSK(-); Site 1: HincII; DNA  
prepared from purified nuclei was randomly sheared,  
end-repaired, size fractionated to enrich for the 0.5 to 5  
kb fraction, ligated into HincII-digested pBSK(-) vector  
and electroporated into E. coli cells. This is a  
methylation filtered library."

## ORIGIN

Query Match 83.3%; Score 15; DB 10; Length 530;

Best Local Similarity 93.3%; Pred. No. 3.2e+03; Indels 0; Gaps 0;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGGCGCAGCGCG 16

DB 24 GAGGGTCCGACGCGG 10

Db

RESULT 49 546 bp mRNA linear EST 29-JAN-2003  
CB138822  
LOCUS K-EST0191737 LSHLK1 Homo sapiens cDNA clone LSHLK1-36-B10 5', mRNA  
sequence.

ACCESSION CB138822

VERSION CB138822.1 GI:28110953

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 546)

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,  
Oh, K.U., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and  
Kim, Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

CONTACT: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 36 row: B column: 10

High quality sequence stop: 546.

Location/Qualifiers

source

1. 546

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="LSHLK1-36-B10"

/sex="M"

/cell\_line="HLK-1"

/lab\_host="Top10"

/clone\_lib="LSHLK1"

/note="Organ: Liver; Vector: pCNS-D2; Site 1: EcoRI;  
Site 2: NotI; The poly (A) + RNA was dephosphorylated with  
bacterial alkaline phosphatase (BAP) and then decapped  
with tabacco acid pyrophosphatase (TAP). The decapped  
intact mRNA was ligated with DNA-RNA linker including  
BcoRI site by treatment of T4 RNA ligase and the first  
strand cDNA was synthesized from oligo dt-selected mRNA by  
priming with dt-tailed vector. The dt-tailed vector was  
adjusted to have about 60nt. The cDNA vector was  
circularized with E. coli DNA ligase after digestion of  
BcoRI which site is also included in vector. An RNA strand

FEATURES  
source  
1. 530

converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells *E. coli* Top10<sup>®</sup> by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

## ORIGIN

Query Match 83.3%; Score 15; DB 6; Length 547;  
 Best Local Similarity 93.3%; Pred. No. 3.2e+03;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGTCGACGCGG 16  
 ||||:||||||  
 Db 17 GAGGTCGACGCGG 31

## RESULT 50

BE552352/c 547 bp mRNA linear EST 10-AUG-2000  
 LOCUS hy06605.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:3196544 3'  
 DEFINITION similar to gb:M62810 MITOCHONDRIAL TRANSCRIPTION FACTOR 1 PRECURSOR  
 (HUMAN); mRNA sequence.

ACCESSION BE552352  
 VERSION BE552352.1 GI:9794044

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.

1 (bases 1 to 547)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.  
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Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
 R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.

cDNA library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LIML, send email to:  
[info@image.llnl.gov](mailto:info@image.llnl.gov)

Seq primer: -40UP from Gibco  
 High quality sequence stop: 481.  
 Location/Qualifiers

1..547

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3196544"

/tissue\_type="pooled germ cell tumors"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP GC6"

/note="Vector: PT73D-Pac (Pharmacia) with a modified  
 polylinker. Site 1: Not I; Site 2: Eco RI; Plasmid DNA  
 from the normalized library NCI-CGAP\_GC4 was prepared, and  
 88 circles were made in vitro. Following HAP purification,  
 this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (clonids  
 1257096-1258631, 1469064-1470983, and 1475592-1476743).  
 Subtraction by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 83.3%; Score 15; DB 2; Length 547;  
 Best Local Similarity 93.3%; Pred. No. 3.2e+03;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGTCGACGCGG 16

Db 533 GAGGTCGACGCGG 518  
 ||||:||||||

Search completed: March 18, 2006, 20:01:40  
 J00 time : 1762.77 secs

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 18:35:23 ; Search time 68.8846 Seconds  
(without alignments)  
464.488 Million cell updates/sec

Title: US-10-800-926-1

Perfect score: 18

Sequence: 1 agagagagagagagagagag 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents NA:\*

1: /cgn2\_6/prodata/1/ina/1/COMB.seq:\*

2: /cgn2\_6/prodata/1/ina/5/COMB.seq:\*

3: /cgn2\_6/prodata/1/ina/6A/COMB.seq:\*

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6: /cgn2\_6/prodata/1/ina/6D/COMB.seq:\*

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8: /cgn2\_6/prodata/1/ina/6F/COMB.seq:\*

9: /cgn2\_6/prodata/1/ina/6G/COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	18	100.0	18	3	US-09-286-098-60 Sequence 60, Appl
C 3	18	100.0	18	3	US-08-960-774-60 Sequence 60, Appl
C 4	18	100.0	18	3	US-09-191-170-54 Sequence 54, Appl
C 5	18	100.0	18	3	US-09-137-619-60 Sequence 60, Appl
C 6	18	100.0	18	3	US-09-954-987B-67 Sequence 67, Appl
C 7	17	94.4	17	2	US-08-465-485A-9 Sequence 9, Appl
C 8	17	94.4	17	2	US-09-080-285-9 Sequence 9, Appl
C 9	17	94.4	17	3	US-09-724-426-9 Sequence 9, Appl
C 10	17	94.4	17	2	US-08-465-485A-8 Sequence 8, Appl
C 11	15	83.3	17	2	US-09-080-285-8 Sequence 8, Appl
C 12	15	83.3	17	3	US-09-724-426-8 Sequence 8, Appl
C 13	15	83.3	17	3	US-09-724-425-8 Sequence 8, Appl
C 14	15	83.3	17	3	US-09-724-425-8 Sequence 8, Appl
C 15	15	83.3	17	3	US-09-724-425-8 Sequence 8, Appl
C 16	15	83.3	17	3	US-09-724-425-8 Sequence 8, Appl
C 17	15	83.3	17	3	US-09-724-425-8 Sequence 8, Appl
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C 23	15	83.3	17	3	US-09-724-425-8 Sequence 8, Appl
C 24	15	83.3	17	3	US-09-724-425-8 Sequence 8, Appl

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C 27	14.4	80.0	767677	3	US-09-949-016-12147 Sequence 12147, A
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C 88	14.4	80.0	4411529	3	US-09-103-840A-1 Sequence 1, Appl
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C 98	13.4	74.4	3007	3	US-08-940-035A-33	Sequence 33, Appl	C 171	13.4	74.4	3794	3	US-10-007-747-27	Sequence 27, Appl
C 99	13.4	74.4	3007	3	US-08-935-105A-33	Sequence 33, Appl	C 172	13.4	74.4	3794	3	US-09-945-901-27	Sequence 27, Appl
C 100	13.4	74.4	3007	3	US-09-648-797-33	Sequence 33, Appl	C 173	13.4	74.4	3861	3	US-09-252-991A-8018	Sequence 8018, Ap
C 101	13.4	74.4	3007	3	US-09-386-123-33	Sequence 33, Appl	C 174	13.4	74.4	3935	2	US-08-231-193A-19	Sequence 19, Appl
C 102	13.4	74.4	3007	3	US-10-038-937-33	Sequence 33, Appl	C 175	13.4	74.4	3935	2	US-08-486-273A-19	Sequence 19, Appl
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C 112	13.4	74.4	3070	3	US-09-386-123-39	Sequence 39, Appl	C 185	13.4	74.4	3935	2	US-08-231-193A-35	Sequence 35, Appl
C 113	13.4	74.4	3070	3	US-10-038-937-39	Sequence 39, Appl	C 186	13.4	74.4	3935	2	US-08-486-273A-35	Sequence 35, Appl
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C 126	13.4	74.4	3155	3	US-09-945-901-13	Sequence 13, Appl	C 199	13.4	74.4	4094	3	US-08-940-086A-29	Sequence 29, Appl
C 127	13.4	74.4	3211	2	US-08-231-193A-21	Sequence 21, Appl	C 200	13.4	74.4	4094	3	US-08-940-035A-29	Sequence 29, Appl
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C 134	13.4	74.4	3211	3	US-09-386-123-21	Sequence 21, Appl	C 207	13.4	74.4	4157	2	US-08-231-193A-25	Sequence 25, Appl
C 135	13.4	74.4	3211	3	US-10-038-937-21	Sequence 21, Appl	C 208	13.4	74.4	4157	2	US-08-486-273A-25	Sequence 25, Appl
C 136	13.4	74.4	3211	3	US-10-007-747-21	Sequence 21, Appl	C 209	13.4	74.4	4157	3	US-08-480-474-25	Sequence 25, Appl
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C 139	13.4	74.4	3274	2	US-08-486-273A-37	Sequence 37, Appl	C 212	13.4	74.4	4157	3	US-08-935-105A-25	Sequence 25, Appl
C 140	13.4	74.4	3274	3	US-08-480-474-37	Sequence 37, Appl	C 213	13.4	74.4	4157	3	US-09-648-797-25	Sequence 25, Appl
C 141	13.4	74.4	3274	3	US-08-940-086A-37	Sequence 37, Appl	C 214	13.4	74.4	4157	3	US-09-386-123-25	Sequence 25, Appl
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C 143	13.4	74.4	3274	3	US-08-935-105A-37	Sequence 37, Appl	C 216	13.4	74.4	4157	3	US-10-007-747-25	Sequence 25, Appl
C 144	13.4	74.4	3274	3	US-09-648-797-37	Sequence 37, Appl	C 217	13.4	74.4	4157	3	US-09-945-901-25	Sequence 25, Appl
C 145	13.4	74.4	3274	3	US-09-386-123-37	Sequence 37, Appl	C 218	13.4	74.4	4158	3	US-09-252-991A-5348	Sequence 5348, Ap
C 146	13.4	74.4	3274	3	US-10-038-937-37	Sequence 37, Appl	C 219	13.4	74.4	4288	2	US-08-231-193A-1	Sequence 1, Appl
C 147	13.4	74.4	3274	3	US-10-007-747-37	Sequence 37, Appl	C 220	13.4	74.4	4288	2	US-08-486-273A-1	Sequence 1, Appl
C 148	13.4	74.4	3274	3	US-09-945-901-37	Sequence 37, Appl	C 221	13.4	74.4	4288	3	US-08-480-474-1	Sequence 1, Appl
C 149	13.4	74.4	3351	3	US-09-252-991A-18871	Sequence 15871, A	C 222	13.4	74.4	4288	3	US-08-940-086A-1	Sequence 1, Appl
C 150	13.4	74.4	3657	3	US-09-252-991A-89898	Sequence 8298, Ap	C 223	13.4	74.4	4288	3	US-08-940-035A-1	Sequence 1, Appl
C 151	13.4	74.4	3731	2	US-08-231-193A-31	Sequence 31, Appl	C 224	13.4	74.4	4288	3	US-08-935-105A-1	Sequence 1, Appl
C 152	13.4	74.4	3731	2	US-08-486-273A-31	Sequence 31, Appl	C 225	13.4	74.4	4288	3	US-09-648-797-1	Sequence 1, Appl
C 153	13.4	74.4	3731	3	US-08-480-474-31	Sequence 31, Appl	C 226	13.4	74.4	4288	3	US-09-386-123-1	Sequence 1, Appl
C 154	13.4	74.4	3731	3	US-08-940-086A-31	Sequence 31, Appl	C 227	13.4	74.4	4288	3	US-10-038-937-1	Sequence 1, Appl
C 155	13.4	74.4	3731	3	US-08-940-035A-31	Sequence 31, Appl	C 228	13.4	74.4	4288	3	US-10-007-747-1	Sequence 1, Appl
C 156	13.4	74.4	3731	3	US-08-935-105A-31	Sequence 31, Appl	C 229	13.4	74.4	4288	3	US-09-945-901-1	Sequence 1, Appl
C 157	13.4	74.4	3731	3	US-09-648-797-31	Sequence 31, Appl	C 230	13.4	74.4	4361	2	US-08-231-193A-23	Sequence 23, Appl
C 158	13.4	74.4	3731	3	US-09-386-123-31	Sequence 31, Appl	C 231	13.4	74.4	4361	2	US-08-486-273A-23	Sequence 23, Appl
C 159	13.4	74.4	3731	3	US-10-038-937-31	Sequence 31, Appl	C 232	13.4	74.4	4361	3	US-08-480-474-23	Sequence 23, Appl
C 160	13.4	74.4	3731	3	US-10-007-747-31	Sequence 31, Appl	C 233	13.4	74.4	4361	3	US-08-940-086A-23	Sequence 23, Appl
C 161	13.4	74.4	3731	3	US-09-945-901-31	Sequence 31, Appl	C 234	13.4	74.4	4361	3	US-08-940-035A-23	Sequence 23, Appl
C 162	13.4	74.4	3794	2	US-08-231-193A-27	Sequence 27, Appl	C 235	13.4	74.4	4361	3	US-08-935-105A-23	Sequence 23, Appl
C 163	13.4	74.4	3794	2	US-08-486-273A-27	Sequence 27, Appl	C 236	13.4	74.4	4361	3	US-09-648-797-23	Sequence 23, Appl
C 164	13.4	74.4	3794	3	US-08-480-474-27	Sequence 27, Appl	C 237	13.4	74.4	4361	3	US-09-386-123-23	Sequence 23, Appl
C 165	13.4	74.4	3794	3	US-08-940-086A-27	Sequence 27, Appl	C 238	13.4	74.4	4361	3	US-10-038-937-23	Sequence 23, Appl
C 166	13.4	74.4	3794	3	US-08-940-035A-27	Sequence 27, Appl	C 239	13.4	74.4	4361	3	US-10-007-747-23	Sequence 23, Appl
C 167	13.4	74.4	3794	3	US-08-935-105A-27	Sequence 27, Appl	C 240	13.4	74.4	4361	3	US-09-945-901-23	Sequence 23, Appl
C 168	13.4	74.4	3794	3	US-09-648-797-27	Sequence 27, Appl	C 241	13.4	74.4	4494	3	US-09-902-540-7532	Sequence 7532, Ap
C 169	13.4	74.4	3794	3	US-09-386-123-27	Sequence 27, Appl	C 242	13.4	74.4	4659	3	US-08-264-578-10	Sequence 10, Appl
C 170	13.4	74.4	3794	3	US-10-038-937-27	Sequence 27, Appl	C 243	13.4	74.4	4659	3	US-08-217-704C-9	Sequence 9, Appl

C 244	13.4	74.4	4659	3	US-08-164-487A-1	Sequence 1, Appl1	C 317	13.2	73.3	481115	3	US-09-949-016-11940	Sequence 11940, A
C 245	13.4	74.4	4953	3	US-09-252-991A-5227	Sequence 5227, Ap	C 318	~13.2	72.2	20	3	US-10-029-598-13	Sequence 12, Appl
C 246	13.4	74.4	6988	3	US-09-902-540-733	Sequence 733, Appl	C 319	13	72.2	20	3	US-09-108-673A-22	Sequence 22, Appl
C 247	13.4	74.4	7796	3	US-09-521-511C-12	Sequence 12, Appl	C 320	13	72.2	972	3	US-09-602-787A-587	Sequence 587, Ap
C 248	13.4	74.4	8176	3	US-09-949-016-1668	Sequence 1668, A	C 321	13	72.2	2478	3	US-09-215-694-31	Sequence 31, Appl
C 249	13.4	74.4	14721	3	US-09-949-016-13507	Sequence 13507, A	C 322	13	72.2	2478	3	US-10-109-310-31	Sequence 31, Appl
C 250	13.4	74.4	16387	3	US-09-902-540-1156	Sequence 1156, Ap	C 323	13	72.2	3285	3	US-09-712-363-13	Sequence 143, Ap
C 251	13.4	74.4	17654	3	US-09-902-540-1161	Sequence 1161, Ap	C 324	13	72.2	10095	3	US-08-822-586-45	Sequence 45, Appl
C 252	13.4	74.4	22118	3	US-09-815-981A-5	Sequence 5, Appl1	C 325	13	72.2	31328	3	US-09-215-694-19	Sequence 19, Appl
C 253	13.4	74.4	25733	3	US-09-902-540-1215	Sequence 1215, Ap	C 326	13	72.2	31328	3	US-10-109-310-19	Sequence 19, Appl
C 254	13.4	74.4	26659	3	US-09-902-540-1217	Sequence 1217, Ap	C 327	13	72.2	36412	3	US-08-311-731A-132	Sequence 132, Ap
C 255	13.4	74.4	26729	3	US-10-283-247-6	Sequence 6, Appl1	C 328	12.8	71.1	50	3	US-10-131-827-4053	Sequence 4053, Ap
C 256	13.4	74.4	28320	3	US-09-902-540-1222	Sequence 1222, Ap	C 329	12.8	71.1	111	2	US-07-750-080A-17	Sequence 17, Appl
C 257	13.4	74.4	70383	3	US-10-283-247-3	Sequence 3, Appl1	C 330	12.8	71.1	111	3	US-08-651-472-17	Sequence 17, Appl
C 258	13.4	74.4	74353	3	US-09-949-016-15336	Sequence 15336, A	C 331	12.8	71.1	111	3	US-08-358-928-17	Sequence 17, Appl
C 259	13.2	73.3	125	3	US-09-513-999C-14561	Sequence 14561, A	C 332	12.8	71.1	208	3	US-09-423-23-1	Sequence 1, Appl1
C 260	13.2	73.3	192	3	US-09-107-433-603	Sequence 603, App	C 333	12.8	71.1	225	3	US-09-252-991A-8443	Sequence 8443, Ap
C 261	13.2	73.3	414	3	US-09-489-039A-282	Sequence 282, App	C 334	12.8	71.1	254	3	US-09-513-999C-14185	Sequence 14185, A
C 262	13.2	73.3	494	3	US-09-270-767-2755	Sequence 2755, Ap	C 335	12.8	71.1	287	3	US-09-313-294A-7202	Sequence 7202, Ap
C 263	13.2	73.3	494	3	US-09-270-767-18037	Sequence 18037, A	C 336	12.8	71.1	293	3	US-09-313-294A-7449	Sequence 7449, Ap
C 264	13.2	73.3	529	3	US-09-621-976-15117	Sequence 15117, A	C 337	12.8	71.1	299	3	US-09-270-767-27137	Sequence 27137, A
C 265	13.2	73.3	532	3	US-09-270-767-9534	Sequence 9534, Ap	C 338	12.8	71.1	320	3	US-09-621-976-389	Sequence 389, App
C 266	13.2	73.3	532	3	US-09-270-767-24816	Sequence 24816, A	C 339	12.8	71.1	352	3	US-09-717-321A-18	Sequence 18, Appl
C 267	13.2	73.3	539	3	US-09-621-976-15114	Sequence 15114, A	C 340	12.8	71.1	352	3	US-09-423-233-3	Sequence 3, Appl1
C 268	13.2	73.3	552	3	US-09-252-991A-8870	Sequence 8870, Ap	C 341	12.8	71.1	378	3	US-09-573-080A-235	Sequence 235, Appl
C 269	13.2	73.3	568	3	US-09-621-976-15109	Sequence 15109, A	C 342	12.8	71.1	398	3	US-09-270-767-16713	Sequence 16713, A
C 270	13.2	73.3	573	3	US-09-621-976-15101	Sequence 15101, A	C 343	12.8	71.1	398	3	US-09-513-999C-32409	Sequence 32409, A
C 271	13.2	73.3	601	3	US-09-949-016-48385	Sequence 48385, A	C 344	12.8	71.1	414	3	US-09-902-540-7384	Sequence 7384, Ap
C 272	13.2	73.3	601	3	US-09-949-016-92697	Sequence 92697, A	C 345	12.8	71.1	537	3	US-09-902-540-3398	Sequence 3398, Ap
C 273	13.2	73.3	601	3	US-09-949-016-146622	Sequence 146622, Sequence 2872, Ap	C 346	12.8	71.1	560	3	US-09-270-767-5624	Sequence 5624, Ap
C 274	13.2	73.3	601	3	US-09-949-002-2874	Sequence 2874, Ap	C 347	12.8	71.1	560	3	US-09-270-767-28906	Sequence 28906, A
C 275	13.2	73.3	601	3	US-09-949-002-2874	Sequence 4878, Ap	C 348	12.8	71.1	583	3	US-09-533-555-1897	Sequence 1897, Ap
C 276	13.2	73.3	601	3	US-09-949-002-4878	Sequence 4880, Ap	C 349	12.8	71.1	595	3	US-09-580-797-37	Sequence 34, Appl
C 277	13.2	73.3	601	3	US-09-949-002-4880	Sequence 4883, Ap	C 350	12.8	71.1	595	3	US-09-580-797-34	Sequence 34, Appl
C 278	13.2	73.3	606	4	US-09-605-703B-1883	Sequence 1883, Ap	C 351	12.8	71.1	599	3	US-09-580-797-37	Sequence 67155, A
C 279	13.2	73.3	667	3	US-10-002-344A-15	Sequence 15, Appl	C 352	12.8	71.1	601	3	US-09-949-016-67155	Sequence 67155, A
C 280	13.2	73.3	690	3	US-09-543-681A-1114	Sequence 1114, Ap	C 353	12.8	71.1	601	3	US-09-949-016-67155	Sequence 67156, A
C 281	13.2	73.3	740	3	US-10-101-464A-140	Sequence 140, App	C 354	12.8	71.1	601	3	US-09-949-016-67155	Sequence 83888, A
C 282	13.2	73.3	832	3	US-09-270-767-5424	Sequence 5424, Ap	C 355	12.8	71.1	601	3	US-09-949-016-83898	Sequence 136862, A
C 283	13.2	73.3	832	3	US-09-270-767-20706	Sequence 20706, A	C 356	12.8	71.1	601	3	US-09-949-016-150119	Sequence 150119, Sequence 2873, Ap
C 284	13.2	73.3	882	3	US-09-452-991A-8977	Sequence 8977, Ap	C 357	12.8	71.1	601	3	US-09-949-002-2873	Sequence 4879, Ap
C 285	13.2	73.3	1590	3	US-09-489-039A-410	Sequence 410, App	C 358	12.8	71.1	601	3	US-09-949-002-4879	Sequence 8, Appl1
C 286	13.2	73.3	1565	3	US-09-902-540-8991	Sequence 8991, Ap	C 359	12.8	71.1	601	3	US-09-580-797-8	Sequence 43, Appl
C 287	13.2	73.3	2287	2	US-08-900-927-2	Sequence 2, Appl1	C 360	12.8	71.1	672	3	US-09-712-363-43	Sequence 5, Appl1
C 288	13.2	73.3	2287	2	US-09-191-279-2	Sequence 2, Appl1	C 361	12.8	71.1	675	3	US-09-580-797-5	Sequence 15097, A
C 289	13.2	73.3	2297	2	US-08-121-713D-63	Sequence 63, Appl	C 362	12.8	71.1	735	3	US-09-252-991A-15097	Sequence 11540, A
C 290	13.2	73.3	2504	2	US-08-835-268-63	Sequence 63, Appl	C 363	12.8	71.1	759	3	US-09-270-767-11540	Sequence 267, App
C 291	13.2	73.3	2504	2	US-08-835-268-63	Sequence 63, Appl	C 364	12.8	71.1	766	3	US-09-495-050A-267	Sequence 95, Appl
C 292	13.2	73.3	2504	2	US-08-833-391-63	Sequence 63, Appl	C 365	12.8	71.1	900	3	US-09-157-688-96	Sequence 10976, A
C 293	13.2	73.3	2504	3	US-09-601-610-63	Sequence 63, Appl	C 366	12.8	71.1	900	3	US-09-270-767-10976	Sequence 14840, A
C 294	13.2	73.3	2504	3	US-09-601-610-63	Sequence 63, Appl	C 367	12.8	71.1	918	3	US-09-252-991A-14840	Sequence 41, Appl
C 295	13.2	73.3	3369	3	US-08-961-527-42	Sequence 42, Appl	C 368	12.8	71.1	952	3	US-09-050-739-41	Sequence 2002, Ap
C 296	13.2	73.3	3369	3	US-08-961-527-42	Sequence 960, App	C 369	12.8	71.1	993	3	US-09-252-991A-2002	Sequence 734, App
C 297	13.2	73.3	10692	3	US-09-902-540-960	Sequence 14401, A	C 370	12.8	71.1	1015	3	US-09-620-312D-734	Sequence 663, App
C 298	13.2	73.3	16455	3	US-09-949-016-14292	Sequence 14401, A	C 371	12.8	71.1	1020	3	US-09-023-655-653	Sequence 4233, Ap
C 299	13.2	73.3	16470	3	US-09-949-016-14601	Sequence 13686, A	C 372	12.8	71.1	1047	3	US-09-902-540-4239	Sequence 9630, Ap
C 300	13.2	73.3	18235	3	US-09-949-016-13686	Sequence 14581, A	C 373	12.8	71.1	1047	3	US-09-902-540-4632	Sequence 14503, A
C 301	13.2	73.3	20875	3	US-09-949-016-15860	Sequence 15860, A	C 374	12.8	71.1	1066	3	US-10-004-115B-35	Sequence 41, Appl
C 302	13.2	73.3	64309	3	US-09-949-016-14581	Sequence 14581, A	C 375	12.8	71.1	1084	3	US-09-902-540-9630	Sequence 94, Appl
C 303	13.2	73.3	68392	3	US-09-949-016-13626	Sequence 13626, A	C 376	12.8	71.1	1155	3	US-09-270-767-11503	Sequence 1875, Ap
C 304	13.2	73.3	69763	3	US-09-949-016-12584	Sequence 12584, A	C 377	12.8	71.1	1155	3	US-10-029-180-41	Sequence 32, Appl
C 305	13.2	73.3	82612	3	US-09-949-016-16823	Sequence 16823, A	C 378	12.8	71.1	1158	3	US-09-984-334-2	Sequence 8, Appl1
C 306	13.2	73.3	112507	3	US-09-949-016-12420	Sequence 12420, A	C 379	12.8	71.1	1173	3	US-09-902-540-5769	Sequence 83, Appl
C 307	13.2	73.3	112507	3	US-09-949-016-12794	Sequence 12794, A	C 380	12.8	71.1	1239	3	US-10-022-180-83	Sequence 2089, Ap
C 308	13.2	73.3	112508	3	US-09-949-016-16589	Sequence 16589, A	C 381	12.8	71.1	1437	3	US-09-252-991A-2089	Sequence 94, Appl
C 309	13.2	73.3	112508	3	US-09-949-016-16590	Sequence 16590, A	C 382	12.8	71.1	1506	3	US-09-758-759-94	Sequence 1875, Ap
C 310	13.2	73.3	131978	3	US-09-949-016-13117	Sequence 13117, A	C 383	12.8	71.1	1506	3	US-09-252-991A-1875	Sequence 32, Appl
C 311	13.2	73.3	150409	3	US-09-949-016-12290	Sequence 12290, A	C 384	12.8	71.1	1582	3	US-08-416-344B-8	Sequence 8, Appl1
C 312	13.2	73.3	150409	3	US-09-949-016-12938	Sequence 12938, A	C 385	12.8	71.1	1623	3	US-09-902-540-4832	Sequence 4832, Ap
C 313	13.2	73.3	188504	3	US-09-949-002-711	Sequence 711, App	C 386	12.8	71.1	1676	3	US-09-902-540-8746	Sequence 8746, Ap
C 314	13.2	73.3	200918	3	US-09-949-002-647	Sequence 647, App	C 387	12.8	71.1	1710	3	US-09-902-540-2988	Sequence 2988, Ap
C 315	13.2	73.3	360470	3	US-09-949-016-13173	Sequence 13173, A	C 388	12.8	71.1	1731	3	US-09-252-991A-8512	Sequence 8512, Ap
C 316	13.2	73.3	455726	3	US-09-949-016-14157	Sequence 14157, A	C 389	12.8	71.1				



C 390	12.8	71.1	1731	3	US-09-328-352-706	Sequence 706, App	463	12.8	71.1	53577	3	US-08-460-215A-1	Sequence 1, App11
C 391	12.8	71.1	1745	3	US-09-857-896A-7	Sequence 7, App11	464	12.8	71.1	63860	3	US-09-949-016-15825	Sequence 15825, A
C 392	12.8	71.1	1929	2	US-07-841-646-26	Sequence 26, App1	465	12.8	71.1	65648	3	US-09-949-016-13285	Sequence 13285, A
C 393	12.8	71.1	1929	6	PCT-US91-07633-3	Sequence 3, App11	466	12.8	71.1	72704	3	US-09-902-540-1273	Sequence 1273, App
C 394	12.8	71.1	2166	3	US-09-902-540-359	Sequence 359, App	467	12.8	71.1	105210	3	US-09-949-016-11158	Sequence 11158, A
C 395	12.8	71.1	2203	3	US-09-902-540-4252	Sequence 4252, App	468	12.8	71.1	109519	3	US-09-738-755-1	Sequence 1, App11
C 396	12.8	71.1	2236	2	US-07-551-080A-18	Sequence 18, App1	469	12.8	71.1	146639	3	US-09-949-016-15449	Sequence 15449, A
C 397	12.8	71.1	2236	2	US-08-551-072-18	Sequence 18, App1	470	12.8	71.1	194915	3	US-09-949-016-15584	Sequence 15584, A
C 398	12.8	71.1	2236	3	US-08-358-928-18	Sequence 18, App1	471	12.8	71.1	271131	3	US-09-949-016-15705	Sequence 15705, A
C 399	12.8	71.1	2236	3	US-09-949-016-55292	Sequence 5292, App	472	12.8	71.1	305491	3	US-09-949-016-17550	Sequence 17550, A
C 400	12.8	71.1	2403	3	US-09-949-016-5293	Sequence 5293, App	473	12.4	68.9	189	3	US-09-313-299A-1847	Sequence 1847, App
C 401	12.8	71.1	2432	3	US-10-104-047-872	Sequence 872, App	474	12.4	68.9	318	3	US-09-902-540-2195	Sequence 2195, App
C 402	12.8	71.1	2634	3	US-08-941-936-1	Sequence 1, App11	475	12.4	68.9	407	3	US-09-270-767-8766	Sequence 8766, App
C 403	12.8	71.1	2666	3	US-09-566-921-3	Sequence 3, App11	476	12.4	68.9	439	3	US-09-621-976-24048	Sequence 24048, App
C 404	12.8	71.1	2714	3	US-09-023-655-928	Sequence 928, App	477	12.4	68.9	481	3	US-09-621-976-24048	Sequence 24048, App
C 405	12.8	71.1	2787	3	US-09-902-540-5793	Sequence 5793, App	478	12.4	68.9	481	3	US-09-640-211A-1840	Sequence 1840, App
C 406	12.8	71.1	2823	3	US-09-252-991A-2840	Sequence 2840, App	479	12.4	68.9	519	3	US-09-640-211A-1554	Sequence 1554, App
C 407	12.8	71.1	3204	3	US-09-252-991A-3126	Sequence 3126, App	480	12.4	68.9	519	3	US-09-252-991A-11147	Sequence 11147, App
C 408	12.8	71.1	3471	3	US-09-902-540-8385	Sequence 8385, App	481	12.4	68.9	526	3	US-09-513-999C-3721	Sequence 3721, App
C 409	12.8	71.1	3797	3	US-09-949-016-3789	Sequence 3789, App	482	12.4	68.9	561	3	US-09-252-991A-391	Sequence 391, App
C 410	12.8	71.1	3802	3	US-09-949-016-905	Sequence 905, App	483	12.4	68.9	600	3	US-09-252-991A-11276	Sequence 11276, App
C 411	12.8	71.1	3846	3	US-09-902-540-2520	Sequence 2520, App	484	12.4	68.9	601	3	US-09-949-016-33458	Sequence 33458, App
C 412	12.8	71.1	3958	3	US-09-949-016-1601	Sequence 1601, App	485	12.4	68.9	601	3	US-09-949-016-33459	Sequence 33459, App
C 413	12.8	71.1	4223	3	US-09-799-451-565	Sequence 565, App	486	12.4	68.9	601	3	US-09-949-016-41093	Sequence 41093, App
C 414	12.8	71.1	4236	3	US-09-902-540-3231	Sequence 3291, App	487	12.4	68.9	601	3	US-09-949-016-41094	Sequence 41094, App
C 415	12.8	71.1	6360	3	US-09-221-017B-835	Sequence 835, App	488	12.4	68.9	601	3	US-09-949-016-55682	Sequence 55682, App
C 416	12.8	71.1	6588	3	US-09-949-016-1076	Sequence 1076, App	489	12.4	68.9	601	3	US-09-949-016-62008	Sequence 62008, App
C 417	12.8	71.1	6739	3	US-09-902-540-901	Sequence 901, App	490	12.4	68.9	601	3	US-09-949-016-66075	Sequence 66075, App
C 418	12.8	71.1	7186	3	US-09-902-540-708	Sequence 708, App	491	12.4	68.9	601	3	US-09-949-016-112317	Sequence 112317, App
C 419	12.8	71.1	7186	3	US-09-902-540-879	Sequence 879, App	492	12.4	68.9	619	3	US-08-998-416-842	Sequence 842, App
C 420	12.8	71.1	7463	3	US-09-902-540-928	Sequence 928, App	493	12.4	68.9	747	3	US-09-252-991A-15739	Sequence 15739, App
C 421	12.8	71.1	11495	3	US-09-056-105-9	Sequence 9, App11	494	12.4	68.9	822	3	US-09-252-991A-15614	Sequence 15614, App
C 422	12.8	71.1	11690	3	US-09-949-016-16592	Sequence 16592, App	495	12.4	68.9	862	3	US-08-998-416-553	Sequence 553, App
C 423	12.8	71.1	11879	3	US-09-949-016-14211	Sequence 14211, App	496	12.4	68.9	873	3	US-09-543-681A-1024	Sequence 1024, App
C 424	12.8	71.1	16187	3	US-09-902-540-1093	Sequence 1093, App	497	12.4	68.9	885	3	US-09-252-991A-12893	Sequence 12893, App
C 425	12.8	71.1	17503	3	US-09-902-540-1114	Sequence 1114, App	498	12.4	68.9	900	3	US-10-059-578A-121	Sequence 121, App
C 426	12.8	71.1	17654	3	US-09-902-540-1161	Sequence 1161, App	499	12.4	68.9	939	3	US-09-351-150A-10	Sequence 10, App
C 427	12.8	71.1	17727	3	US-09-902-540-1152	Sequence 1152, App	500	12.4	68.9	1087	3	US-09-489-039A-2291	Sequence 2291, App
C 428	12.8	71.1	18031	3	US-09-902-540-1180	Sequence 1180, App	501	12.4	68.9	1098	3	US-09-902-540-5144	Sequence 5144, App
C 429	12.8	71.1	21358	3	US-09-973-278-789	Sequence 789, App	502	12.4	68.9	1029	3	US-09-489-039A-336	Sequence 336, App
C 430	12.8	71.1	21676	3	US-09-973-278-792	Sequence 792, App	503	12.4	68.9	1086	3	US-09-902-540-8095	Sequence 8095, App
C 431	12.8	71.1	22143	3	US-09-949-016-15583	Sequence 15983, App	504	12.4	68.9	1107	3	US-09-252-991A-932	Sequence 932, App
C 432	12.8	71.1	22339	3	US-09-949-016-12411	Sequence 12411, App	505	12.4	68.9	1158	3	US-09-724-623-8	Sequence 8, App11
C 433	12.8	71.1	22339	3	US-09-949-016-16154	Sequence 16154, App	506	12.4	68.9	1161	3	US-09-808-387-5	Sequence 5, App11
C 434	12.8	71.1	24791	3	US-09-902-540-1211	Sequence 1211, App	507	12.4	68.9	1246	3	US-09-691-270A-19	Sequence 19, App1
C 435	12.8	71.1	25370	3	US-09-949-016-12109	Sequence 12109, App	508	12.4	68.9	1344	3	US-09-303-518D-127	Sequence 127, App
C 436	12.8	71.1	25370	3	US-09-949-016-12109	Sequence 12109, App	509	12.4	68.9	1350	3	US-09-902-540-4545	Sequence 4545, App
C 437	12.8	71.1	25376	3	US-09-949-016-15880	Sequence 15880, App	510	12.4	68.9	1420	3	US-09-270-767-11140	Sequence 11140, App
C 438	12.8	71.1	25976	3	US-10-418-036-23	Sequence 23, App1	511	12.4	68.9	1446	3	US-09-252-991A-7984	Sequence 7984, App
C 439	12.8	71.1	28567	3	US-10-418-036-23	Sequence 23, App1	512	12.4	68.9	1497	3	US-09-489-039A-398	Sequence 398, App
C 440	12.8	71.1	30782	3	US-09-949-016-13724	Sequence 13724, App	513	12.4	68.9	1527	3	US-09-252-991A-1035	Sequence 1035, App
C 441	12.8	71.1	31720	3	US-09-949-016-15947	Sequence 15947, App	514	12.4	68.9	1587	3	US-09-902-540-6357	Sequence 6357, App
C 442	12.8	71.1	33536	3	US-09-949-016-17034	Sequence 17034, App	515	12.4	68.9	1599	3	US-09-252-991A-1021	Sequence 1021, App
C 443	12.8	71.1	33536	3	US-09-949-016-17034	Sequence 17034, App	516	12.4	68.9	1674	3	US-09-808-387-3	Sequence 3, App11
C 444	12.8	71.1	33536	3	US-09-949-016-17035	Sequence 17035, App	517	12.4	68.9	1687	3	US-09-270-767-12792	Sequence 12792, App
C 445	12.8	71.1	39982	3	US-09-820-924-3	Sequence 3, App11	518	12.4	68.9	1725	3	US-09-270-767-12792	Sequence 12792, App
C 446	12.8	71.1	39982	3	US-10-369-626-3	Sequence 3, App11	519	12.4	68.9	1776	3	US-09-799-451-497	Sequence 497, App
C 447	12.8	71.1	47184	3	US-09-949-016-12647	Sequence 12647, App	520	12.4	68.9	1818	3	US-09-902-540-5126	Sequence 5126, App
C 448	12.8	71.1	47184	3	US-09-949-016-15531	Sequence 15531, App	521	12.4	68.9	1873	3	US-09-821-803A-1	Sequence 1, App11
C 449	12.8	71.1	51043	3	US-09-949-016-12739	Sequence 12739, App	522	12.4	68.9	1967	3	US-09-902-540-2665	Sequence 2665, App
C 450	12.8	71.1	51046	3	US-09-949-016-13946	Sequence 13946, App	523	12.4	68.9	2001	3	US-09-252-991A-483	Sequence 483, App
C 451	12.8	71.1	51671	3	US-09-949-016-12068	Sequence 12068, App	524	12.4	68.9	2005	3	US-10-104-047-175	Sequence 175, App
C 452	12.8	71.1	51671	3	US-09-949-016-15962	Sequence 15962, App	525	12.4	68.9	2085	3	US-09-352-990-9	Sequence 9, App11
C 453	12.8	71.1	51754	3	US-09-949-016-15009	Sequence 15009, App	526	12.4	68.9	2295	3	US-09-270-767-1016	Sequence 1016, App
C 454	12.8	71.1	51754	3	US-09-949-016-15011	Sequence 15011, App	527	12.4	68.9	2295	3	US-09-270-767-15298	Sequence 15298, App
C 455	12.8	71.1	51754	3	US-09-949-016-15011	Sequence 15011, App	528	12.4	68.9	2331	3	US-09-698-341-1	Sequence 1, App11
C 456	12.8	71.1	51754	3	US-09-949-016-15012	Sequence 15012, App	529	12.4	68.9	2337	2	US-09-906-925-5	Sequence 5, App11
C 457	12.8	71.1	51754	3	US-09-949-016-15275	Sequence 15275, App	530	12.4	68.9	2592	3	US-09-902-540-2500	Sequence 2500, App
C 458	12.8	71.1	51754	3	US-09-949-016-15276	Sequence 15276, App	531	12.4	68.9	2613	3	US-09-902-540-6510	Sequence 6510, App
C 459	12.8	71.1	51754	3	US-09-949-016-15277	Sequence 15277, App	532	12.4	68.9	2714	3	US-09-774-528-161	Sequence 161, App
C 460	12.8	71.1	51754	3	US-09-949-016-15278	Sequence 15278, App	533	12.4	68.9	2724	3	US-10-120-988-161	Sequence 161, App
C 461	12.8	71.1	53526	3	US-08-658-136-2	Sequence 2, App11	534	12.4	68.9	2724	3	US-09-902-540-410	Sequence 410, App
C 462	12.8	71.1	53577	3	US-08-658-136-1	Sequence 1, App11	535	12.4	68.9	2840	3	US-10-087-167-1	Sequence 1, App11

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537	12.4	68.9	3447	3	US-09-949-016-1944	Sequence 1944, App
538	12.4	68.9	3526	3	US-09-175-713-4	Sequence 4, App1
539	12.4	68.9	3648	3	US-09-902-540-624	Sequence 624, App
540	12.4	68.9	3839	3	US-09-845-248B-56	Sequence 56, App1
541	12.4	68.9	3839	3	US-09-845-248B-57	Sequence 57, App1
542	12.4	68.9	3840	3	US-09-845-248B-55	Sequence 55, App1
543	12.4	68.9	4079	3	US-09-016-434-1412	Sequence 1412, App
544	12.4	68.9	5255	3	US-09-698-341-4	Sequence 4, App1
545	12.4	68.9	5392	2	US-08-803-852B-1	Sequence 1, App1
546	12.4	68.9	5392	2	US-08-803-852B-1	Sequence 1, App1
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548	12.4	68.9	5392	3	US-09-635-359B-1	Sequence 1, App1
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550	12.4	68.9	7490	3	US-09-949-016-17606	Sequence 17606, A
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555	12.4	68.9	11425	3	US-09-949-016-13480	Sequence 13480, A
556	12.4	68.9	11612	3	US-09-902-540-981	Sequence 981, App
557	12.4	68.9	13706	3	US-09-902-540-1134	Sequence 1134, App
558	12.4	68.9	13987	2	US-08-804-227C-13	Sequence 13, App1
559	12.4	68.9	14541	3	US-09-902-540-1159	Sequence 1159, App
560	12.4	68.9	15644	3	US-09-902-540-1133	Sequence 1133, App
561	12.4	68.9	15945	3	US-09-949-016-17271	Sequence 17271, A
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565	12.4	68.9	20026	3	US-09-949-016-13147	Sequence 13147, A
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568	12.4	68.9	28058	3	US-09-902-540-1252	Sequence 1252, App
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571	12.4	68.9	38564	3	US-09-734-673-3	Sequence 3, App1
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573	12.4	68.9	44377	2	US-08-804-198-1	Sequence 1, App1
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576	12.4	68.9	61198	3	US-09-949-016-17248	Sequence 17248, A
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578	12.4	68.9	62728	3	US-09-949-016-12539	Sequence 12539, A
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632	12.2	67.8	126	2	US-08-446-374-8	Sequence 8, App1
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C 684	12.2	67.8	601	3	US-09-949-016-21636	Sequence 21636, A	757	12.2	67.8	601	3	US-09-949-016-17765	Sequence 17765, A
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C 700	12.2	67.8	601	3	US-09-949-016-59772	Sequence 59772, A	773	12.2	67.8	601	3	US-09-949-016-20054	Sequence 20054, A
C 701	12.2	67.8	601	3	US-09-949-016-59773	Sequence 59773, A	774	12.2	67.8	601	3	US-09-949-016-20646	Sequence 20646, A
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C 706	12.2	67.8	601	3	US-09-949-016-62754	Sequence 62754, A	779	12.2	67.8	601	3	US-09-949-002-8156	Sequence 8156, A
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C 713	12.2	67.8	601	3	US-09-949-016-79853	Sequence 79853, A	786	12.2	67.8	601	3	US-09-533-559-5595	Sequence 5595, A
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C 841	12.2	67.8	1219	3	US-09-252-991A-7567	Sequence 166, App	C 914	12.2	67.8	2086	3	US-09-072-435-1	Sequence 1, Appl
C 842	12.2	67.8	1224	3	US-09-252-991A-10778	Sequence 7567, Ap	C 915	12.2	67.8	2089	3	US-10-104-047-1055	Sequence 1055, Ap
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C 856	12.2	67.8	1335	3	US-09-902-540-451	Sequence 451, App	C 929	12.2	67.8	2382	3	US-09-270-767-11211	Sequence 11211, A
C 857	12.2	67.8	1341	3	US-09-252-991A-16544	Sequence 16544, A	C 930	12.2	67.8	2406	3	US-09-252-991A-15562	Sequence 15562, A
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C 859	12.2	67.8	1381	3	US-09-270-767-10523	Sequence 10523, App	C 932	12.2	67.8	2538	3	US-10-104-047-1207	Sequence 1207, Ap
C 860	12.2	67.8	1386	3	US-09-602-777A-199	Sequence 199, App	C 933	12.2	67.8	2549	3	US-09-252-991A-15666	Sequence 15666, A
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C 868	12.2	67.8	1464	3	US-09-328-352-3361	Sequence 3361, Ap	C 941	12.2	67.8	2657	3	US-09-902-540-6188	Sequence 6188, Ap
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C 871	12.2	67.8	1485	2	US-08-446-380-3	Sequence 3, Appl	C 944	12.2	67.8	2758	3	US-09-221-017B-441	Sequence 441, App
C 872	12.2	67.8	1485	2	US-08-446-380-3	Sequence 3, Appl	C 945	12.2	67.8	2821	3	US-09-135-010A-115	Sequence 115, App
C 873	12.2	67.8	1485	2	US-08-446-382-3	Sequence 3, Appl	C 946	12.2	67.8	2821	3	US-09-597-735-115	Sequence 115, App
C 874	12.2	67.8	1485	2	US-08-446-382-3	Sequence 3, Appl	C 947	12.2	67.8	2821	3	US-09-597-732-115	Sequence 115, App
C 875	12.2	67.8	1485	2	US-08-275-487-3	Sequence 3, Appl	C 948	12.2	67.8	2821	3	US-09-597-731-115	Sequence 115, App
C 876	12.2	67.8	1485	2	US-09-252-991A-7612	Sequence 7612, Ap	C 949	12.2	67.8	2823	3	US-10-104-047-854	Sequence 854, App
C 877	12.2	67.8	1485	6	PCT-US95-08919-3	Sequence 3, Appl	C 950	12.2	67.8	2824	3	US-09-949-016-32	Sequence 32, Appl
C 878	12.2	67.8	1509	3	US-09-149-476-179	Sequence 179, App	C 951	12.2	67.8	2896	3	US-10-104-047-432	Sequence 432, App
C 879	12.2	67.8	1512	3	US-09-252-991A-1551	Sequence 1551, App	C 952	12.2	67.8	3029	2	US-08-275-488A-6	Sequence 6, Appl
C 880	12.2	67.8	1530	3	US-09-149-476-306	Sequence 306, App	C 953	12.2	67.8	3029	2	US-08-275-488A-6	Sequence 6, Appl
C 881	12.2	67.8	1530	3	US-09-902-540-9066	Sequence 9066, Ap	C 954	12.2	67.8	3029	2	US-08-446-380-6	Sequence 6, Appl
C 882	12.2	67.8	1620	2	US-08-275-488A-5	Sequence 5, Appl	C 955	12.2	67.8	3029	2	US-08-446-380-6	Sequence 6, Appl
C 883	12.2	67.8	1620	2	US-08-275-488A-5	Sequence 5, Appl	C 956	12.2	67.8	3029	2	US-08-446-380-6	Sequence 6, Appl
C 884	12.2	67.8	1620	2	US-08-446-380-5	Sequence 5, Appl	C 957	12.2	67.8	3029	2	US-08-446-380-6	Sequence 6, Appl
C 885	12.2	67.8	1620	2	US-08-446-380-5	Sequence 5, Appl	C 958	12.2	67.8	3029	2	US-08-446-380-6	Sequence 6, Appl
C 886	12.2	67.8	1620	2	US-08-446-380-5	Sequence 5, Appl	C 959	12.2	67.8	3029	6	PCT-US95-08919-6	Sequence 6, Appl
C 887	12.2	67.8	1620	2	US-08-445-801-5	Sequence 5, Appl	C 960	12.2	67.8	3133	3	US-09-193-069-1	Sequence 1, Appl
C 888	12.2	67.8	1620	2	US-08-275-487-5	Sequence 5, Appl	C 961	12.2	67.8	3133	3	US-09-973-278-829	Sequence 829, App
C 889	12.2	67.8	1620	6	PCT-US95-08919-5	Sequence 5, Appl	C 962	12.2	67.8	3181	3	US-09-135-021-1	Sequence 1, Appl
C 890	12.2	67.8	1659	3	US-09-252-991A-15717	Sequence 15717, A	C 963	12.2	67.8	3181	3	US-09-135-021-1	Sequence 1, Appl
C 891	12.2	67.8	1677	3	US-09-252-991A-1616	Sequence 1616, Ap	C 964	12.2	67.8	3181	3	US-09-135-021-1	Sequence 1, Appl
C 892	12.2	67.8	1686	3	US-09-902-540-9069	Sequence 9069, Ap	C 965	12.2	67.8	3181	3	US-09-444-871-1	Sequence 1, Appl
C 893	12.2	67.8	1686	3	US-09-252-991A-14463	Sequence 14463, Ap	C 966	12.2	67.8	3181	3	US-09-597-735-1	Sequence 1, Appl
C 894	12.2	67.8	1707	3	US-09-526-993-5	Sequence 5, Appl	C 967	12.2	67.8	3181	3	US-09-444-871-1	Sequence 1, Appl
C 895	12.2	67.8	1737	3	US-09-252-991A-7335	Sequence 7335, Ap	C 968	12.2	67.8	3181	3	US-09-597-735-1	Sequence 1, Appl
C 896	12.2	67.8	1753	3	US-09-634-338-403	Sequence 403, App	C 969	12.2	67.8	3182	3	US-09-597-735-1	Sequence 1, Appl
C 897	12.2	67.8	1762	3	US-09-265-383-2	Sequence 2, Appl	C 970	12.2	67.8	3182	3	US-09-135-021-5	Sequence 5, Appl
C 898	12.2	67.8	1771	3	US-09-270-767-12615	Sequence 12615, A	C 971	12.2	67.8	3196	3	US-09-221-017B-114	Sequence 314, App
C 899	12.2	67.8	1776	3	US-09-252-991A-12189	Sequence 12189, A	C 972	12.2	67.8	3196	3	US-09-704-449-1	Sequence 1, Appl
C 900	12.2	67.8	1806	3	US-09-252-991A-5253	Sequence 5253, Ap	C 973	12.2	67.8	3224	3	US-09-526-993-2	Sequence 2, Appl

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C 974 12.2 67.8 3352 3 US-10-101-464A-868 Sequence 868, App
C 975 12.2 67.8 3356 2 US-08-162-809-9 Sequence 9, Appl
C 976 12.2 67.8 3567 3 US-10-011-146-1 Sequence 1, Appl
C 977 12.2 67.8 3588 3 US-09-302-540-4681 Sequence 4681, Ap
C 978 12.2 67.8 3591 2 US-08-162-809-13 Sequence 13, Appl
C 979 12.2 67.8 3650 3 US-09-949-016-5637 Sequence 5637, Ap
C 980 12.2 67.8 3725 3 US-10-160-719A-13 Sequence 13, Appl
C 981 12.2 67.8 3725 3 US-10-160-719A-13 Sequence 13, Appl
C 982 12.2 67.8 3725 3 US-10-160-719A-41 Sequence 41, Appl
C 983 12.2 67.8 3725 3 US-10-209-059-45 Sequence 45, Appl
C 984 12.2 67.8 3768 3 US-09-332-5228-7 Sequence 7, Appl
C 985 12.2 67.8 3768 3 US-08-506-2968-20 Sequence 20, Appl
C 986 12.2 67.8 4345 3 US-09-949-016-2755 Sequence 2755, Ap
C 987 12.2 67.8 4380 3 US-08-955-565A-3 Sequence 3, Appl
C 988 12.2 67.8 4506 3 US-08-178-257-1 Sequence 1, Appl
C 989 12.2 67.8 4580 2 US-08-674-351-1 Sequence 8, Appl
C 990 12.2 67.8 4702 2 US-08-038-682-8 Sequence 8, Appl
C 991 12.2 67.8 4702 2 US-08-302-832-8 Sequence 8, Appl
C 992 12.2 67.8 4702 2 US-08-530-198-8 Sequence 8, Appl
C 993 12.2 67.8 4702 2 US-08-469-880-8 Sequence 8, Appl
C 994 12.2 67.8 4702 2 US-08-728-470-8 Sequence 8, Appl
C 995 12.2 67.8 4702 2 US-08-719-641-8 Sequence 8, Appl
C 996 12.2 67.8 4761 3 US-09-302-540-739 Sequence 739, App
C 997 12.2 67.8 4794 2 US-08-617-697-7 Sequence 7, Appl
C 998 12.2 67.8 4803 2 US-08-617-697-8 Sequence 8, Appl
C 999 12.2 67.8 4853 2 US-08-793-824-1 Sequence 1, Appl
C1000 12.2 67.8 4941 3 US-09-252-991A-5741 Sequence 5741, Ap
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## ALIGNMENTS

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RESULT 1
US-09-030-701-28/c
; Sequence 28, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
; TITLE OF INVENTION: UNMETHYLATED CPG DINUCLEOTIDE IN THE TREATMENT OF
; TITLE OF INVENTION: LPS-ASSOCIATED DISORDERS
; FILE REFERENCE: C1039/7011
; CURRENT APPLICATION NUMBER: US/09/030, 701B
; CURRENT FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/039, 405
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-030-701-28
```

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Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.7;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AGAGGGUCCGACCGCGUA 18
Db 18 AGAGGGTCCGACCGCGTA 1
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## RESULT 2

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US-09-286-098-60/c
; Sequence 60, Application US/09286098
; Patent No. 6218371
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Weiner, George
```

```
; TITLE OF INVENTION: Methods and Products for Stimulating the
; TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
; TITLE OF INVENTION: CYCOKINES
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/286, 098
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,729
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-286-098-60
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```
Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.7;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AGAGGGUCCGACCGCGUA 18
Db 18 AGAGGGTCCGACCGCGTA 1
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RESULT 3
US-08-960-774-60/c
; Sequence 60, Application US/08960774
; Patent No. 6239116
; GENERAL INFORMATION:
; APPLICANT: Krieg et al.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,774
; FILING DATE: 30-October-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial No. 6239116 08/738,652
; FILING DATE: October 30, 1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08918/012001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-960-774-60
```

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Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.7;
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Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCCACGCCGUA 18

Db 18 AGAGGUGCCACGCCGUA 1

RESULT 4  
US-09-191-170-54/c  
Sequence 54, Application US/09191170

Patent No. 6429199

GENERAL INFORMATION:

APPLICANT: Kriegl, Arthur M.

APPLICANT: Hartmann, Gunther

TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules

TITLE OF INVENTION: for Activating Dendritic Cells

FILE REFERENCE: C1039/7017

CURRENT APPLICATION NUMBER: US/09/191,170

EARLIER FILING DATE: 1998-11-13

EARLIER APPLICATION NUMBER: US 08/960,774

EARLIER FILING DATE: 1997-10-30

EARLIER APPLICATION NUMBER: US 08/738,652

EARLIER FILING DATE: 1996-10-30

EARLIER APPLICATION NUMBER: US 08/386,063

EARLIER FILING DATE: 1995-02-07

EARLIER APPLICATION NUMBER: US 08/276,358

EARLIER FILING DATE: 1994-07-15

NUMBER OF SEQ ID NOS: 99

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 54

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: synthetic oligonucleotide

US-09-191-170-54

Query Match

Best Local Similarity 100.0%; Score 18; DB 3; Length 18;

Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCCACGCCGUA 18

Db 18 AGAGGUGCCACGCCGUA 1

RESULT 5  
US-09-337-619-60/c  
Sequence 60, Application US/09337619

Patent No. 6653292

GENERAL INFORMATION:

APPLICANT: Kriegl, Arthur M.

TITLE OF INVENTION: Methods of Treating Cancer Using

FILE REFERENCE: C1039/7021/HCL

CURRENT APPLICATION NUMBER: US/09/337,619

EARLIER FILING DATE: 1999-06-21

EARLIER APPLICATION NUMBER: US 08/960,774

EARLIER FILING DATE: 1997-10-30

EARLIER APPLICATION NUMBER: US 08/738,652

EARLIER FILING DATE: 1996-10-30

EARLIER APPLICATION NUMBER: US 08/386,063

EARLIER FILING DATE: 1995-02-07

EARLIER APPLICATION NUMBER: US 08/276,358

NUMBER OF SEQ ID NOS: 123

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 60

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic Oligonucleotide

US-09-337-619-60

Query Match

Best Local Similarity 100.0%; Score 18; DB 3; Length 18;

Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCCACGCCGUA 18

Db 18 AGAGGUGCCACGCCGUA 1

RESULT 6  
US-09-954-987B-67/c

Sequence 67, Application US/09954987B

Patent No. 6943240

GENERAL INFORMATION:

APPLICANT: Stefan Bauer

APPLICANT: Grayson B. Lipford

APPLICANT: Hermann Wagner

TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF

FILE REFERENCE: C1041/7016 (AMS)

CURRENT APPLICATION NUMBER: US/09/954,987B

EARLIER FILING DATE: 2001-09-17

EARLIER APPLICATION NUMBER: US 60/233,035

EARLIER FILING DATE: 2000-09-15

EARLIER APPLICATION NUMBER: US 60/263,657

EARLIER FILING DATE: 2001-01-23

EARLIER APPLICATION NUMBER: US 60/291,726

EARLIER FILING DATE: 2001-05-17

EARLIER APPLICATION NUMBER: US 60/300,210

EARLIER FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 230

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 67

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic oligonucleotide

US-09-954-987B-67

Query Match

Best Local Similarity 100.0%; Score 18; DB 3; Length 18;

Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGCCACGCCGUA 18

Db 18 AGAGGUGCCACGCCGUA 1

RESULT 7  
US-08-465-485A-9/c

Sequence 9, Application US/08465485A

Patent No. 5831066

GENERAL INFORMATION:

APPLICANT: Reed, John

TITLE OF INVENTION: Regulation of bcl-2 Gene Expression

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSER: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

STREET: 1755 S. Jefferson Davis Hwy., Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:



APPLICATION NUMBER: US/08/465,485A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/124,256  
FILING DATE: 20-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/840,716  
FILING DATE: 21-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/288,692  
FILING DATE: 22-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Fortney, Andrew D.  
REGISTRATION NUMBER: 34,600  
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (408) 436-2070  
TELEFAX: (408) 436-2075  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ANTI-SENSE: YES  
US-08-465-485A-9

Query Match 94.4%; Score 17; DB 2; Length 17;  
Best Local Similarity 88.2%; Pred. No. 19;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GAGGGUCCGACGGCGUA 18  
Db 17 GAGGGTCGACGCGGTA 1

## RESULT 8

US-09-080-285-9/c  
Sequence 9, Application US/09080285  
Patent No. 6040181  
GENERAL INFORMATION:  
APPLICANT: Reed, John  
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
STEERT, 1755 S. Jefferson Davis Hwy., Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/080,285  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/465,485  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/124,256  
FILING DATE: 20-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/840,716  
FILING DATE: 21-FEB-1992  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/288,692  
FILING DATE: 22-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Fortney, Andrew D.  
REGISTRATION NUMBER: 34,600  
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (408) 436-2070  
TELEFAX: (408) 436-2075  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ANTI-SENSE: YES  
US-09-080-285-9

Query Match 94.4%; Score 17; DB 3; Length 17;  
Best Local Similarity 88.2%; Pred. No. 19;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GAGGGUCCGACGGCGUA 18  
Db 17 GAGGGTCGACGCGGTA 1

## RESULT 9

US-09-724-426-9/c  
Sequence 9, Application US/09724426  
Patent No. 6414134  
GENERAL INFORMATION:  
APPLICANT: Reed, John  
TITLE OF INVENTION: Regulation of BCL-2 Gene Expression  
FILE REFERENCE: 10412-024  
CURRENT APPLICATION NUMBER: US/09/724,426  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: Patent version 3.0  
SEQ ID NO 9  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-724-426-9

Query Match 94.4%; Score 17; DB 3; Length 17;  
Best Local Similarity 88.2%; Pred. No. 19;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GAGGGUCCGACGGCGUA 18  
Db 17 GAGGGTCGACGCGGTA 1

## RESULT 10

US-09-724-425-9/c  
Sequence 9, Application US/09724425  
Patent No. 6841541  
GENERAL INFORMATION:  
APPLICANT: Reed, John C.  
TITLE OF INVENTION: REGULATION OF BCL-2 GENE EXPRESSION  
FILE REFERENCE: 04040/1200990-US7  
CURRENT APPLICATION NUMBER: US/09/724,425  
CURRENT FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: US 09/375,514  
PRIOR FILING DATE: 1999-08-17  
PRIOR APPLICATION NUMBER: US 09/080,285  
PRIOR FILING DATE: 1998-05-18  
PRIOR APPLICATION NUMBER: US 08/465,485  
PRIOR FILING DATE: 1995-06-05  
PRIOR APPLICATION NUMBER: US 08/124,256  
PRIOR FILING DATE: 1993-09-20



PRIOR APPLICATION NUMBER: US 07/840,716  
PRIOR FILING DATE: 1992-02-21  
PRIOR APPLICATION NUMBER: US 07/288,692  
PRIOR FILING DATE: 1988-12-22  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 9  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-724-425-9

Query Match 94.4%; Score 17; DB 3; Length 17;  
Best Local Similarity 88.2%; Pred. No. 19;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGAGGUGGCACGCGUA 18  
17 AGAGGTCGACGCGTA 1

RESULT 11  
US-08-465-485A-8/c  
Sequence 8, Application US/08465485A  
Patent No. 5831066  
GENERAL INFORMATION:  
APPLICANT: Reed, John  
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
P.C.  
STREET: 1755 S. Jefferson Davis Hwy., Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,485A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/124,256  
FILING DATE: 20-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/840,716  
FILING DATE: 21-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/288,692  
FILING DATE: 22-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Fortney, Andrew D.  
REGISTRATION NUMBER: 34,600  
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (408) 436-2070  
TELEFAX: (408) 436-2075  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULAR TYPE: DNA (genomic)  
ANTI-SENSE: YES  
US-08-465-485A-8

Query Match 83.3%; Score 15; DB 2; Length 17;

Best Local Similarity 93.3%; Pred. No. 1.9e+02;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGGCACGCG 15  
15 AGAGGTCGACGCG 1

RESULT 12  
US-09-080-285-8/c  
Sequence 8, Application US/09080285  
Patent No. 6040181  
GENERAL INFORMATION:  
APPLICANT: Reed, John  
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
P.C.  
STREET: 1755 S. Jefferson Davis Hwy., Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/080,285  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/465,485  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/124,256  
FILING DATE: 20-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/840,716  
FILING DATE: 21-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/288,692  
FILING DATE: 22-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Fortney, Andrew D.  
REGISTRATION NUMBER: 34,600  
REFERENCE/DOCKET NUMBER: 3335-070-55, CONT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (408) 436-2070  
TELEFAX: (408) 436-2075  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULAR TYPE: DNA (genomic)  
ANTI-SENSE: YES  
US-09-080-285-8

Query Match 83.3%; Score 15; DB 3; Length 17;  
Best Local Similarity 93.3%; Pred. No. 1.9e+02;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUGGCACGCG 15  
15 AGAGGTCGACGCG 1

RESULT 13  
US-09-724-426-8/c

```

; Sequence 8, Application US/09724426
; Patent No. 6414134
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of BCL-2 Gene Expression
; FILE REFERENCE: 10412-024
; CURRENT APPLICATION NUMBER: US/09/724,426
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 8
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-724-426-8

Query Match      83.3%; Score 15; DB 3; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.9e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGAGGUGCGACGCG 15
Db      15 AGAGGTCGACGCG 1

RESULT 14
US-09-724-425-8/c
; Sequence 8, Application US/09724425
; Patent No. 6841541
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: REGULATION OF BCL-2 GENE EXPRESSION
; FILE REFERENCE: 04040/120090-US7
; CURRENT APPLICATION NUMBER: US/09/724,425
; CURRENT FILING DATE: 2000-11-28
; PRIOR FILING DATE: 1999-08-17
; PRIOR FILING DATE: 1998-05-18
; PRIOR FILING DATE: 1998-05-18
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/465,485
; PRIOR FILING DATE: 1993-09-20
; PRIOR APPLICATION NUMBER: US 07/840,716
; PRIOR FILING DATE: 1992-02-21
; PRIOR APPLICATION NUMBER: US 07/288,692
; PRIOR FILING DATE: 1988-12-22
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-724-425-8

Query Match      83.3%; Score 15; DB 3; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.9e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGAGGUGCGACGCG 15
Db      15 AGAGGTCGACGCG 1

RESULT 15
US-09-108-673A-25/c
; Sequence 25, Application US/09108673A
; Patent No. 6887906
; GENERAL INFORMATION:
; APPLICANT: Ching-Leou Teng and Greg Hardee
; TITLE OF INVENTION: Compositions and Methods for the Delivery of
; TITLE OF INVENTION: Oligonucleotides via the Alimentary Canal
; NUMBER OF SEQUENCES: 132
```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 6887906.ris LLP
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/108,673A
; FILING DATE: July 1, 1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/886,829
; FILING DATE: 01-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: 1SIS-3105
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568 3439
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; FEATURE:
; OTHER INFORMATION: Antisense to bcl-2 mRNA
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: WO 95/08350 (SEQ ID NO: 8)
; FILING DATE: 20-SEP-1994
; PUBLICATION DATE: 30-MAR-1995
; US-09-108-673A-25

Query Match      83.3%; Score 15; DB 3; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.9e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 AGAGGUGCGACGCG 15
Db      15 AGAGGTCGACGCG 1

RESULT 16
US-09-949-016-2432
; Sequence 2432, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2432
; LENGTH: 955
; TYPE: DNA
; ORGANISM: Human
```

US-09-949-016-2432

Query Match

Best Local Similarity 83.3%; Score 15; DB 3; Length 955;  
Pred. No. 1.8e+02; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGG 16

DB 134 GAGGTCGCACGCGG 148

RESULT 17

US-09-949-016-2433  
Sequence 2433, Application US/09949016  
Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATEDFILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2433

LENGTH: 955

TYPE: DNA

ORGANISM: Human

US-09-949-016-2433

Query Match

Best Local Similarity 83.3%; Score 15; DB 3; Length 955;  
Pred. No. 1.8e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGG 16

DB 134 GAGGTCGCACGCGG 148

RESULT 18

US-09-949-016-4795  
Sequence 4795, Application US/09949016  
Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATEDFILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4795

LENGTH: 2036

TYPE: DNA

ORGANISM: Human

US-09-949-016-4795

Query Match

Best Local Similarity 83.3%; Score 15; DB 3; Length 2036;  
Pred. No. 1.8e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGG 16

DB 134 GAGGTCGCACGCGG 148

RESULT 19

US-09-949-016-14174  
Sequence 14174, Application US/09949016  
Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATEDFILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 14174

LENGTH: 12993

TYPE: DNA

ORGANISM: Human

US-09-949-016-14174

Query Match

Best Local Similarity 83.3%; Score 15; DB 3; Length 12993;  
Pred. No. 1.8e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGGUCCGACGCGG 16

DB 2134 GAGGTCGCACGCGG 2148

RESULT 20

US-09-949-016-14175  
Sequence 14175, Application US/09949016  
Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATEDFILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 14175

LENGTH: 12993

TYPE: DNA

ORGANISM: Human

FEATURES:

NAME/KEY: misc\_feature

LOCATION: (1)...(12993)

OTHER INFORMATION: n = A,T,C or G

US-09-949-016-14175

Query Match 83.3%; Score 15; DB 3; Length 12993;  
Best Local Similarity 93.3%; Pred. No. 1.8e+02;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGGCG 16  
Db 2134 GAGGUGCGACGGCG 2148

RESULT 21  
US-09-949-016-16537  
Sequence 16537, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 16537  
LENGTH: 14587  
TYPE: DNA  
ORGANISM: Human  
FEATURES:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(14587)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-16537

Query Match 83.3%; Score 15; DB 3; Length 14587;  
Best Local Similarity 93.3%; Pred. No. 1.7e+02;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACGGCG 16  
Db 2134 GAGGUGCGACGGCG 2148

RESULT 22  
US-07-841-651-1/C  
Sequence 1, Application US/07841651  
Patent No. 5410031  
GENERAL INFORMATION:  
APPLICANT: Pajor, Ana M  
TITLE OF INVENTION: Cloning and Functional Expression of a  
Mammalian Na+/Nucleoside Cotransporter: A Member of the  
SGLT Family  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Sheldon E. Mak  
STREET: 225 South Lake Avenue, Ninth Floor  
CITY: Pasadena  
STATE: California  
COUNTRY: USA  
ZIP: 91101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/841,651  
FILING DATE: 19920224

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandel, Saralynn  
REGISTRATION NUMBER: 31,853  
REFERENCE/DOCKET NUMBER: 8772  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (818) 796-4000  
TELEFAX: (818) 795-6321  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2238 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Oryctolagus cuniculus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 7..2022  
US-07-841-651-1

Query Match 80.0%; Score 14.4; DB 2; Length 2238;  
Best Local Similarity 87.5%; Pred. No. 3.6e+02;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGGCG 16  
Db 1548 AGAGGUGCGACGGCG 1533

RESULT 23  
US-08-311-731A-138/C  
Sequence 138, Application US/08311731A  
Patent No. 6583266  
GENERAL INFORMATION:  
APPLICANT: SMITH, DOUGLAS  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES  
RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LARVAE FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 411  
CORRESPONDENCE ADDRESS:  
ADDRESSER: WOLF, GREENFIELD & SACKS, P.C.  
STREET: 600 ATLANTIC AVENUE  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/311,731A  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: GATES, EDWARD R.  
REGISTRATION NUMBER: 31,616  
REFERENCE/DOCKET NUMBER: C0044/7125  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/720-3500  
TELEFAX: 617/720-2441  
INFORMATION FOR SEQ ID NO: 138:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35961 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Mycobacterium leprae  
US-08-311-731A-138

Query Match  
Best Local Similarity 80.0%; Score 14.4; DB 3; Length 35961;  
Best Local Similarity 87.5%; Pred. No. 3.5e+02;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGG 16  
DB 1594 AGAGGCTCGACCGG 1579

RESULT 24  
US-09-952-060-31/c  
Sequence 31, Application US/09952060  
Patent No. 6733993  
GENERAL INFORMATION:  
APPLICANT: Emili, Emilio A.  
APPLICANT: Youil, Rima  
APPLICANT: Bett, Andrew J.  
APPLICANT: Chen, Ling  
APPLICANT: Kaslow, David C.  
APPLICANT: Shiver, John W.  
APPLICANT: Toner, Timothy J.  
APPLICANT: Casimiro, Danilo R.  
TITLE OF INVENTION: ENHANCED FIRST GENERATION ADENOVIRUS  
TITLE OF INVENTION: VACCINES EXPRESSING CODON OPTIMIZED HIV1-GAG, POL, NEF AND  
TITLE OF INVENTION: MODIFICATIONS  
FILE REFERENCE: 20747Y  
CURRENT APPLICATION NUMBER: US/09/952,060  
CURRENT FILING DATE: 2001-09-14  
PRIOR APPLICATION NUMBER: PCT/US01/28861  
PRIOR FILING DATE: 2001-09-14  
PRIOR APPLICATION NUMBER: 60/317,814  
PRIOR FILING DATE: 2001-09-07  
PRIOR APPLICATION NUMBER: 60/279,056  
PRIOR FILING DATE: 2001-03-27  
PRIOR APPLICATION NUMBER: 60/233,180  
PRIOR FILING DATE: 2000-09-15  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 31  
LENGTH: 36620  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Codon optimized DNA encoding pMRKADSHIV-1 nef,  
OTHER INFORMATION: noncoding  
US-09-952-060-31

Query Match  
Best Local Similarity 80.0%; Score 14.4; DB 3; Length 36620;  
Best Local Similarity 87.5%; Pred. No. 3.5e+02;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGG 16  
DB 25690 AGAGGCTCGACCGG 25675

RESULT 25  
US-09-952-060-26/c  
Sequence 26, Application US/09952060  
Patent No. 6733993  
GENERAL INFORMATION:  
APPLICANT: Emili, Emilio A.  
APPLICANT: Youil, Rima  
APPLICANT: Bett, Andrew J.  
APPLICANT: Chen, Ling  
APPLICANT: Kaslow, David C.

APPLICANT: Shiver, John W.  
APPLICANT: Toner, Timothy J.  
APPLICANT: Casimiro, Danilo R.  
TITLE OF INVENTION: ENHANCED FIRST GENERATION ADENOVIRUS  
TITLE OF INVENTION: VACCINES EXPRESSING CODON OPTIMIZED HIV1-GAG, POL, NEF AND  
TITLE OF INVENTION: MODIFICATIONS  
FILE REFERENCE: 20747Y  
CURRENT APPLICATION NUMBER: US/09/952,060  
CURRENT FILING DATE: 2001-09-14  
PRIOR APPLICATION NUMBER: PCT/US01/28861  
PRIOR FILING DATE: 2001-09-14  
PRIOR APPLICATION NUMBER: 60/317,814  
PRIOR FILING DATE: 2001-09-07  
PRIOR APPLICATION NUMBER: 60/279,056  
PRIOR FILING DATE: 2001-03-27  
PRIOR APPLICATION NUMBER: 60/233,180  
PRIOR FILING DATE: 2000-09-15  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 26  
LENGTH: 37474  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: DNA encoding pMRKAD5 HIV-1 gag, noncoding  
US-09-952-060-26

Query Match  
Best Local Similarity 80.0%; Score 14.4; DB 3; Length 37474;  
Best Local Similarity 87.5%; Pred. No. 3.5e+02;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGG 16  
DB 26555 AGAGGCTCGACCGG 26540

RESULT 26  
US-09-952-060-29/c  
Sequence 29, Application US/09952060  
Patent No. 6733993  
GENERAL INFORMATION:  
APPLICANT: Emili, Emilio A.  
APPLICANT: Youil, Rima  
APPLICANT: Bett, Andrew J.  
APPLICANT: Chen, Ling  
APPLICANT: Kaslow, David C.  
APPLICANT: Shiver, John W.  
APPLICANT: Toner, Timothy J.  
APPLICANT: Casimiro, Danilo R.  
TITLE OF INVENTION: ENHANCED FIRST GENERATION ADENOVIRUS  
TITLE OF INVENTION: VACCINES EXPRESSING CODON OPTIMIZED HIV1-GAG, POL, NEF AND  
TITLE OF INVENTION: MODIFICATIONS  
FILE REFERENCE: 20747Y  
CURRENT APPLICATION NUMBER: US/09/952,060  
CURRENT FILING DATE: 2001-09-14  
PRIOR APPLICATION NUMBER: PCT/US01/28861  
PRIOR FILING DATE: 2001-09-14  
PRIOR APPLICATION NUMBER: 60/317,814  
PRIOR FILING DATE: 2001-09-07  
PRIOR APPLICATION NUMBER: 60/279,056  
PRIOR FILING DATE: 2001-03-27  
PRIOR APPLICATION NUMBER: 60/233,180  
PRIOR FILING DATE: 2000-09-15  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 29  
LENGTH: 38519  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Codon optimized DNA encoding pMRKADSHIV-1 pol,  
OTHER INFORMATION: noncoding  
US-09-952-060-29

Query Match 80.0%; Score 14.4; DB 3; Length 36519;  
Best Local Similarity 87.5%; Pred. No. 3.5e+02;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUGCGCAGCGG 16  
DB 27589 AGAGGUGCGCAGCGG 27574

RESULT 27  
US-09-949-016-12147/c  
Sequence 12147, Application US/09949016

Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
PRIOR FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12147  
LENGTH: 767677  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(767677)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-12147

Query Match 80.0%; Score 14.4; DB 3; Length 767677;  
Best Local Similarity 93.8%; Pred. No. 3.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUGCGCAGCGG 16  
DB 516926 AGAGGUGCGCAGCGG 516911

RESULT 28  
US-09-949-016-17361/c  
Sequence 17361, Application US/09949016

Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
PRIOR FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 17361  
LENGTH: 767677  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature

LOCATION: (1)...(767677)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-17361

Query Match 80.0%; Score 14.4; DB 3; Length 767677;  
Best Local Similarity 93.8%; Pred. No. 3.1e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAGGUGCGCAGCGG 16  
DB 516926 AGAGGUGCGCAGCGG 516911

RESULT 29  
US-09-103-840A-2  
Sequence 2, Application US/09103840A

Patent No. 6294328  
GENERAL INFORMATION:  
APPLICANT: FLEISCHMAN, Robert D.  
APPLICANT: WHITE, Owen R.  
APPLICANT: FRASER, Claire M.  
APPLICANT: VENTER, John C.  
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
TUBERCULOSIS  
FILE REFERENCE: 24366-20007.00  
CURRENT APPLICATION NUMBER: US/09/103,840A  
PRIOR FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 4403765  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
FEATURE:  
OTHER INFORMATION: CDC 1551  
OTHER INFORMATION: "n" bases at various positions throughout the sequence  
OTHER INFORMATION: represent a, t, c or g  
US-09-103-840A-2

Query Match 80.0%; Score 14.4; DB 3; Length 4403765;  
Best Local Similarity 81.2%; Pred. No. 2.2e+02;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGUGCGCAGCGG 17  
DB 789126 GAGGUGCGCAGCGG 789141

RESULT 30  
US-09-103-840A-2/c  
Sequence 2, Application US/09103840A

Patent No. 6294328  
GENERAL INFORMATION:  
APPLICANT: FLEISCHMAN, Robert D.  
APPLICANT: WHITE, Owen R.  
APPLICANT: FRASER, Claire M.  
APPLICANT: VENTER, John C.  
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
TUBERCULOSIS  
FILE REFERENCE: 24366-20007.00  
CURRENT APPLICATION NUMBER: US/09/103,840A  
PRIOR FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 4403765  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
FEATURE:  
OTHER INFORMATION: CDC 1551  
OTHER INFORMATION: "n" bases at various positions throughout the sequence  
OTHER INFORMATION: represent a, t, c or g  
US-09-103-840A-2

Query Match 80.0%; Score 14.4; DB 3; Length 4403765;  
Best Local Similarity 87.5%; Pred. No. 2.2e+02;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGGCGCGACGCGGUA 18  
|||||  
DB 991739 AGGCGCGACGCGGTA 991724

RESULT 31  
US-09-103-840A-1  
; Sequence 1, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; FILE REFERENCE: 24366-20007.00  
; CURRENT FILING DATE: US/09/103,840A  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4411529  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; OTHER INFORMATION: H37Rv  
US-09-103-840A-1

Query Match 80.0%; Score 14.4; DB 3; Length 4411529;  
Best Local Similarity 81.2%; Pred. No. 2.2e+02;  
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GAGGCGCGACGCGGU 17  
|||||  
DB 787164 GAGGCGCGACGCGGT 787179

RESULT 32  
US-09-103-840A-1/c  
; Sequence 1, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; FILE REFERENCE: 24366-20007.00  
; CURRENT FILING DATE: US/09/103,840A  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4411529  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; OTHER INFORMATION: H37Rv  
US-09-103-840A-1

Query Match 80.0%; Score 14.4; DB 3; Length 4411529;  
Best Local Similarity 87.5%; Pred. No. 2.2e+02;  
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGGCGCGACGCGGUA 18  
|||||  
DB 991738 AGGCGCGACGCGGTA 991723

RESULT 33  
US-08-465-485A-10/c  
; Sequence 10, Application US/08465485A  
; Patent No. 5831066  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John  
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: P.C.  
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,485A  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/124,256  
FILING DATE: 20-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/840,716  
FILING DATE: 21-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/288,692  
FILING DATE: 22-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Portney, Andrew D.  
REGISTRATION NUMBER: 34,600  
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (408) 436-2070  
TELEFAX: (408) 436-2075  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ANTI-SENSE: YES  
US-08-465-485A-10

Query Match 77.8%; Score 14; DB 2; Length 17;  
Best Local Similarity 85.7%; Pred. No. 6.2e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCGCGACGCGGUA 18  
|||||  
DB 17 GCGCGACGCGGTA 4

RESULT 34  
US-09-080-285-10/c  
; Sequence 10, Application US/09080285  
; Patent No. 6040181  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John  
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: P.C.  
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400



CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/080,285  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/465,485  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/124,256  
FILING DATE: 20-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/840,716  
FILING DATE: 21-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/288,692  
FILING DATE: 22-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Fortney, Andrew D.  
REGISTRATION NUMBER: 34,600  
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (408) 436-2070  
TELEFAX: (408) 436-2075  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ANTI-SENSE: YES  
US-09-080-285-10

Query Match 77.8%; Score 14; DB 3; Length 17;  
Best Local Similarity 85.7%; Pred. No. 6.2e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGUCGACGCGGUA 18  
||:|||||||:  
Db 17 GGTCGACGCGGTA 4

RESULT 35  
US-09-724-426-10/c  
Sequence 10, Application US/09724426  
Patent No. 641134  
GENERAL INFORMATION:  
APPLICANT: Reed, John  
TITLE OF INVENTION: Regulation of BCL-2 Gene Expression  
FILE REFERENCE: 10412-024  
CURRENT APPLICATION NUMBER: US/09/724,426  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 10  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-724-426-10

Query Match 77.8%; Score 14; DB 3; Length 17;  
Best Local Similarity 85.7%; Pred. No. 6.2e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGUCGACGCGGUA 18  
||:|||||||:  
Db 17 GGTCGACGCGGTA 4

RESULT 36  
US-09-724-425-10/c  
Sequence 10, Application US/09724425  
Patent No. 6841541  
GENERAL INFORMATION:  
APPLICANT: Reed, John C.  
TITLE OF INVENTION: REGULATION OF BCL-2 GENE EXPRESSION  
FILE REFERENCE: 04040/1200990-US7  
CURRENT APPLICATION NUMBER: US/09/724,425  
CURRENT FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: US 09/375,514  
PRIOR FILING DATE: 1999-08-17  
PRIOR APPLICATION NUMBER: US 09/080,285  
PRIOR FILING DATE: 1998-05-18  
PRIOR APPLICATION NUMBER: US 08/465,485  
PRIOR FILING DATE: 1995-06-05  
PRIOR APPLICATION NUMBER: US 08/124,256  
PRIOR FILING DATE: 1993-09-20  
PRIOR APPLICATION NUMBER: US 07/840,716  
PRIOR FILING DATE: 1992-02-21  
PRIOR APPLICATION NUMBER: US 07/288,692  
PRIOR FILING DATE: 1988-12-22  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 10  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-724-425-10

Query Match 77.8%; Score 14; DB 3; Length 17;  
Best Local Similarity 85.7%; Pred. No. 6.2e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGUCGACGCGGUA 18  
||:|||||||:  
Db 17 GGTCGACGCGGTA 4

RESULT 37  
US-09-108-673A-26/c  
Sequence 26, Application US/09108673A  
Patent No. 6887906  
GENERAL INFORMATION:  
APPLICANT: Ching-Leou Teng and Greg Hardee  
TITLE OF INVENTION: Compositions and Methods for the Delivery of  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Woodcock Washburn Kurtz Mackiewicz & No. 6887906r1s LLP  
STREET: One Liberty Place, 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERECT 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/108,673A  
FILING DATE: July 1, 1998  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/886,829  
FILING DATE: 01-JUL-1997  
ATTORNEY/AGENT INFORMATION:

NAME: Paul K. Legard  
REGISTRATION NUMBER: 38,534  
REFERENCE/DOCKET NUMBER: ISIS-3105  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
FEATURE:  
OTHER INFORMATION: Antisense to bcl-2 mRNA  
PUBLICATION INFORMATION:  
DOCUMENT NUMBER: WO 95/08350 (SEQ ID NO: 9)  
FILING DATE: 20-SEP-1994  
PUBLICATION DATE: 30-MAR-1995  
US-09-108-673A-26

Query Match  
Best Local Similarity 77.8%; Score 14; DB 3; Length 17;  
Best Local Similarity 85.7%; Pred. No. 6.2e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGUGCGACCGCGUA 18  
DB 17 GGTCGCACGCGTA 4

RESULT 38  
US-09-108-673A-27/c  
Sequence 27, Application US/09108673A  
Patent No. 6887906  
GENERAL INFORMATION:  
APPLICANT: Ching-Leou Teng and Greg Hardee  
TITLE OF INVENTION: Compositions and Methods for the Delivery of  
TITLE OF INVENTION: Oligonucleotides Via the Alimentary Canal  
NUMBER OF SEQUENCES: 132  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 6887906ris LLP  
STREET: One Liberty Place, 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/108,673A  
FILING DATE: JULY 1, 1998  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/886,829  
FILING DATE: 01-JUL-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul K. Legard  
REGISTRATION NUMBER: 38,534  
REFERENCE/DOCKET NUMBER: ISIS-3105  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
FEATURE:

OTHER INFORMATION: Antisense to bcl-2 mRNA  
PUBLICATION INFORMATION:  
DOCUMENT NUMBER: WO 95/08350 (SEQ ID NO: 10)  
FILING DATE: 20-SEP-1994  
PUBLICATION DATE: 30-MAR-1995  
US-09-108-673A-27

Query Match  
Best Local Similarity 77.8%; Score 14; DB 3; Length 17;  
Best Local Similarity 85.7%; Pred. No. 6.2e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGUGCGACCGCGUA 18  
DB 17 GGTCGCACGCGTA 4

RESULT 39  
US-09-270-767-5572/c  
Sequence 5572, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5572  
LENGTH: 397  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
US-09-270-767-5572

Query Match  
Best Local Similarity 77.8%; Score 14; DB 3; Length 397;  
Best Local Similarity 92.9%; Pred. No. 5.9e+02;  
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACCGCG 15  
DB 34 GAGGTCGCACGCG 21

RESULT 40  
US-09-270-767-20854/c  
Sequence 20854, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 20854  
LENGTH: 397  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
US-09-270-767-20854

Query Match  
Best Local Similarity 77.8%; Score 14; DB 3; Length 397;  
Best Local Similarity 92.9%; Pred. No. 5.9e+02;  
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GAGGUGCGACCGCG 15  
DB 34 GAGGTCGCACGCG 21

RESULT 41  
US-09-676-519-19  
Sequence 19, Application US/09676519

Patent No. 6737508  
GENERAL INFORMATION:  
APPLICANT: PELLETER, JERRY  
APPLICANT: GROES, PHILIPPE  
APPLICANT: DUBOW, MICHAEL  
TITLE OF INVENTION: DNA SEQUENCES FROM STAPHYLOCOCCUS AUREUS BACTERIOPHAGES  
FILE REFERENCE: 073406-0404  
CURRENT FILING DATE: 2000-09-28  
CURRENT APPLICATION NUMBER: US/09/676,519  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: 60/110,992  
PRIOR FILING DATE: 1998-12-03  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 19  
LENGTH: 43576  
TYPE: DNA  
ORGANISM: Staphylococcus bacteriophage  
US-09-676-519-19

Query Match 76.7%; Score 13.8; DB 3; Length 43576;  
Best Local Similarity 92.9%; Pred. No. 5.5e+02;

Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGGUCGACGCGC 14  
|||||:|||||

DB 31337 AGAGGTCGACGCGC 31350

RESULT 42  
US-10-019-455A-15/C  
Sequence 15, Application US/10019455A  
Patent No. 6797483

GENERAL INFORMATION:  
APPLICANT: ITOH, YASUAKI  
APPLICANT: NISHI, KAZUORI  
APPLICANT: OGI, KAZUHIRO  
APPLICANT: OKUBO, SHOICHI  
APPLICANT: MOGI, SHINICHI  
APPLICANT: NOGUCHI, YUKO  
TITLE OF INVENTION: NOVEL PEPTIDE AND DNA THEREOF  
FILE REFERENCE: 56804-46342  
CURRENT APPLICATION NUMBER: US/10/019,455A  
CURRENT FILING DATE: 2002-04-22  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 24  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-019-455A-15

Query Match 76.7%; Score 13.8; DB 3; Length 24;  
Best Local Similarity 82.4%; Pred. No. 7.8e+02;

Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGGUCGACGCGGUA 18  
|||||:|||||

DB 16 GATGGGCGACGCGGTA 2

RESULT 43  
US-09-270-767-7758

Sequence 7758, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7758  
LENGTH: 335  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
FEATURE:  
OTHER INFORMATION: n means any nucleotide  
US-09-270-767-7758

Query Match 76.7%; Score 13.8; DB 3; Length 335;  
Best Local Similarity 76.5%; Pred. No. 7.5e+02;

Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGGUCGACGCGGUA 18  
|||||:|||||

DB 91 GAGATCGCACGCGATA 107

RESULT 44  
US-09-270-767-23040

Sequence 23040, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 23040  
LENGTH: 335  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
FEATURE:  
OTHER INFORMATION: n means any nucleotide  
US-09-270-767-23040

Query Match 76.7%; Score 13.8; DB 3; Length 335;  
Best Local Similarity 76.5%; Pred. No. 7.5e+02;

Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGGUCGACGCGGUA 18  
|||||:|||||

DB 91 GAGATCGCACGCGATA 107

RESULT 45  
US-09-513-999C-2747/C

Sequence 2747, Application US/09513999C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclert, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: 59, US2, REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 2747  
LENGTH: 364  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:

NAME/KEY: CDS  
LOCATION: 27..362  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 18  
OTHER INFORMATION: w=a or t  
US-09-513-999C-2747

Query Match 76.7%; Score 13.8; DB 3; Length 364;  
Best Local Similarity 76.5%; Pred. No. 7.4e+02;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GAGGGGCGCAGCGGUA 18  
DB 73 GAGGGTCCGCTCGGTA 57

RESULT 46

US-09-270-767-25712/C  
Sequence 25712, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 25712  
LENGTH: 523  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
US-09-270-767-25712

Query Match 76.7%; Score 13.8; DB 3; Length 523;  
Best Local Similarity 76.5%; Pred. No. 7.5e+02;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGU 17  
DB 151 AGGGGTCCAGCAGCGGT 135

RESULT 47

US-09-270-767-10334/C  
Sequence 10334, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 10334  
LENGTH: 600  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
US-09-270-767-10334

Query Match 76.7%; Score 13.8; DB 3; Length 600;  
Best Local Similarity 76.5%; Pred. No. 7.4e+02;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGU 17  
DB 228 AGTGGGTCCAGCAGCGGT 212

RESULT 48  
US-09-949-016-150767/C

Sequence 150767, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 150767  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-150767

Query Match 76.7%; Score 13.8; DB 3; Length 601;  
Best Local Similarity 76.5%; Pred. No. 7.4e+02;  
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGU 17  
DB 163 AGAGGTCCAGCAGCGGT 147

RESULT 49

US-09-252-991A-8441  
Sequence 8441, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 8441  
LENGTH: 1107  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-8441

Query Match 76.7%; Score 13.8; DB 3; Length 1107;  
Best Local Similarity 82.4%; Pred. No. 7.4e+02;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGAGGUGCGACGCGGU 17  
DB 1031 AGAAGGCGCAGCGGT 1047

RESULT 50

US-09-902-540-9637/C  
Sequence 9637, Application US/09902540  
Patent No. 6833447  
GENERAL INFORMATION:  
APPLICANT: Goldman, Barry S.  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Wiegand, Roger C.  
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849)B  
 ; CURRENT APPLICATION NUMBER: US/09/902,540  
 ; CURRENT FILING DATE: 2001-07-10  
 ; PRIOR APPLICATION NUMBER: 60/217,883  
 ; PRIOR FILING DATE: 2000-07-10  
 ; NUMBER OF SEQ ID NOS: 16825  
 ; SEQ ID NO 9637  
 ; LENGTH: 1236  
 ; TYPE: DNA  
 ; ORGANISM: Myxococcus xanthus  
 US-09-902-540-9637

Query Match 76.7%; Score 13.8; DB 3; Length 1236;  
 Best Local Similarity 82.4%; Pred. No. 7.4e+02;  
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 GAGGGGUGCGACGGCGGUA 18  
 Db 494 GTGGGGCGCACGGCGTA 478

Search completed: March 18, 2006, 18:39:20  
 Job time : 99.8846 secs

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 18:34:54 ; Search time 401.923 Seconds  
(without alignments)  
331.640 Million cell updates/sec

Title: US-10-800-926-3  
Perfect score: 20  
Sequence: 1 agguacagccagcagcagca 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 332346308 residues  
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : N Geneseq\_21:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*
- 14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	4	AAFP9262
2	20	100.0	20	6	ABSL7907
3	20	100.0	20	6	ABSL8704
4	20	100.0	20	9	ACD96963
5	20	100.0	20	9	ADB36764
6	20	100.0	20	13	ADU89707
7	20	100.0	20	14	ADW79936
8	18	90.0	5253	10	ABT40830
9	18	90.0	5253	13	ADV39876
10	16.8	84.0	720	3	AAZ50957
11	16.8	84.0	735	11	ABD09355
12	16.8	84.0	145068	13	ABD33090
13	16.4	82.0	246	3	AAFI0633
14	16.4	82.0	246	13	ADU54674
15	16.4	82.0	246	14	ADZ92677
16	16.4	82.0	1308	13	ADX13768
17	16.4	82.0	31632	9	ADA03035
18	16.4	82.0	31632	9	ADA65319
19	16.4	82.0	31632	10	ADB72773

20	16.4	82.0	96599	9	ADA02933	AdA02933 Mouse Bra
21	16.4	82.0	96599	10	ADB72671	AdB72671 Mouse Bra
22	16.4	82.0	96599	12	ADC85413	AdC85413 Mouse Bra
23	16.4	82.0	96599	10	ADM74528	AdM74528 Murine ca
24	16	80.0	2550	4	ABL20341	ABl20341 Drosophill
25	16	80.0	2668	4	ABL09903	ABl09903 Drosophill
26	16	80.0	4972	4	ABL20340	ABl20340 Drosophill
27	16	80.0	4989	4	ABL09902	ABl09902 Drosophill
28	16	80.0	90616	12	ADQ97596	AdQ97596 Mouse can
29	16	80.0	96599	10	ADC85298	AdC85298 Human Egr
30	16	80.0	96600	10	ADA02819	AdA02819 Mouse Sos
31	16	80.0	96600	12	ADB72557	AdB72557 Mouse Sos
32	16	80.0	96600	10	ADM74414	AdM74414 Murine ca
33	16	80.0	144411	12	ADP74214	AdP74214 Equine he
34	16	80.0	144486	12	ADP74215	AdP74215 Equine he
35	16	80.0	145444	12	ADP74213	AdP74213 Equine he
36	16	80.0	145596	12	ADP74202	AdP74202 Equine he
37	16	80.0	241748	14	ADZ13116	AdZ13116 Murine ca
38	15.8	79.0	411	11	ABD15945	ABd15945 Pseudomon
39	15.8	79.0	537	11	ABD16211	ABd16211 Pseudomon
40	15.8	79.0	542	5	ABV15922	ABv15922 Human pro
41	15.8	79.0	592	5	ABV45722	ABv45722 Human pro
42	15.8	79.0	693	5	AA889740	AA889740 DNA encod
43	15.8	79.0	978	4	ABL04139	ABl04139 Drosophill
44	15.8	79.0	1023	13	AD514617	ADs14617 Pseudomon
45	15.8	79.0	1044	11	ABD16472	ABd16472 Pseudomon
46	15.8	79.0	1057	3	AAZ61623	AAz61623 cDNA enco
47	15.8	79.0	1057	4	AA899556	AA899556 Skin cell
48	15.8	79.0	1057	6	ABL34708	ABl34708 Rat cDNA
49	15.8	79.0	1452	11	ABD16075	ABd16075 Pseudomon
50	15.8	79.0	1890	4	AA899799	AA899799 Skin cell
51	15.8	79.0	1890	6	ABL34951	ABl34951 Rat cDNA
52	15.8	79.0	2004	3	AAZ61757	AAz61757 cDNA enco
53	15.8	79.0	2004	4	AA899690	AA899690 Skin cell
54	15.8	79.0	2004	6	ABL34842	ABl34842 Rat cDNA
55	15.8	79.0	2040	4	AAH16586	AAh16586 Human cDN
56	15.8	79.0	2412	8	ACA47376	ACa47376 Prokaryot
57	15.8	79.0	2550	11	ABD16350	ABd16350 Pseudomon
58	15.8	79.0	2704	4	AA833172	AA833172 DNA encod
59	15.8	79.0	3265	4	ABL04138	ABl04138 Drosophill
60	15.8	79.0	15051	4	ABL03732	ABl03732 Drosophill
61	15.8	79.0	19183	4	AAK64938	AAk64938 Human imm
62	15.8	79.0	19183	4	ABL36434	ABl36434 Human mus
63	15.8	79.0	19183	8	ABX59422	ABx59422 Human mus
64	15.8	79.0	19183	12	AD030172	AD030172 Human mus
65	15.8	79.0	43256	12	ADQ97736	AdQ97736 Mouse can
66	15.4	77.0	249	11	ABD17329	ABd17329 Pseudomon
67	15.4	77.0	448	3	AAZ93530	AAz93530 Expanstin
68	15.4	77.0	1286	13	ADZ77960	AdZ77960 Plant ful
69	15.4	77.0	1353	13	ADT42162	Adt42162 Bacterial
70	15.4	77.0	1367	9	ADA03078	AdA03078 Mouse mCG
71	15.4	77.0	1367	9	ADA65362	AdA65362 Mouse mCG
72	15.4	77.0	1367	10	ADB72816	AdB72816 Mouse mCG
73	15.4	77.0	1367	10	ADC26998	AdC26998 Mouse mCG
74	15.4	77.0	1367	11	ADZ27156	AdZ27156 Mouse can
75	15.4	77.0	1515	9	ADA03082	AdA03082 Human PRD
76	15.4	77.0	1515	9	ADA65366	AdA65366 Human PRD
77	15.4	77.0	1515	10	ADH72820	ADh72820 Human PRD
78	15.4	77.0	1515	10	ADC27002	ADc27002 Human car
79	15.4	77.0	1515	11	AD127160	AD127160 Human cod
80	15.4	77.0	1837	14	ADZ25585	AdZ25585 Mouse ubl
81	15.4	77.0	2111	5	ABV27899	ABv27899 Human pro
82	15.4	77.0	2111	5	ABV22063	ABv22063 Human pro
83	15.4	77.0	2129	4	ABA88920	ABa88920 Escherich
84	15.4	77.0	2208	9	ADA03081	AdA03081 Human PRD
85	15.4	77.0	2208	9	ADA65365	AdA65365 Human PRD
86	15.4	77.0	2208	10	ADB72819	AdB72819 Human PRD
87	15.4	77.0	2208	10	ADC27001	ADc27001 Human car
88	15.4	77.0	2208	10	AD50280	Ad50280 Human PFM
89	15.4	77.0	2208	11	AD127159	AD127159 Human cDN
90	15.4	77.0	3504	9	ADA03079	AdA03079 Mouse mCG
91	15.4	77.0	3504	9	ADA65363	AdA65363 Mouse mCG
92	15.4	77.0	3504	10	ADB72817	AdB72817 Mouse mCG

93	15.4	77.0	3504	10	ADC26999	Adc26999	Mouse	cat	c 166	15.2	76.0	2673	4	AA552580	AA552580 E. coli D
94	15.4	77.0	3504	11	ADL27157	Adl27157	Mouse	cod	c 167	15.2	76.0	2673	8	ACA18973	ACA18973 Prokaryot
95	15.4	77.0	8210	6	ABK92506	Abk92506	Human	pro	c 168	15.2	76.0	2673	10	ADP48813	ADP48813 Bacteriell
96	15.4	77.0	9511	2	AAQ38221	Aaq38221	NAMHB	vir	c 169	15.2	76.0	2730	13	ACF70806	ACF70806 Photocarb
97	15.4	77.0	26565	6	ABR78924	Ab78924	E. coli	C	c 170	15.2	76.0	2832	4	ABL07249	ABL07249 Drosophill
98	15.4	77.0	26565	10	ADH80491	Adh80491	Escherich		c 171	15.2	76.0	3013	4	ABL07332	ABL07332 Drosophill
99	15.4	77.0	27920	11	ACN44776	Acn44776	Mouse	gen	c 172	15.2	76.0	3636	4	ABL08950	ABL08950 Drosophill
100	15.4	77.0	28956	9	ADA02963	Ada02963	Mouse	lck	c 173	15.2	76.0	3637	4	ABL08950	ABL08950 Drosophill
101	15.4	77.0	28956	10	ADH72701	Adh72701	Mouse	lck	c 174	15.2	76.0	4181	4	ABL11702	ABL11702 Drosophill
102	15.4	77.0	28956	10	ADH72701	Adh72701	Mouse	lck	c 175	15.2	76.0	5004	4	ABL18692	ABL18692 Drosophill
103	15.4	77.0	28956	12	ADM74558	Adm74558	Murine	ca	c 176	15.2	76.0	6240	4	ABL06443	ABL06443 Drosophill
104	15.4	77.0	28956	12	ADM74558	Adm74558	Murine	ca	c 177	15.2	76.0	6970	6	ABL14623	ABL14623 Drosophill
105	15.4	77.0	47322	13	ABD33395	Abd33395	Murine	ca	c 178	15.2	76.0	6970	6	ABL14623	ABL14623 Drosophill
106	15.4	77.0	63626	10	ADC27000	Adc27000	Human	cat	c 179	15.2	76.0	9933	4	ABL06442	ABL06442 Drosophill
107	15.4	77.0	63720	9	ADA03080	Ada03080	Human	PRD	c 180	15.2	76.0	10200	4	ABL14622	ABL14622 Drosophill
108	15.4	77.0	63720	9	ADA03080	Ada03080	Human	PRD	c 181	15.2	76.0	10397	4	ABL14362	ABL14362 Drosophill
109	15.4	77.0	63720	10	ADB72818	Adb72818	Human	PRD	c 182	15.2	76.0	10397	4	ABL14362	ABL14362 Drosophill
110	15.4	77.0	63908	11	ADL27158	Adl27158	Human	gen	c 183	15.2	76.0	14820	4	AA546246	AA546246 Drosophill
111	15.4	77.0	63915	11	ACN44660	Acn44660	Mouse	mCG	c 184	15.2	76.0	21437	13	ABD33476	ABD33476 Drosophill
112	15.4	77.0	90442	9	ADA66361	Ada66361	Mouse	mCG	c 185	15.2	76.0	21437	14	ABL07248	ABL07248 Drosophill
113	15.4	77.0	90442	9	ADA66361	Ada66361	Mouse	mCG	c 186	15.2	76.0	21966	4	ABD33264	ABD33264 Human can
114	15.4	77.0	90442	10	ADB72815	Adb72815	Mouse	mCG	c 187	15.2	76.0	21966	4	ABD33264	ABD33264 Human can
115	15.4	77.0	90442	10	ADC26997	Adc26997	Mouse	cat	c 188	15.2	76.0	41061	13	ADP90165	ADP90165 Human gen
116	15.4	77.0	90442	11	ADL27155	Adl27155	Mouse	gen	c 189	15.2	76.0	46649	10	ADP90165	ADP90165 Human gen
117	15.4	77.0	110000	11	ACN43984	Acn43984	Mouse	gen	c 190	15.2	76.0	46649	10	ADP90165	ADP90165 Human gen
118	15.4	77.0	165221	11	ACN44524	Acn44524	Murine	ca	c 191	15.2	76.0	52287	13	ADU50859	ADU50859 Human thl
119	15.4	77.0	165799	11	ADZ13004	Adz13004	Murine	ca	c 192	15.2	76.0	52287	14	ADZ42275	ADZ42275 Human thl
120	15.4	77.0	173810	6	ABN85752	Abn85752	Mouse	chr	c 193	15.2	76.0	58687	12	ADQ97534	ADQ97534 Mouse can
121	15.2	76.0	390	12	ADP28781	Adp28781	Human	sec	c 194	15.2	76.0	76410	11	ACN43894	ACN43894 Human gen
122	15.2	76.0	390	12	ADP28781	Adp28781	Human	sec	c 195	15.2	76.0	80557	6	ABX09142	ABX09142 Mycobacte
123	15.2	76.0	393	6	ABK75698	Abk75698	Bacillue		c 196	15.2	76.0	87331	11	ACN44038	ACN44038 Human apo
124	15.2	76.0	419	5	ABV26657	Abv26657	Human	pro	c 197	15.2	76.0	100137	12	AAI99682	AAI99682 Human gen
125	15.2	76.0	419	5	ABV26657	Abv26657	Human	pro	c 198	15.2	76.0	100137	12	AAI99682	AAI99682 Human gen
126	15.2	76.0	433	5	ABV10446	Abv10446	Human	pro	c 199	15.2	76.0	110000	4	AAI99683	AAI99683 Human gen
127	15.2	76.0	433	5	ABV10446	Abv10446	Human	pro	c 200	15.2	76.0	110000	6	ABX08336	ABX08336 Human gen
128	15.2	76.0	468	5	ABV31616	Abv31616	Human	pro	c 201	15.2	76.0	110000	10	ACPF67367	ACPF67367 Human gen
129	15.2	76.0	476	9	ACH43255	Ach43255	Human	foe	c 202	15.2	76.0	110000	10	ACPF67367	ACPF67367 Human gen
130	15.2	76.0	546	11	ABD16480	Abd16480	Pseudomon		c 203	15.2	76.0	110000	10	ACPF67367	ACPF67367 Human gen
131	15.2	76.0	577	12	ADB28782	Adb28782	Human	sec	c 204	15.2	76.0	110000	12	ADJ25985	ADJ25985 Human gen
132	15.2	76.0	577	12	ADB28782	Adb28782	Human	sec	c 205	15.2	76.0	110000	12	ADJ25985	ADJ25985 Human gen
133	15.2	76.0	598	6	ABN65119	Abn65119	Human	can	c 206	15.2	76.0	110000	12	ADN97989	ADN97989 Human gen
134	15.2	76.0	807	10	ABN28804	Abn28804	N. gonorr		c 207	15.2	76.0	110000	12	ADN97989	ADN97989 Human gen
135	15.2	76.0	813	13	AAZ54114	Aaz54114	Neisseria		c 208	15.2	76.0	110000	14	ABE85185	ABE85185 Human gen
136	15.2	76.0	816	12	ADP28783	Adp28783	Human	sec	c 209	15.2	76.0	118544	12	ADQ97100	ADQ97100 Human gen
137	15.2	76.0	828	10	ABX38805	Abx38805	N. gonorr		c 210	15.2	76.0	148697	12	ADL08108	ADL08108 Human gen
138	15.2	76.0	924	2	AAH33554	Aah33554	Rice	beta	c 211	15.2	76.0	241748	14	ADZ13116	ADZ13116 Murine ca
139	15.2	76.0	933	4	AAH31763	Aah31763	Human	OLF	c 212	15.2	76.0	249999	8	ABE80229	ABE80229 Human tra
140	15.2	76.0	936	5	AAZ42418	Aaz42418	Human	CDN	c 213	15.2	76.0	383	2	AAQ39782	AAQ39782 Human bra
141	15.2	76.0	936	5	AAZ42418	Aaz42418	Human	CDN	c 214	15.2	76.0	383	2	AAQ39782	AAQ39782 Human bra
142	15.2	76.0	936	5	AAZ42418	Aaz42418	Human	CDN	c 215	15.2	76.0	383	2	AAQ39782	AAQ39782 Human bra
143	15.2	76.0	937	6	ABK37704	Abk37704	DNA	encod	c 216	15.2	76.0	540	12	ACH78325	ACH78325 Human gen
144	15.2	76.0	939	10	ABZ77887	Abz77887	Human	G P	c 217	15.2	76.0	540	12	ACH78325	ACH78325 Human gen
145	15.2	76.0	939	10	ABZ77887	Abz77887	Human	G P	c 218	15.2	76.0	540	12	ACH78325	ACH78325 Human gen
146	15.2	76.0	942	6	AAD28707	Aad28707	Human	G-P	c 219	15.2	76.0	540	12	ACH78325	ACH78325 Human gen
147	15.2	76.0	1035	2	AAH33564	Aah33564	Rice	Gns2	c 220	15.2	76.0	540	12	ACH78325	ACH78325 Human gen
148	15.2	76.0	1060	14	AE655645	Ae655645	Rice	geno	c 221	15.2	76.0	540	12	ACH78325	ACH78325 Human gen
149	15.2	76.0	1125	13	ADK31234	Adk31234	Plant	full	c 222	15.2	76.0	540	12	ACH78325	ACH78325 Human gen
150	15.2	76.0	1207	12	ADN60386	Adn60386	B. lichen		c 223	15.2	76.0	540	12	ACH78325	ACH78325 Human gen
151	15.2	76.0	1336	10	ADC86048	Adc86048	Human	GPC	c 224	15.2	76.0	540	12	ACH78325	ACH78325 Human gen
152	15.2	76.0	1351	10	ABX17879	Abx17879	Human	GPC	c 225	15.2	76.0	540	12	ACH78325	ACH78325 Human gen
153	15.2	76.0	1380	4	ABL21703	AbL21703	Drosophill		c 226	15.2	76.0	540	12	ACH78325	ACH78325 Human gen
154	15.2	76.0	1401	13	ADT48137	Adt48137	Bacteriell		c 227	15.2	76.0	540	12	ACH78325	ACH78325 Human gen
155	15.2	76.0	1447	4	ABL08951	AbL08951	Drosophill		c 228	15.2	76.0	540	12	ACH78325	ACH78325 Human gen
156	15.2	76.0	1449	5	AA55077	AA55077	DNA	encod	c 229	15.2	76.0	540	12	ACH78325	ACH78325 Human gen
157	15.2	76.0	1485	8	ADA70022	Ada70022	Rice	gene	c 230	15.2	76.0	540	12	ACH78325	ACH78325 Human gen
158	15.2	76.0	1485	12	ADU39593	Adu39593	Plant	CDN	c 231	15.2	76.0	540	12	ACH78325	ACH78325 Human gen
159	15.2	76.0	1521	11	ABD16222	Abd16222	Pseudomon		c 232	15.2	76.0	540	12	ACH78325	ACH78325 Human gen
160	15.2	76.0	1596	11	ABD15934	Abd15934	Pseudomon		c 233	15.2	76.0	540	12	ACH78325	ACH78325 Human gen
161	15.2	76.0	1803	8	ACA43814	AcA43814	Prokaryot		c 234	15.2	76.0	540	12	ACH78325	ACH78325 Human gen
162	15.2	76.0	1812	13	AD556727	Ad556727	Bacteriell		c 235	15.2	76.0	540	12	ACH78325	ACH78325 Human gen
163	15.2	76.0	2153	12	ADN60386	Adn60386	B. lichen		c 236	15.2	76.0	540	12	ACH78325	ACH78325 Human gen
164	15.2	76.0	2230	12	AAH33530	Aah33530	Rice	Beta	c 237	15.2	76.0	540	12	ACH78325	ACH78325 Human gen
165	15.2	76.0	2278	4	ABL18693	AbL18693	Drosophill		c 238	15.2	76.0	540	12	ACH78325	ACH78325 Human gen



C 239	15	75.0	110000	2	AAV21209.13	Continuation (14 o	312	14.8	74.0	1327	10	ADG63542	AdG63542 Human EST
240	15	75.0	110000	12	ADN47591_00	AdA47591 Thymococ	313	14.8	74.0	1327	10	ADG66642	AdG66642 Human EST
241	15	75.0	110000	12	ADN47209_00	AdA47209 Thymococ	314	14.8	74.0	1327	10	ADG68766	AdG68766 Human EST
242	15	75.0	110000	12	ADN47960_00	AdA47960 Thymococ	315	14.8	74.0	1327	10	ADG62826	AdG62826 Human EST
C 243	15	75.0	130427	13	ADV35011	AdV35011 Murine CD	316	14.8	74.0	1327	10	ADG67891	AdG67891 Human EST
244	15	75.0	174424	6	ABL68122	AbL68122 Ovary can	317	14.8	74.0	1327	10	ADG64121	AdG64121 Human EST
245	15	75.0	181343	12	ADQ19573	AdQ19573 Human sof	318	14.8	74.0	1327	10	ADG62266	AdG62266 Human EST
C 246	15	75.0	203070	11	ACN44012	ACN44012 Mouse gen	319	14.8	74.0	1327	10	ADG62202	AdG62202 Human EST
C 247	15	75.0	349980	5	AAE66431	AAE66431 Pyrococu	320	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
248	14.8	74.0		6	AAE65668	AAE65668 Human map	321	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
249	14.8	74.0		6	ABN44229	ABN44229 Human sp1	322	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
C 250	14.8	74.0	122	4	AAH69048	AAH69048 Human cer	323	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
C 251	14.8	74.0	142	5	ABV14161	ABV14161 Human pro	324	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
C 252	14.8	74.0	143	4	AAI24766	AAI24766 Human bre	325	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
C 253	14.8	74.0	156	6	ABV96778	ABV96778 Human pen	326	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
C 254	14.8	74.0	225	5	ABV35255	ABV35255 Human pro	327	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
C 255	14.8	74.0	306	5	ABV04992	ABV04992 Human pro	328	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
256	14.8	74.0	374	3	AAE09681	AAE09681 Human sec	329	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
257	14.8	74.0	319	5	ABV62097	ABV62097 Human pro	330	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
258	14.8	74.0	319	5	ABV61963	ABV61963 Human pro	331	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
259	14.8	74.0	319	5	ABV62161	ABV62161 Human pro	332	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
260	14.8	74.0	373	4	AAE39292	AAE39292 Novel hum	333	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
261	14.8	74.0	383	6	ABV94272	ABV94272 Breast ca	334	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
C 262	14.8	74.0	400	13	ADU14457	ADU14457 Solid tum	335	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
C 263	14.8	74.0	413	8	ACA57174	ACA57174 Human adi	336	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
C 264	14.8	74.0	442	10	ACD92577	ACD92577 Human col	337	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
265	14.8	74.0	452	5	AAE85751	AAE85751 DNA encod	338	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
266	14.8	74.0	453	8	ABX44179	ABX44179 Bovine ES	339	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
267	14.8	74.0	470	5	AAE85750	AAE85750 DNA encod	340	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
268	14.8	74.0	477	6	ABV94827	ABV94827 Human pan	341	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
C 269	14.8	74.0	493	9	ADF79945	ADF79945 Leukaemia	342	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
270	14.8	74.0	498	9	ACH45106	ACH45106 Human foe	343	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
271	14.8	74.0	527	11	ACN86393	ACN86393 Breast ca	344	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
C 272	14.8	74.0	539	3	AAE76755	AAE76755 Human ORF	345	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
C 273	14.8	74.0	569	13	ADG50581	ADG50581 Novel can	346	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
C 274	14.8	74.0	584	4	AAE52546	AAE52546 Human ova	347	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
C 275	14.8	74.0	669	14	AEA33895	AEA33895 DNA encod	348	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
276	14.8	74.0	672	10	ADG76022	ADG76022 DNA homol	349	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
277	14.8	74.0	707	10	ADK5393	ADK5393 Plant DNA	350	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
278	14.8	74.0	708	4	ADL13115	ADL13115 Human mem	351	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
279	14.8	74.0	708	12	ADJ10374	ADJ10374 Human cel	352	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
280	14.8	74.0	708	12	ADJ10374	ADJ10374 Human cel	353	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
281	14.8	74.0	714	8	ADA50521	ADA50521 Human pro	354	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
C 282	14.8	74.0	775	4	AAH04875	AAH04875 Human CDN	355	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
283	14.8	74.0	796	6	ABK30337	ABK30337 Human G-P	356	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
284	14.8	74.0	810	6	ABG94226	ABG94226 FLO11 gen	357	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
C 285	14.8	74.0	884	2	AAZ41356	AAZ41356 Human nor	358	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
C 286	14.8	74.0	957	5	AAE76824	AAE76824 DNA encod	359	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
C 287	14.8	74.0	966	3	AAE62320	AAE62320 Arabidops	360	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
C 288	14.8	74.0	969	3	AAE35676	AAE35676 Arabidops	361	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
C 289	14.8	74.0	1016	7	ADK04583	ADK04583 Human pho	362	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
C 290	14.8	74.0	1052	8	ADL48772	ADL48772 Mouse kal	363	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
291	14.8	74.0	1122	10	ADB37681	ADB37681 Anti-RNA	364	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
292	14.8	74.0	1173	11	ABD07557	ABD07557 Pseudomon	365	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
293	14.8	74.0	1173	14	ACT170547	ACT170547 M. xanthu	366	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
C 294	14.8	74.0	1278	12	ADP07647	ADP07647 Human sec	367	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
295	14.8	74.0	1278	10	ADP07647	ADP07647 Human sec	368	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
296	14.8	74.0	1323	4	AAI90399	AAI90399 Human NOV	369	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
297	14.8	74.0	1327	2	AAZ34034	AAZ34034 Human pol	370	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
298	14.8	74.0	1327	3	AAE78495	AAE78495 Human EST	371	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
299	14.8	74.0	1327	3	AAE78495	AAE78495 Human EST	372	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
300	14.8	74.0	1327	8	AAE58237	AAE58237 Human EST	373	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
301	14.8	74.0	1327	8	AAE63602	AAE63602 Novel hum	374	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
302	14.8	74.0	1327	8	AAE63602	AAE63602 Novel hum	375	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
303	14.8	74.0	1327	8	AAE63602	AAE63602 Novel hum	376	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
304	14.8	74.0	1327	8	AAE63602	AAE63602 Novel hum	377	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
305	14.8	74.0	1327	9	AAE63602	AAE63602 Novel hum	378	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
306	14.8	74.0	1327	9	AAE63602	AAE63602 Novel hum	379	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
307	14.8	74.0	1327	9	AAE63602	AAE63602 Novel hum	380	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
308	14.8	74.0	1327	9	AAE63602	AAE63602 Novel hum	381	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
309	14.8	74.0	1327	10	AAE63602	AAE63602 Novel hum	382	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
310	14.8	74.0	1327	10	AAE63602	AAE63602 Novel hum	383	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST
311	14.8	74.0	1327	10	AAE63602	AAE63602 Novel hum	384	14.8	74.0	1327	10	ADG61835	AdG61835 Human EST

385	14.8	74.0	2056	6	ABV94273	Breast c8	458	14.8	74.0	3143	12	ADP23503	Adf23503 Human CDN
386	14.8	74.0	2056	10	ADP81427	Adf81427 Leukemia	459	14.8	74.0	3143	12	ADP23486	Adf23486 Human CDN
387	14.8	74.0	2068	5	AA844943	AA844943 CDNA enco	460	14.8	74.0	3143	12	ADP26953	Adf26953 Human CDN
388	14.8	74.0	2079	5	AA844942	AA844942 CDNA enco	461	14.8	74.0	3143	12	ADP27589	Adf27589 Human CDN
389	14.8	74.0	2085	13	AD549931	Ad549931 Bacterial	462	14.8	74.0	3143	12	ADP41183	Adf41183 Human CDN
390	14.8	74.0	2095	8	ABX63665	ABX63665 Human CDN	463	14.8	74.0	3143	12	ADP32862	Adf32862 Human CDN
391	14.8	74.0	2098	5	AA844944	AA844944 CDNA enco	464	14.8	74.0	3143	12	ADP25228	Adf25228 Human CDN
392	14.8	74.0	2217	11	ACL30450	ACL30450 Rice ablo	465	14.8	74.0	3143	12	ADP26329	Adf26329 Human CDN
393	14.8	74.0	2238	10	ACC69003	ACC69003 Human neu	466	14.8	74.0	3143	12	ADP34118	Adf34118 Human CDN
394	14.8	74.0	2328	11	ACL30010	ACL30010 Rice ablo	467	14.8	74.0	3143	12	ADP46355	Adf46355 Human CDN
395	14.8	74.0	2356	6	ABZ11172	ABZ11172 Human mem	468	14.8	74.0	3143	12	ADG50341	Adg50341 Human CDN
396	14.8	74.0	2356	12	ADM43690	ADM43690 Novel hum	469	14.8	74.0	3143	12	ADG59717	Adg59717 Human CDN
397	14.8	74.0	2409	6	ABK31797	ABK31797 DNA enco	470	14.8	74.0	3143	12	ADG549717	Adg549717 Human CDN
398	14.8	74.0	2503	2	AA055347	AA055347 Sequence	471	14.8	74.0	3143	12	ADG48469	Adg48469 Human CDN
399	14.8	74.0	2587	12	ADQ67506	ADQ67506 Novel hum	472	14.8	74.0	3143	12	ADG49093	Adg49093 Human CDN
400	14.8	74.0	2587	4	AB112987	AB112987 Drosophill	473	14.8	74.0	3143	12	ADG50965	Adg50965 Human CDN
401	14.8	74.0	2672	4	AD110378	AD110378 Human mem	474	14.8	74.0	3143	12	ADG58909	Adg58909 Human CDN
402	14.8	74.0	2672	10	AD110378	AD110378 Human cel	475	14.8	74.0	3143	12	ADG62365	Adg62365 Human CDN
403	14.8	74.0	2706	12	ADJ46902	ADJ46902 Human tra	476	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
404	14.8	74.0	2706	13	ADT43813	ADT43813 Bacterial	477	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
405	14.8	74.0	2801	6	ABQ61196	ABQ61196 Human PRO	478	14.8	74.0	3143	12	ADH25390	Adh25390 Human CDN
406	14.8	74.0	2832	12	ADP78171	ADP78171 Human ext	479	14.8	74.0	3143	12	ADU50123	Adu50123 Human CDN
407	14.8	74.0	2850	12	ADQ83547	ADQ83547 Human tum	480	14.8	74.0	3143	12	ADW49402	Adw49402 Human CDN
408	14.8	74.0	2950	13	ACN40467	ACN40467 Human tum	481	14.8	74.0	3143	12	ADZ52063	Adz52063 Human CDN
409	14.8	74.0	2981	10	ADB62165	ADB62165 Human CDN	482	14.8	74.0	3191	5	AA669084	AA669084 Human sec
410	14.8	74.0	3042	4	AAK53428	AAK53428 Human pol	483	14.8	74.0	3257	13	ADP25056	Adp25056 PRO polyp
411	14.8	74.0	3042	4	ABX13628	ABX13628 Human cyt	484	14.8	74.0	3257	13	ADP17583	Adp17583 DNA enco
412	14.8	74.0	3104	4	AD113116	AD113116 Human mem	485	14.8	74.0	3257	14	ADY20098	Ady20098 DNA enco
413	14.8	74.0	3104	4	AD110376	AD110376 Human cel	486	14.8	74.0	3412	6	ABK34689	ABK34689 Human CDN
414	14.8	74.0	3104	12	ADJ46902	ADJ46902 Human tra	488	14.8	74.0	3412	6	ABK34707	ABK34707 Human CDN
415	14.8	74.0	3143	2	AA234033	AA234033 Human PRO	489	14.8	74.0	3505	10	ADP60955	Adp60955 DNA demet
416	14.8	74.0	3143	3	AACT8494	AACT8494 Human PRO	490	14.8	74.0	3505	10	ACN39327	ACN39327 Tumour-as
417	14.8	74.0	3143	3	AACT8494	AACT8494 Human PRO	491	14.8	74.0	3546	13	ADV43514	Adv43514 Human pcy
418	14.8	74.0	3143	3	AACT8494	AACT8494 Human PRO	492	14.8	74.0	3660	14	ADU70923	Adu70923 Full leng
419	14.8	74.0	3143	8	ACR71755	ACR71755 Human sec	493	14.8	74.0	3704	4	AB108628	AB108628 Drosophill
420	14.8	74.0	3143	8	ACR71755	ACR71755 Human sec	494	14.8	74.0	3724	6	AA066256	AA066256 Sequence
421	14.8	74.0	3143	8	ACR71755	ACR71755 Human sec	495	14.8	74.0	3727	2	ABR84147	ABR84147 Human CDN
422	14.8	74.0	3143	8	ACR71755	ACR71755 Human sec	496	14.8	74.0	3727	8	ACR34551	ACR34551 Gene enco
423	14.8	74.0	3143	9	AD29747	AD29747 Novel hum	497	14.8	74.0	3727	8	ACR34551	ACR34551 Gene enco
424	14.8	74.0	3143	9	AD29747	AD29747 Novel hum	498	14.8	74.0	3727	8	ACR34551	ACR34551 Gene enco
425	14.8	74.0	3143	9	AD29747	AD29747 Novel hum	499	14.8	74.0	3727	8	ACR34551	ACR34551 Gene enco
426	14.8	74.0	3143	9	AD29747	AD29747 Novel hum	500	14.8	74.0	3727	8	ACR34551	ACR34551 Gene enco
427	14.8	74.0	3143	9	AD29747	AD29747 Novel hum	501	14.8	74.0	3727	8	ACR34551	ACR34551 Gene enco
428	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	502	14.8	74.0	3734	5	AD162304	AD162304 Human ova
429	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	503	14.8	74.0	3734	5	AD162304	AD162304 Human ova
430	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	504	14.8	74.0	3734	5	AD162304	AD162304 Human ova
431	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	505	14.8	74.0	3734	5	AD162304	AD162304 Human ova
432	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	506	14.8	74.0	3734	5	AD162304	AD162304 Human ova
433	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	507	14.8	74.0	3734	5	AD162304	AD162304 Human ova
434	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	508	14.8	74.0	3734	5	AD162304	AD162304 Human ova
435	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	509	14.8	74.0	3734	5	AD162304	AD162304 Human ova
436	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	510	14.8	74.0	3734	5	AD162304	AD162304 Human ova
437	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	511	14.8	74.0	3734	5	AD162304	AD162304 Human ova
438	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	512	14.8	74.0	3734	5	AD162304	AD162304 Human ova
439	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	513	14.8	74.0	3734	5	AD162304	AD162304 Human ova
440	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	514	14.8	74.0	3734	5	AD162304	AD162304 Human ova
441	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	515	14.8	74.0	3734	5	AD162304	AD162304 Human ova
442	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	516	14.8	74.0	3734	5	AD162304	AD162304 Human ova
443	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	517	14.8	74.0	3734	5	AD162304	AD162304 Human ova
444	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	518	14.8	74.0	3734	5	AD162304	AD162304 Human ova
445	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	519	14.8	74.0	3734	5	AD162304	AD162304 Human ova
446	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	520	14.8	74.0	3734	5	AD162304	AD162304 Human ova
447	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	521	14.8	74.0	3734	5	AD162304	AD162304 Human ova
448	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	522	14.8	74.0	3734	5	AD162304	AD162304 Human ova
449	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	523	14.8	74.0	3734	5	AD162304	AD162304 Human ova
450	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	524	14.8	74.0	3734	5	AD162304	AD162304 Human ova
451	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	525	14.8	74.0	3734	5	AD162304	AD162304 Human ova
452	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	526	14.8	74.0	3734	5	AD162304	AD162304 Human ova
453	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	527	14.8	74.0	3734	5	AD162304	AD162304 Human ova
454	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	528	14.8	74.0	3734	5	AD162304	AD162304 Human ova
455	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	529	14.8	74.0	3734	5	AD162304	AD162304 Human ova
456	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	530	14.8	74.0	3734	5	AD162304	AD162304 Human ova
457	14.8	74.0	3143	10	ADB76390	ADB76390 Human PRO	531	14.8	74.0	3734	5	AD162304	AD162304 Human ova

C 531	14.8	74.0	15650	5	ABA16364	AbA16364 Human ner	C 604	14.4	72.0	1589	6	ABE65715	ABe65715 Mouse gen
C 532	14.8	74.0	15650	5	ABA15903	AbA15903 Human ner	C 605	14.4	72.0	1605	13	ADS63748	AdS63748 Bacterial
C 533	14.8	74.0	17659	10	ADB67031	AdB67031 Mouse Gal	C 606	14.4	72.0	1628	13	ADS63381	AdS63381 Bacterial
C 534	14.8	74.0	18352	12	ADG44924	AdG44924 Mouse cat	C 607	14.4	72.0	1636	4	ABL01957	ABl01957 Drosophill
C 535	14.8	74.0	18698	10	ADB67026	AdB67026 Mouse Gal	C 608	14.4	72.0	1704	4	ABL02081	ABl02081 Drosophill
C 536	14.8	74.0	20757	14	ACL64726	ACl64726 M. xanthu	C 609	14.4	72.0	1720	6	ABE65714	ABe65714 Mouse gen
C 537	14.8	74.0	21005	14	ABE27718	ABe27718 Mouse Csa	C 610	14.4	72.0	1777	13	ADZ11498	AdZ11498 House mou
C 538	14.8	74.0	21779	13	ABE26691	ABe26691 Mouse can	C 611	14.4	72.0	1809	14	ADZ62411	AdZ62411 Murine 26
C 539	14.8	74.0	21779	14	ADZ12836	AdZ12836 Murine ca	C 612	14.4	72.0	1865	4	AAH84131	AAh84131 Gorilla o
C 540	14.8	74.0	21898	9	ADA03041	AdA03041 Mouse mCG	C 613	14.4	72.0	1996	4	AAE26656	AAe26656 Human gen
C 541	14.8	74.0	21898	9	ADA66325	AdA66325 Mouse mCG	C 614	14.4	72.0	1996	8	ABX74005	ABx74005 Human nov
C 542	14.8	74.0	21898	10	ADB72779	AdB72779 Mouse mCG	C 615	14.4	72.0	2002	6	ABE63412	ABe63412 Rat seque
C 543	14.8	74.0	21898	11	ADL27119	ADe27119 Mouse gen	C 616	14.4	72.0	2002	10	ADBS7807	ADbS7807 Toxicity-
C 544	14.8	74.0	24602	14	ACL64739	ACl64739 M. xanthu	C 617	14.4	72.0	2002	10	ADBS2326	ADbS2326 Primary r
C 545	14.8	74.0	25973	10	ADB67041	AdB67041 Mouse Gal	C 618	14.4	72.0	2002	13	ADVA0780	ADvA0780 Rat cardl
C 546	14.8	74.0	28136	4	AAK69755	AAk69755 Human Imm	C 619	14.4	72.0	2018	13	ADK60319	ADk60319 Plant ful
C 547	14.8	74.0	28534	11	ADB67028	AdB67028 Mouse Gal	C 620	14.4	72.0	2037	4	ABL05583	ABl05583 Drosophill
C 548	14.8	74.0	33097	11	ACN44008	ACn44008 Mouse gen	C 621	14.4	72.0	2126	4	AAE26659	AAe26659 Human gen
C 549	14.8	74.0	36047	10	ADE95869	ADe95869 Mouse NfK	C 622	14.4	72.0	2126	4	AAE26657	AAe26657 Human gen
C 550	14.8	74.0	36048	9	ADA02621	AdA02621 Mouse NfK	C 623	14.4	72.0	2126	8	ABX74006	ABx74006 Human nov
C 551	14.8	74.0	36048	11	ADB72359	AdB72359 Mouse NfK	C 624	14.4	72.0	2126	8	ABX74008	ABx74008 Human nov
C 552	14.8	74.0	39405	13	ACN44704	ACn44704 Mouse gen	C 625	14.4	72.0	2127	12	ADOS3548	ADoS3548 Human nov
C 553	14.8	74.0	49914	13	ABD33262	ABd33262 Murine ca	C 626	14.4	72.0	2227	4	AAK75488	AAk75488 Human Imm
C 554	14.8	74.0	55235	4	AAK67426	AAk67426 Human Imm	C 627	14.4	72.0	2252	13	ABD33375	ABd33375 Murine ca
C 555	14.8	74.0	77530	13	ABD33240	ABd33240 Murine ca	C 628	14.4	72.0	2401	6	ABL34943	ABl34943 Murine CD
C 556	14.8	74.0	79256	13	ABD33177	ABd33177 Murine ca	C 629	14.4	72.0	2401	6	ABL34943	ABl34943 Murine CD
C 557	14.8	74.0	79256	13	ABD33177	ABd33177 Murine ca	C 630	14.4	72.0	2411	3	AAZ61680	AAz61680 CDNA enco
C 558	14.8	74.0	96389	9	ADA02675	AdA02675 Mouse Top	C 631	14.4	72.0	2411	3	AAZ61783	AAz61783 CDNA enco
C 559	14.8	74.0	96389	10	ADB72413	AdB72413 Mouse Top	C 632	14.4	72.0	2411	4	AAZ61783	AAz61783 CDNA enco
C 560	14.8	74.0	96389	10	ADB72413	AdB72413 Mouse Top	C 633	14.4	72.0	2411	4	AAZ61783	AAz61783 CDNA enco
C 561	14.8	74.0	96593	9	ADA02885	AdA02885 Mouse Blm	C 634	14.4	72.0	2411	6	ABL34765	ABl34765 Murine CD
C 562	14.8	74.0	96593	12	ADB72623	AdB72623 Mouse Blm	C 635	14.4	72.0	2411	6	ABL34765	ABl34765 Murine CD
C 563	14.8	74.0	96593	12	ADM74480	AdM74480 Murine ca	C 636	14.4	72.0	2502	13	ADBS95168	ADBS95168 Human the
C 564	14.8	74.0	96594	10	ADM74480	AdM74480 Murine ca	C 637	14.4	72.0	2502	13	ADBS95168	ADBS95168 Human the
C 565	14.8	74.0	104062	11	ACN44458	ACn44458 Human gen	C 638	14.4	72.0	2502	13	ADBS95168	ADBS95168 Human the
C 566	14.8	74.0	105305	11	ACN44458	ACn44458 Human gen	C 639	14.4	72.0	2502	13	ADBS95168	ADBS95168 Human the
C 567	14.8	74.0	107304	13	ABD33230	ABd33230 Murine ca	C 640	14.4	72.0	2532	4	ABL05228	ABl05228 Drosophill
C 568	14.8	74.0	114793	4	AAO08215	AAo08215 Human gen	C 641	14.4	72.0	2635	12	ADOC64717	ADoC64717 Novel hum
C 569	14.8	74.0	117328	13	ABD33286	ABd33286 Mouse can	C 642	14.4	72.0	2669	10	ADVA7092	ADvA7092 Human gen
C 570	14.8	74.0	121129	13	ABD33446	ABd33446 Murine ca	C 643	14.4	72.0	2680	10	ADVA7092	ADvA7092 Human gen
C 571	14.8	74.0	122779	12	ADQ97053	ADq97053 Mouse can	C 644	14.4	72.0	2925	4	ABL15708	ABl15708 Drosophill
C 572	14.8	74.0	141463	11	ACN43862	ACn43862 Human gen	C 645	14.4	72.0	3147	4	ABL14769	ABl14769 Drosophill
C 573	14.8	74.0	168325	11	ACN44484	ACn44484 Mouse gen	C 646	14.4	72.0	3229	14	ADZ62912	AdZ62912 Murine De
C 574	14.8	74.0	168407	13	ABD33266	ABd33266 Murine ca	C 647	14.4	72.0	3434	7	ABL06652	ABl06652 Drosophill
C 575	14.8	74.0	174600	12	ADQ97520	ADq97520 Mouse can	C 648	14.4	72.0	3591	7	ADZ29341	ADz29341 Mouse Mmp
C 576	14.8	74.0	180026	14	ADQ97752	ADq97752 Mouse can	C 649	14.4	72.0	3614	4	ABL05218	ABl05218 Drosophill
C 577	14.8	74.0	240000	12	ADZ12006	AdZ12006 Mouse ste	C 650	14.4	72.0	3738	12	ACN45219	ACn45219 Human gen.
C 578	14.8	74.0	349981	10	ADZ12006	AdZ12006 Mouse ste	C 651	14.4	72.0	3857	11	ACN45219	ACn45219 Human gen.
C 579	14.4	72.0	22	10	ACC78647	ACC78647 P. obesus	C 652	14.4	72.0	3890	12	ADOC64364	ADoC64364 Novel hum
C 580	14.4	72.0	215	6	ADFS7265	ADfS7265 Urogenita	C 653	14.4	72.0	4018	12	ADL15892	ADL15892 Mouse pro
C 581	14.4	72.0	313	6	ABQ98681	ABq98681 Human ORP	C 654	14.4	72.0	4094	12	ADOS35742	ADoS35742 Novel mou
C 582	14.4	72.0	354	6	ABH78635	ABh78635 Human ATP	C 655	14.4	72.0	4094	12	ADOS35742	ADoS35742 Novel mou
C 583	14.4	72.0	426	14	ADV90659	ADv90659 P. obesus	C 656	14.4	72.0	4121	13	ADRO7934	ADrO7934 Pull leng
C 584	14.4	72.0	431	10	ADV90659	ADv90659 P. obesus	C 657	14.4	72.0	4160	4	ABL01956	ABl01956 Drosophill
C 585	14.4	72.0	436	6	ABE184130	ABe184130 Human ova	C 658	14.4	72.0	4550	2	AAZ01025	AAz01025 Partial m
C 586	14.4	72.0	443	6	ABO97010	ABo97010 Mouse ES	C 659	14.4	72.0	4600	13	ADRE88391	ADRe88391 Nocardia
C 587	14.4	72.0	474	4	AAE554184	AAe554184 Pseudomon	C 660	14.4	72.0	4600	13	ADRE88391	ADRe88391 Nocardia
C 588	14.4	72.0	489	4	ABE105229	ABe105229 Drosophill	C 661	14.4	72.0	4600	13	ADRE88391	ADRe88391 Nocardia
C 589	14.4	72.0	501	2	AAV68447	AAv68447 Strawber	C 662	14.4	72.0	4848	5	AAE67953	AAe67953 DNA enco
C 590	14.4	72.0	508	13	ADR30364	ADr30364 Mouse gen	C 663	14.4	72.0	4888	2	AAV22134	AAv22134 Rice glut
C 591	14.4	72.0	513	6	ABE83872	ABe83872 DNA enco	C 664	14.4	72.0	5008	4	ABL02080	ABl02080 Drosophill
C 592	14.4	72.0	513	10	ADBA46045	ADbA46045 Canb fusi	C 665	14.4	72.0	5190	4	ABL05582	ABl05582 Drosophill
C 593	14.4	72.0	556	10	ADBA4538	ADbA4538 Mouse mit	C 666	14.4	72.0	6307	9	ADAL19460	ADaL19460 Mouse LPT
C 594	14.4	72.0	618	10	ADDD3113	ADd3113 Mouse mit	C 667	14.4	72.0	6660	10	ADL133741	ADl133741 Mouse LPT
C 595	14.4	72.0	628	13	ADQ58641	ADq58641 Novel can	C 668	14.4	72.0	7568	4	ABL14768	ABl14768 Drosophill
C 596	14.4	72.0	674	10	ADDD3113	ADd3113 Mouse mit	C 669	14.4	72.0	7568	4	ABL14768	ABl14768 Drosophill
C 597	14.4	72.0	816	5	AAE26438	AAe26438 Pseudomon	C 670	14.4	72.0	9731	4	AAK72933	AAk72933 Human Imm
C 598	14.4	72.0	816	5	AAE26438	AAe26438 Pseudomon	C 671	14.4	72.0	9733	4	AAK72933	AAk72933 Human Imm
C 599	14.4	72.0	1096	14	ADDD35244	ADdD35244 Mouse mit	C 672	14.4	72.0	9733	4	AAK85097	AAk85097 Human Imm
C 600	14.4	72.0	1147	14	ADZ62425	AdZ62425 Murine 26	C 673	14.4	72.0	10591	12	ADOS9810	ADoS9810 Novel hum
C 601	14.4	72.0	1233	13	ADT46873	ADt46873 Bacterial	C 674	14.4	72.0	11546	13	ADU73266	ADu73266 Plasmid P
C 602	14.4	72.0	1407	13	ADT45913	ADt45913 Bacterial	C 675	14.4	72.0	13462	10	ADBE8453	ADbE8453 Mouse DCA
C 603	14.4	72.0	1467	13	ADS64133	AdS64133 Bacterial	C 676	14.4	72.0	20762	11	ACN44092	ACn44092 Mouse gen

677	14.4	72.0	21558	11	ACN45060	ACN45060 Mouse gen	750	14.4	72.0	51705	10	ADB72461	Adb72461 Mouse Syk
C 678	14.4	72.0	21562	11	ACN45004	ACN45004 Mouse gen	751	14.4	72.0	51705	10	ADBS971	Adbs971 Mouse Syk
679	14.4	72.0	22312	11	ACN44324	ACN44324 Mouse gen	752	14.4	72.0	52637	13	ADBS7083	Adbs7083 Mouse can
C 680	14.4	72.0	22965	11	ABD33374	ABD33374 Murine ca	C 753	14.4	72.0	52920	13	ABD33498	Abd33498 Murine ca
681	14.4	72.0	23070	9	ADBD2507	ADBD2507 Mouse Wnt	C 754	14.4	72.0	53981	11	ACN44928	ACN44928 Mouse gen
682	14.4	72.0	23070	10	ADBD72245	ADBD72245 Mouse Wnt	C 755	14.4	72.0	54037	13	ABD33333	ABD33332 Murine ca
683	14.4	72.0	23070	10	ADBS9755	ADBS9755 Mouse Wnt	C 756	14.4	72.0	54303	9	ABD32752	ABD32752 Mouse can
684	14.4	72.0	23611	13	ABD33108	ABD33108 Murine ca	C 757	14.4	72.0	54355	10	ADBD2753	Adbd2753 Mouse Mor
685	14.4	72.0	23611	13	ACN45136	ACN45136 Mouse gen	758	14.4	72.0	54355	10	ADBS2491	Adbs2491 Mouse Mor
C 686	14.4	72.0	23938	11	ACN45136	ACN45136 Mouse gen	759	14.4	72.0	54355	10	ADBS2491	Adbs2491 Mouse Mor
687	14.4	72.0	23982	14	AD212503	AD212503 Murine ca	760	14.4	72.0	55435	12	ADN74338	Adn74338 Murine ca
C 688	14.4	72.0	24495	13	ABD32636	ABD32636 Mouse can	761	14.4	72.0	55544	11	ACN45112	ACN45112 Mouse gen
C 689	14.4	72.0	24990	11	ACN45218	ACN45218 Human gen	762	14.4	72.0	56793	11	ACN45112	ACN45112 Mouse gen
C 690	14.4	72.0	25469	11	ACN44880	ACN44880 Mouse gen	763	14.4	72.0	57860	13	ADBD3663	Adbd3663 Mouse can
C 691	14.4	72.0	25545	11	ACN44876	ACN44876 Mouse gen	C 764	14.4	72.0	58053	13	ABD32663	ABD32663 Mouse gen
692	14.4	72.0	25913	4	AAK70862	AAK70862 Human Imm	C 765	14.4	72.0	58540	11	ACN44640	ACN44640 Mouse gen
C 693	14.4	72.0	26064	11	ACN44812	ACN44812 Mouse gen	C 766	14.4	72.0	61791	13	ABD33484	ABD33484 Murine ca
C 694	14.4	72.0	26307	11	ACN44140	ACN44140 Mouse gen	C 767	14.4	72.0	63411	12	ADBD3426	ADBD3426 Mouse gen
695	14.4	72.0	27383	12	ADQ59497	ADQ59497 Human can	768	14.4	72.0	63761	13	ADBS9515	ADBS9515 Human can
696	14.4	72.0	27898	14	AD213868	AD213868 Murine ca	769	14.4	72.0	64482	12	ADBS9515	ADBS9515 Human can
697	14.4	72.0	28027	11	ACN45020	ACN45020 Mouse gen	C 770	14.4	72.0	64482	12	ADBS9515	ADBS9515 Human can
698	14.4	72.0	28903	11	ACN44636	ACN44636 Mouse gen	C 771	14.4	72.0	64482	12	ADBS9515	ADBS9515 Human can
699	14.4	72.0	28932	11	ACN44352	ACN44352 Mouse gen	C 772	14.4	72.0	64482	14	AD213896	Ad213896 Murine ca
C 700	14.4	72.0	29377	11	ACN44988	ACN44988 Mouse gen	C 773	14.4	72.0	65559	11	ACN44408	ACN44408 Mouse gen
C 701	14.4	72.0	29560	13	ABD33580	ABD33580 Murine ca	C 774	14.4	72.0	65559	11	ACN44408	ACN44408 Mouse gen
C 702	14.4	72.0	30304	13	ABD32631	ABD32631 Mouse can	C 775	14.4	72.0	66681	13	ABD33333	ABD33333 Murine ca
C 703	14.4	72.0	30310	6	AAU38253	AAU38253 Genomic D	C 776	14.4	72.0	668370	11	ACN45024	ACN45024 Mouse gen
C 704	14.4	72.0	30659	11	ACN43884	ACN43884 Mouse gen	C 777	14.4	72.0	68370	11	ACN45024	ACN45024 Mouse gen
C 705	14.4	72.0	30752	11	ACN44344	ACN44344 Mouse gen	C 778	14.4	72.0	68497	11	ACN45024	ACN45024 Mouse gen
C 706	14.4	72.0	31946	11	ACN44096	ACN44096 Mouse gen	C 779	14.4	72.0	69515	11	ACN44660	ACN44660 Mouse gen
C 707	14.4	72.0	32185	11	ACN45120	ACN45120 Mouse gen	C 780	14.4	72.0	69966	13	ABD32713	ABD32713 Mouse gen
C 708	14.4	72.0	32858	4	ABL29482	ABL29482 Drosophila	C 781	14.4	72.0	70215	12	ADQ9761	ADQ9761 Mouse can
709	14.4	72.0	33000	10	ADBS6849	ADBS6849 Murine DC	782	14.4	72.0	71594	12	ADQ9761	ADQ9761 Mouse can
710	14.4	72.0	33500	11	ACN44036	ACN44036 Mouse gen	783	14.4	72.0	72507	11	ADQ97602	ADQ97602 Mouse can
711	14.4	72.0	33551	13	ABD32675	ABD32675 Mouse can	784	14.4	72.0	76644	12	ADQ97602	ADQ97602 Mouse can
712	14.4	72.0	34123	11	ACN45036	ACN45036 Mouse gen	C 785	14.4	72.0	77530	13	ABD33240	ABD33240 Murine tu
713	14.4	72.0	34319	9	ADAI3460	ADAI3460 Mouse rho	C 786	14.4	72.0	79467	9	ADBD2717	ADBD2717 Mouse Nfa
714	14.4	72.0	34319	9	ADAI3460	ADAI3460 Mouse rho	C 787	14.4	72.0	79467	9	ADBD2717	ADBD2717 Mouse Nfa
715	14.4	72.0	34319	10	ADQ47145	ADQ47145 Mouse gen	C 788	14.4	72.0	79467	10	ADBS9515	ADBS9515 Human can
C 716	14.4	72.0	34319	11	ACN44940	ACN44940 Mouse gen	C 789	14.4	72.0	79467	10	ADBS9515	ADBS9515 Human can
C 717	14.4	72.0	35359	3	AAZ29063	AAZ29063 Murine Tg	C 790	14.4	72.0	80275	12	ADQ97310	ADQ97310 Mouse can
C 718	14.4	72.0	35828	14	ADW28713	ADW28713 Murine ge	C 791	14.4	72.0	80275	12	ADQ97310	ADQ97310 Mouse can
C 719	14.4	72.0	37723	11	ACN44856	ACN44856 Mouse gen	C 792	14.4	72.0	80321	11	ACN45012	ACN45012 Mouse gen
720	14.4	72.0	38977	11	ACN44728	ACN44728 Human can	C 793	14.4	72.0	80423	13	ABD32576	ABD32576 Mouse can
721	14.4	72.0	39801	6	ABK63462	ABK63462 Human CDN	794	14.4	72.0	83180	11	ACN44784	ACN44784 Mouse gen
722	14.4	72.0	40116	8	ABZ26080	ABZ26080 Mouse DNa	795	14.4	72.0	83943	13	ABD33881	ABD33881 Mouse can
723	14.4	72.0	40463	11	ACN44904	ACN44904 Mouse gen	796	14.4	72.0	84410	13	ABD33551	ABD33551 Mouse can
C 724	14.4	72.0	40633	11	ACN43848	ACN43848 Mouse gen	797	14.4	72.0	86804	12	ADQ97700	ADQ97700 Mouse can
C 725	14.4	72.0	42179	11	ACN45160	ACN45160 Mouse gen	798	14.4	72.0	88421	6	AAU40781	AAU40781 Murine g
C 726	14.4	72.0	42379	12	ADQ97660	ADQ97660 Mouse can	C 799	14.4	72.0	88441	12	ADQ97097	ADQ97097 Mouse can
C 727	14.4	72.0	42514	11	ACN44164	ACN44164 Mouse gen	C 800	14.4	72.0	88493	13	ABD33522	ABD33522 Murine ca
C 728	14.4	72.0	42952	12	ADQ93609	ADQ93609 Murine ca	C 801	14.4	72.0	88493	13	ABD33522	ABD33522 Murine ca
729	14.4	72.0	43572	13	ABD33614	ABD33614 Murine ca	C 802	14.4	72.0	88607	12	ADQ97648	ADQ97648 Mouse can
C 730	14.4	72.0	43672	11	ACN44232	ACN44232 Mouse gen	C 803	14.4	72.0	88853	11	ACN43904	ACN43904 Mouse gen
C 731	14.4	72.0	43672	11	ACN44232	ACN44232 Mouse gen	C 804	14.4	72.0	89213	13	ABD33614	ABD33614 Murine ca
732	14.4	72.0	43799	14	AD21270	AD21270 Murine ca	C 805	14.4	72.0	90351	13	ABD33651	ABD33651 Mouse can
733	14.4	72.0	44529	14	AD21270	AD21270 Murine ca	C 806	14.4	72.0	90351	13	ABD33651	ABD33651 Mouse can
734	14.4	72.0	44728	13	ABD32556	ABD32556 Mouse can	807	14.4	72.0	90650	13	ADBS9504	ADBS9504 Mouse gen
C 735	14.4	72.0	44972	11	ACN44080	ACN44080 Mouse gen	808	14.4	72.0	91071	11	ACN44004	ACN44004 Mouse gen
C 736	14.4	72.0	46336	13	ABD33221	ABD33221 Murine ca	C 809	14.4	72.0	92076	12	ABD33368	ABD33368 Mouse can
737	14.4	72.0	46338	13	ABD33451	ABD33451 Murine ca	C 810	14.4	72.0	92969	12	ADQ97202	ADQ97202 Mouse can
738	14.4	72.0	46625	14	AD212788	AD212788 Murine ca	C 811	14.4	72.0	94720	9	ADBS9502	ADBS9502 Mouse can
C 739	14.4	72.0	46730	14	AD212788	AD212788 Murine ca	C 812	14.4	72.0	94720	9	ADBD2654	ADBD2654 Human STR
C 740	14.4	72.0	47745	11	ACN44160	ACN44160 Mouse gen	C 813	14.4	72.0	95489	12	ADQ97298	ADQ97298 Mouse can
C 741	14.4	72.0	48974	2	AAK55300	AAK55300 Mouse Pre	C 814	14.4	72.0	95489	12	ADQ97298	ADQ97298 Mouse can
C 742	14.4	72.0	49349	13	ADBS6997	ADBS6997 Mouse can	C 815	14.4	72.0	96389	9	ADBD2675	ADBD2675 Mouse Top
C 743	14.4	72.0	49349	14	AD212842	AD212842 Murine ca	816	14.4	72.0	96389	10	ADBS9523	ADBS9523 Mouse Top
C 744	14.4	72.0	50605	12	ADQ97801	ADQ97801 Murine ca	817	14.4	72.0	96389	10	ADBS9523	ADBS9523 Mouse Top
C 745	14.4	72.0	50657	13	ABD33455	ABD33455 Murine ca	C 818	14.4	72.0	96593	9	ADBD2651	ADBD2651 Mouse Ras
C 746	14.4	72.0	51198	11	ACN45000	ACN45000 Mouse gen	C 819	14.4	72.0	96593	10	ADBS7239	ADBS7239 Mouse Ras
C 747	14.4	72.0	51323	13	ABD32784	ABD32784 Mouse can	C 820	14.4	72.0	96593	10	ADBS7239	ADBS7239 Mouse Ras
748	14.4	72.0	51664	11	ACN44432	ACN44432 Mouse can	C 821	14.4	72.0	98638	12	ADQ97919	ADQ97919 Mouse can
749	14.4	72.0	51705	9	ADBD2723	ADBD2723 Mouse Syk	C 822	14.4	72.0	98638	12	ADQ97919	ADQ97919 Mouse can

C 823	14.4	72.0	98642	11	ACN44584	ACN44584 Mouse gen	C 896	14.4	72.0	254087	11	ACN43996	ACN43996 Mouse gen
C 824	14.4	72.0	100554	11	ACN44624	ACN44624 Mouse gen	C 897	14.4	72.0	256525	11	ACN44148	ACN44148 Mouse gen
C 825	14.4	72.0	100866	12	ADQ97263	ADQ97263 Mouse gen	C 898	14.4	72.0	263744	10	ADP08271	ADP08271 Mouse gen
C 826	14.4	72.0	101241	11	ACN44740	ACN44740 Mouse gen	C 899	14.4	72.0	295096	11	ACN44068	ACN44068 Mouse gen
C 827	14.4	72.0	101241	11	ACN44740	ACN44740 Mouse gen	C 900	14.4	72.0	295096	11	ACN44743	ACN44743 Mouse gen
C 828	14.4	72.0	104932	14	ABE96642	ABE96642 Human STA	C 901	14.4	72.0	349980	5	AAH41225	AAH41225 Pyrococcus
C 829	14.4	72.0	108566	13	ABD32933	ABD32933 Mouse can	C 902	14.2	71.0	48	11	ADMO9644	ADMO9644 Human PTG
C 830	14.4	72.0	108845	13	ABD32542	ABD32542 Mouse can	C 903	14.2	71.0	65	6	ABN30215	ABN30215 Rat splic
C 831	14.4	72.0	110000	11	ACN43984	ACN43984 Mouse gen	C 904	14.2	71.0	92	14	ACT61456	ACT61456 Human col
C 832	14.4	72.0	110000	12	ADQ97328	ADQ97328 Mouse gen	C 905	14.2	71.0	189	6	ABQ90472	ABQ90472 M. capuli
C 833	14.4	72.0	110000	13	ABD32627	ABD32627 Mouse gen	C 906	14.2	71.0	201	13	ADBS6522	ADBS6522 Human aut
C 834	14.4	72.0	110000	13	ABD32966	ABD32966 Mouse gen	C 907	14.2	71.0	209	6	ABL75000	ABL75000 Corn tabs
C 835	14.4	72.0	110000	13	ABD32594	ABD32594 Mouse can	C 908	14.2	71.0	248	4	AAH57322	AAH57322 Human pan
C 836	14.4	72.0	110000	13	ABD32594	ABD32594 Mouse can	C 909	14.2	71.0	265	6	ABN20351	ABN20351 Human ORF
C 837	14.4	72.0	110000	13	ABD32594	ABD32594 Mouse can	C 910	14.2	71.0	271	6	ABN75867	ABN75867 Human ORF
C 838	14.4	72.0	110000	13	ABD32811	ABD32811 Mouse can	C 911	14.2	71.0	291	2	AAO05616	AAO05616 Nue minig
C 839	14.4	72.0	110000	13	ABD32859	ABD32859 Mouse can	C 912	14.2	71.0	317	12	ACH93866	ACH93866 Human gen
C 840	14.4	72.0	110021	13	ABD32859	ABD32859 Mouse can	C 913	14.2	71.0	317	12	ACH93866	ACH93866 Human gen
C 841	14.4	72.0	110218	11	ACN44744	ACN44744 Mouse gen	C 914	14.2	71.0	325	2	AAQ59424	AAQ59424 Human bra
C 842	14.4	72.0	114633	12	ADQ97873	ADQ97873 Mouse gen	C 915	14.2	71.0	363	4	AAI24487	AAI24487 Human bra
C 843	14.4	72.0	114633	12	ADQ97873	ADQ97873 Mouse gen	C 916	14.2	71.0	378	12	ACH83114	ACH83114 Human gen
C 844	14.4	72.0	118864	12	ADQ97849	ADQ97849 Mouse can	C 917	14.2	71.0	385	9	ACL21990	ACL21990 DNA clone
C 845	14.4	72.0	121129	13	ABD33446	ABD33446 Mouse can	C 918	14.2	71.0	385	14	ADY98815	ADY98815 T. reesei
C 846	14.4	72.0	123920	13	ADV34995	ADV34995 Mouse gen	C 919	14.2	71.0	407	4	AAI14960	AAI14960 Human bre
C 847	14.4	72.0	123920	13	ADV34995	ADV34995 Mouse gen	C 920	14.2	71.0	408	4	AAI38850	AAI38850 Novel hum
C 848	14.4	72.0	124289	14	AD213200	AD213200 Mouse gen	C 921	14.2	71.0	420	14	ACT62322	ACT62322 Human col
C 849	14.4	72.0	124289	14	AD213200	AD213200 Mouse gen	C 922	14.2	71.0	423	5	AAI67559	AAI67559 Novel hum
C 850	14.4	72.0	130427	13	ADV35011	ADV35011 Mouse gen	C 923	14.2	71.0	435	8	ABT07008	ABT07008 Human ova
C 851	14.4	72.0	137454	12	ADQ97388	ADQ97388 Mouse can	C 924	14.2	71.0	435	8	ABX72886	ABX72886 Human ova
C 852	14.4	72.0	142976	13	ABD32612	ABD32612 Mouse can	C 925	14.2	71.0	455	5	AAI80374	AAI80374 DNA encod
C 853	14.4	72.0	144179	11	ACN44188	ACN44188 Mouse gen	C 926	14.2	71.0	459	9	ACH28567	ACH28567 Human adu
C 854	14.4	72.0	147433	11	ACN44752	ACN44752 Mouse gen	C 927	14.2	71.0	460	11	ACN84982	ACN84982 Breast ca
C 855	14.4	72.0	153995	13	ABD33534	ABD33534 Mouse gen	C 928	14.2	71.0	461	4	AAI14575	AAI14575 Probe #45
C 856	14.4	72.0	154504	12	ADQ59431	ADQ59431 Human can	C 929	14.2	71.0	461	4	ABAS6299	ABAS6299 Human foe
C 857	14.4	72.0	154504	12	ADQ59431	ADQ59431 Human can	C 930	14.2	71.0	461	4	AAI35942	AAI35942 Probe #46
C 858	14.4	72.0	155350	10	ADL13861	ADL13861 Osteocarth	C 931	14.2	71.0	461	4	ABR45788	ABR45788 Human bre
C 859	14.4	72.0	155350	13	ABD33514	ABD33514 Murine ca	C 932	14.2	71.0	461	4	ABR45788	ABR45788 Human bre
C 860	14.4	72.0	155692	14	AD213384	AD213384 Murine ca	C 933	14.2	71.0	461	4	AAK25940	AAK25940 Probe #44
C 861	14.4	72.0	158405	13	ADV35010	ADV35010 Murine cd	C 934	14.2	71.0	461	4	AAK04480	AAK04480 Human bra
C 862	14.4	72.0	158405	13	ADV35010	ADV35010 Murine cd	C 935	14.2	71.0	461	4	ABR25637	ABR25637 Human liv
C 863	14.4	72.0	163701	13	ABD33351	ABD33351 Murine ca	C 936	14.2	71.0	461	5	AAI04385	AAI04385 Probe #43
C 864	14.4	72.0	163701	14	AD213376	AD213376 Murine ca	C 937	14.2	71.0	461	6	ABR04553	ABR04553 Human gen
C 865	14.4	72.0	167739	9	AD582858	AD582858 Murine tu	C 938	14.2	71.0	472	9	ACH26762	ACH26762 Human adu
C 866	14.4	72.0	168407	13	ABD33266	ABD33266 Murine ca	C 939	14.2	71.0	475	12	ADK52055	ADK52055 Human ato
C 867	14.4	72.0	170279	13	ABD32686	ABD32686 Mouse can	C 940	14.2	71.0	476	4	AAK82826	AAK82826 Human imm
C 868	14.4	72.0	171936	6	ABE56565	ABE56565 Human STL	C 941	14.2	71.0	476	4	AAK82825	AAK82825 Human imm
C 869	14.4	72.0	171936	6	ABE56565	ABE56565 Human STL	C 942	14.2	71.0	481	5	AAI80373	AAI80373 DNA encod
C 870	14.4	72.0	171936	12	ADN16205	ADN16205 Mouse sul	C 943	14.2	71.0	488	9	ACL21998	ACL21998 DNA clone
C 871	14.4	72.0	171936	12	ADN16205	ADN16205 Mouse sul	C 944	14.2	71.0	491	9	ACL21986	ACL21986 DNA clone
C 872	14.4	72.0	174600	12	ADQ97520	ADQ97520 Mouse can	C 945	14.2	71.0	495	9	ACL21994	ACL21994 DNA clone
C 873	14.4	72.0	175603	12	ADQ97554	ADQ97554 Mouse can	C 946	14.2	71.0	495	9	ACL21974	ACL21974 DNA clone
C 874	14.4	72.0	177049	12	ADQ59413	ADQ59413 Human can	C 947	14.2	71.0	496	9	ACH44189	ACH44189 Human foe
C 875	14.4	72.0	177049	14	ADQ21688	ADQ21688 Murine ca	C 948	14.2	71.0	502	14	ADU74712	ADU74712 Human col
C 876	14.4	72.0	178024	12	ADQ97721	ADQ97721 Human can	C 949	14.2	71.0	515	9	ACH35420	ACH35420 Human end
C 877	14.4	72.0	192992	13	ABD33866	ABD33866 Mouse can	C 950	14.2	71.0	518	5	AAI93993	AAI93993 Primer sp
C 878	14.4	72.0	197775	11	ACN44416	ACN44416 Mouse gen	C 951	14.2	71.0	518	14	ADY63420	ADY63420 Human clo
C 879	14.4	72.0	197775	11	ACN44416	ACN44416 Mouse gen	C 952	14.2	71.0	520	9	ACL21978	ACL21978 DNA clone
C 880	14.4	72.0	198161	6	ABR83564	ABR83564 Human CDN	C 953	14.2	71.0	522	4	AAI56615	AAI56615 DNA encod
C 881	14.4	72.0	198161	13	ADQ17348	ADQ17348 Human sof	C 954	14.2	71.0	523	9	ACL21991	ACL21991 DNA clone
C 882	14.4	72.0	202351	11	ACN44504	ACN44504 Mouse gen	C 955	14.2	71.0	524	12	ACH76621	ACH76621 Human gen
C 883	14.4	72.0	202351	11	ACN44504	ACN44504 Mouse gen	C 956	14.2	71.0	528	9	ACL21975	ACL21975 DNA clone
C 884	14.4	72.0	203132	13	ABD33364	ABD33364 Murine ca	C 957	14.2	71.0	532	12	ACH21982	ACH21982 DNA clone
C 885	14.4	72.0	203132	13	ABD33364	ABD33364 Murine ca	C 958	14.2	71.0	533	12	ACH80166	ACH80166 Human gen
C 886	14.4	72.0	203132	14	ADZ13443	ADZ13443 Murine ca	C 959	14.2	71.0	540	11	ACL47487	ACL47487 Rice abio
C 887	14.4	72.0	203132	14	ADZ13443	ADZ13443 Murine ca	C 960	14.2	71.0	540	12	ADU74893	ADU74893 Plant CDN
C 888	14.4	72.0	204803	12	ADQ97348	ADQ97348 Mouse can	C 961	14.2	71.0	549	3	AAI95332	AAI95332 Cat filea
C 889	14.4	72.0	205388	12	ADQ97560	ADQ97560 Mouse can	C 962	14.2	71.0	555	9	ADA93289	ADA93289 Maize gen
C 890	14.4	72.0	208765	12	ADQ97430	ADQ97430 Mouse can	C 963	14.2	71.0	555	10	ABT40967	ABT40967 Toxicity
C 891	14.4	72.0	215980	6	AAI38337	AAI38337 Complemen	C 964	14.2	71.0	555	11	ADU12129	ADU12129 Maize CDN
C 892	14.4	72.0	215980	6	AAI38337	AAI38337 Complemen	C 965	14.2	71.0	555	11	ACL4571	ACL4571 Rice abio
C 893	14.4	72.0	225583	11	ADV34981	ADV34981 Murine gen	C 966	14.2	71.0	563	9	ACL21984	ACL21984 DNA clone
C 894	14.4	72.0	233060	11	ACN43912	ACN43912 Mouse gen	C 967	14.2	71.0	573	9	ACL21995	ACL21995 DNA clone
C 895	14.4	72.0	247461	13	ABD33153	ABD33153 Murine ca	C 968	14.2	71.0	576	9	ACL21988	ACL21988 DNA clone

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c 969 14.2 71.0 578 9 AC121993 DNA clone
c 970 14.2 71.0 578 12 ACH69414 Human gen
c 971 14.2 71.0 579 2 AAX01704 Human ant
c 972 14.2 71.0 579 2 AAX01712 Human ant
c 973 14.2 71.0 579 2 AAX01705 Human ant
c 974 14.2 71.0 579 2 AAX01708 Human ant
c 975 14.2 71.0 579 2 AAX01713 Human ant
c 976 14.2 71.0 580 12 ADE77004 Human ant
c 977 14.2 71.0 585 4 AAB28816 Drosophila
c 978 14.2 71.0 594 8 ACA23424 Prokaryot
c 979 14.2 71.0 598 9 AC121976 DNA clone
c 980 14.2 71.0 600 9 AC121977 DNA clone
c 981 14.2 71.0 600 14 AD270322 Human CDN
c 982 14.2 71.0 603 2 AAV88562 EST clone
c 983 14.2 71.0 603 2 AC121997 DNA clone
c 984 14.2 71.0 603 9 AC121996 DNA clone
c 985 14.2 71.0 606 11 ABD11974 Pseudomon
c 986 14.2 71.0 618 13 ADT46051 Bacterial
c 987 14.2 71.0 621 9 AC121992 DNA clone
c 988 14.2 71.0 621 11 ABD07359 Pseudomon
c 989 14.2 71.0 622 9 AC121981 DNA clone
c 990 14.2 71.0 627 6 ABS61473 Prostate
c 991 14.2 71.0 627 14 AC159924 Human col
c 992 14.2 71.0 637 14 AC166578 M. xanthu
c 993 14.2 71.0 633 9 AC121980 DNA clone
c 994 14.2 71.0 635 9 AC121983 DNA clone
c 995 14.2 71.0 641 5 AAS91654 DNA encod
c 996 14.2 71.0 642 6 ABZ08504 Human leu
c 997 14.2 71.0 649 9 AC122000 DNA clone
c 998 14.2 71.0 649 9 AC121999 DNA clone
c 999 14.2 71.0 654 11 ADJ12138 Maize CDN
1000 14.2 71.0 654 11 AC134693 Rice abio
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## ALIGNMENTS

## RESULT 1

AAFP99262 standard; DNA; 20 BP.

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XX ID AAFP99262 standard; DNA; 20 BP.
XX AC AAFP99262;
XX DT 12-JUN-2001 (first entry)
XX DE Immunostimulatory nucleic acid #378.
XX KM Vaccine; cytopathic; virucidal; bactericidal; fungicidal; anti-parasitic;
XX KM immunostimulatory; tumour; viral infection; bacterial infection;
XX KM fungal infection; parasitic infection; cancer; asthma;
XX KM infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX OS Synthetic.
XX PN WO200123972-A2.
XX PD 05-APR-2001.
XX PF 25-SEP-2000; 2000WO-US026383.
XX PR 25-SEP-1999; 99US-0156113P.
XX PR 27-SEP-1999; 99US-0156135P.
XX PR 23-AUG-2000; 2000US-0227436P.
XX PA (IOWA ) UNIV IOWA RES FOUND.
XX PA (COLE-) COLEY PHARM GMBH.
XX PI Kriegl AM, Schetter C, Vollmer J;
XX DR MPI, 2001-273485/28.
XX PT Vaccinating against tumors, infectious diseases, allergies and asthma
XX using immunostimulatory Py-rich and TG nucleic acids.
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XX PS Claim 101; Page 46; 338pp; English.
XX CC The present invention relates to a method for stimulating an immune
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XX response. The method comprises administering an immunostimulatory nucleic
XX acid to a non-rodent subject in sufficient quantity to stimulate an
XX immune response. The present sequence is one such immunostimulatory
XX nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
XX (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
XX against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
XX and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
XX haemophilus, campylobacter, clostridium, bactericidia coli and/or
XX staphylococcus), fungal antigens and/or parasitic antigens. The method is
XX also useful for preventing cancer, asthma, infectious disease, allergy or
XX immune deficiency. The present sequence can also be used to redirect a
XX Th2 to a Th1 immune response and to activate immune cells. Note: the
XX present sequence may have a phosphorothioate backbone
```

SQ Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;

Best Local Similarity 90.0%; Pred. No. 9.3; Mismatches 0; Gaps 0;

Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AGGUAACAGCCAGACUACGA 20
Db 1 AGGTACAGCCAGACUACGA 20
|||:|||||:|||||:|||||
|||:|||||:|||||:|||||
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## RESULT 2

ABS77907 standard; DNA; 20 BP.

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XX ID ABS77907 standard; DNA; 20 BP.
XX AC ABS77907;
XX DT 13-DEC-2002 (first entry)
XX DE Angiogenesis inhibitory oligonucleotide #391.
XX KM Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
XX KM tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
XX KM diabetic retinopathy; retinopathy of prematurity; macular degeneration;
XX KM corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
XX KM rubecosis; Osler-Weber Syndrome; myocardial angiogenesis;
XX KM plaque neovascularisation; telangiectasia; haemophillic joint;
XX KM angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
XX KM scleroderma; hypertrophic scar.
XX OS Synthetic.
XX PN WO200253141-A2.
XX PD 11-JUL-2002.
XX PF 14-DEC-2001; 2001WO-US048458.
XX PR 14-DEC-2000; 2000US-025534P.
XX PA (COLE-) COLEY PHARM GROUP INC.
XX PI Bratzler RJ;
XX DR MPI; 2002-566690/60.
XX PT Inhibiting angiogenesis in a subject, involves administering at least one
XX antiangiogenic nucleic acid molecule to the subject.
XX PS Claim 2; Page 26; 276pp; English.
XX CC The invention relates to inhibiting angiogenesis in a subject, comprising
XX administering at least one antiangiogenic nucleic acid molecule. Also
XX included is a kit comprising a first container housing the antiangiogenic
XX nucleic acids, and instructions for administering them to a subject
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CC having a condition characterised by unwanted angiogenesis. The method is  
CC useful for inhibiting angiogenesis associated with solid tumour growth.  
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
CC rubosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophilic joints, angiodiroma,  
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
CC acid of the invention  
XX

XX SQ Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 90.0%; Pred. No. 9.3;  
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUACGA 20  
DB 1 AGGTACAGCCAGACTACGA 20

RESULT 3  
ABL38704  
ID ABL38704 standard; DNA; 20 BP.

XX ABL38704;

XX 16-APR-2002 (first entry)

XX Immunostimulatory nucleic acid SEQ ID NO: 68.

XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;  
XX angiogenesis; metastasis; cytotoxic; ss.

XX Synthetic.

XX WO200197843-A2.

XX 27-DEC-2001.

XX 22-JUN-2001; 2001WO-US020154.

XX 22-JUN-2000; 2000US-0213346P.

XX (IOWA) UNIV IOWA RES FOUND.

XX Weiner G, Hartmann G;

XX WPI, 2002-154611/20.

XX The present invention relates to methods for treating or preventing  
XX cancer, involving administering to a subject having or at risk of  
XX developing cancer immunostimulatory nucleic acids that induce expression  
XX of cell surface antigens and antibodies. The methods are useful for  
XX treating or preventing cancer such as basal cell carcinoma, bladder  
XX cancer, bone cancer, brain and central nervous system (CNS) cancer,  
XX breast cancer, cervical cancer, colon and rectum cancer, connective  
XX tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx  
XX cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
XX Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
XX cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
XX cancer, stomach cancer, testicular cancer, and uterine cancer. The  
XX present sequence is an immunostimulatory oligonucleotide described in the  
XX exemplification of the invention

SQ Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 90.0%; Pred. No. 9.3;  
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUACGA 20  
DB 1 AGGTACAGCCAGACTACGA 20

RESULT 4  
ACD99693

ID ACD99693 standard; DNA; 20 BP.

XX ACD99693;

XX 25-SEP-2003 (first entry)

XX Immunostimulatory nucleic acid #379.

XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
XX antifungal; gene therapy; vaccine; non-allergic inflammatory disease;  
XX psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
XX inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.

XX Synthetic.

XX US2003050268-A1.

XX 13-MAR-2003.

XX 29-MAR-2002; 2002US-00112653.

XX 29-MAR-2001; 2001US-0279642P.

XX (KRIE/) KRIE A M.

XX (BERG/) BERG D J.

XX Kriegl AM, Berg DJ;

XX WPI, 2003-521815/49.

XX The invention describes a method of treating non-allergic inflammatory  
XX disease comprising administering to a subject having or at risk of  
XX developing a non-allergic inflammatory disease an immunostimulatory  
XX nucleic acid for prevention or treatment of the disease. The method is  
XX useful for treating non-allergic inflammatory diseases, such as  
XX psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
XX Crohn's disease, ulcerative colitis or Crohn's disease.  
XX This sequence represents an immunostimulatory nucleic acid

XX Disclousure; Page 19; 22pp; English.

XX The present invention relates to methods for treating or preventing  
XX cancer, involving administering to a subject having or at risk of  
XX developing cancer immunostimulatory nucleic acids that induce expression  
XX of cell surface antigens and antibodies. The methods are useful for  
XX treating or preventing cancer such as basal cell carcinoma, bladder  
XX cancer, bone cancer, brain and central nervous system (CNS) cancer,  
XX breast cancer, cervical cancer, colon and rectum cancer, connective  
XX tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx  
XX cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-  
XX Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian  
XX cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin  
XX cancer, stomach cancer, testicular cancer, and uterine cancer. The  
XX present sequence is an immunostimulatory oligonucleotide described in the  
XX exemplification of the invention

XX SQ Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 20;  
Best Local Similarity 90.0%; Pred. No. 9.3;  
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUACGA 20  
DB 1 AGGTACAGCCAGACTACGA 20

RESULT 5  
ADB36764

ID ADB36764 standard; DNA; 20 BP.



AC ADB36764;  
 XX 04-DEC-2003 (first entry)  
 XX Immunostimulatory nucleic acid #378.  
 DE Immunostimulatory nucleic acid #378.  
 XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
 KM hypo-responsive subject; immunostimulatory.  
 XX Synthetic.  
 OS US2003087848-A1.  
 PN 08-MAY-2003.  
 XX 02-FEB-2001; 2001US-00776479.  
 PF 03-FEB-2000; 2000US-0179991P.  
 PR (BRAT/) BRATZLER R L.  
 PA (PETE/) PETERSEN D M.  
 PA (FOUR/) FOURON Y.  
 XX Bratzler RL, Petersen DM, Fouron Y;  
 PI WPI, 2003-657977/62.  
 DR Treating and/or preventing allergy or asthma using an immunostimulatory  
 PT nucleic acid alone or in combination with an asthma/allergy medicament.  
 XX Disclosure; Page 10; 221pp; English.  
 XX The invention relates to a method of treating or preventing allergy or  
 CC asthma which comprises administering to a subject a poly-G nucleic acid  
 CC in an aerosol formulation. The methods and compositions of the present  
 CC invention are useful for diagnosing and/or treating asthma and allergy  
 CC especially in a hypo-responsive subject. The present sequence represents  
 CC an immunostimulatory nucleic acid of the invention.  
 CC  
 XX Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 20; DB 9; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 9.3;  
 Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGGUAACGCCAGGACTACGA 20  
 DB 1 AGGTAACGCCAGGACTACGA 20  
 RESULT 6  
 ADU89707  
 ID ADU89707 standard; DNA; 20 BP.  
 XX  
 AC ADU89707;  
 XX  
 DT 10-FEB-2005 (first entry)  
 XX  
 DE Allergic response suppressor oligonucleotide #391.  
 XX  
 KM ss; antiasthmatic; antiallergic; dermatological; antiinflammatory;  
 KM antibacterial; antiviral; immunoglobulin E antagonist; allergy;  
 KM immunostimulant; asthma; rhinitis; urticaria; dermatitis;  
 KM bacterial infection; viral infection.  
 XX  
 OS Synthetic.  
 XX  
 PN US2004235774-A1.  
 PF 25-NOV-2004.  
 XX 23-APR-2004; 2004US-00831778.  
 XX

PR 03-FEB-2000; 2000US-0179991P.  
 PR 02-FEB-2001; 2001US-00776479.  
 XX (BRAT/) BRATZLER R L.  
 PA (PETE/) PETERSEN D M.  
 PA (FOUR/) FOURON Y.  
 XX Bratzler RL, Petersen DM, Fouron Y;  
 PI WPI, 2004-833006/82.  
 DR Suppressing allergies, including asthma, rhinitis, urticaria and atopic  
 PT dermatitis, in a subject, comprises administering a first and second dose  
 PT of an immunostimulatory nucleic acid.  
 XX Disclosure; SEQ ID NO 391; 235pp; English.  
 PS  
 XX The invention relates to a method of suppressing a symptom of an allergic  
 CC response in a subject by administering a first and second dose of an  
 CC immunostimulatory nucleic acid that comprises a nucleotide sequence  
 CC comprising 5'-cg-3', and where the second dose is administered from 1 day  
 CC to 8 weeks after the first dose. The methods and compositions of the  
 CC present invention are useful for the treatment or prevention of asthma  
 CC and allergy, including rhinitis, urticaria and atopic dermatitis, using  
 CC an immunostimulatory nucleic acid alone or in combination with other  
 CC medicaments. They can also be used in preventing bacterial and viral  
 CC infections. This sequence represents an oligonucleotide used in the  
 CC method of the invention.  
 CC  
 XX Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 20; DB 13; Length 20;  
 Best Local Similarity 90.0%; Pred. No. 9.3;  
 Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGGUAACGCCAGGACTACGA 20  
 DB 1 AGGTAACGCCAGGACTACGA 20  
 RESULT 7  
 ADW79936  
 ID ADW79936 standard; RNA; 20 BP.  
 XX  
 AC ADW79936;  
 XX  
 DT 21-APR-2005 (first entry)  
 XX  
 DE Bacterial immunomodulatory Cpg oligoribonucleotide, SEQ ID NO:3.  
 XX  
 KM Immune modulation; immune stimulation; bacterial infection; infection;  
 KM endotoxic shock; antibacterial; antimicrobial; immunomodulator;  
 KM immunostimulant; adjuvant; ss.  
 XX  
 OS Bacteria.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 18..19  
 FT /\*tag= a  
 FT /note= "Cpg dinucleotide"  
 XX  
 PN US2005032731-A1.  
 PD 10-FEB-2005.  
 XX  
 PF 15-MAR-2004; 2004US-00800926.  
 XX 11-MAY-1993; 93US-00059745.  
 PR 20-JAN-1995; 95US-00376175.  
 PR 18-AUG-1995; 95US-00517016.  
 PR 29-OCT-1996; 96US-00739264.  
 PR 17-NOV-1998; 98US-00193653.  
 PR 18-JUN-2001; 2001US-00883550.  
 XX

XX (MARS/) MARSHALL W B.  
 XX Marshall WE;  
 PI WPI: 2005-161694/17.  
 DR  
 XX Composition for modulating and/or stimulating immune system of animal  
 PT useful for withstanding microbial infections and lethality of endotoxic  
 PT shock, comprises low molecular weight oligoribonucleotide from bacteria.  
 XX  
 XX Claim 5; SEQ ID NO 3; 17pp; English.  
 XX  
 XX The invention relates to a composition for modulating and/or stimulating  
 CC the immune system of an animal, comprising bacterial oligoribonucleotides  
 CC (ORN) with a molecular weight of less than 10 kD. The bacterial ORNs are  
 CC preferably ADW79334-ADW79336, contain Cpg motifs and are resistant to  
 CC RNase. Bacteria produce RNase-resistant Cpg ORNs in response to stressors  
 CC such as a change in environment, including the neutral pH they encounter  
 CC when they colonize animals. The immune systems of animals have co-evolved  
 CC to recognize such Cpg ORNs as being derived from bacteria, and has  
 CC adapted a non-toxic alerting response to their release from bacteria. The  
 CC invention also relates to a method for the preparation of the bacterial  
 CC ORNs by subjecting bacteria to one or more periods of stress, separating  
 CC the ORNs and media from the bacteria, and filtering the separated product  
 CC to remove substances with a molecular weight of more than 10 kD, and a  
 CC method of using the filtrate to modulate/stimulate the immune system of  
 CC an animal to withstand microbial infection. The composition and methods  
 CC of the invention are useful for modulating and/or stimulating the immune  
 CC system of animals (including humans, poultry and livestock), particularly  
 CC to withstand microbial infections or the onset of endotoxic shock. The  
 CC compositions may be administered orally (e.g., as a food supplement) or  
 CC parentally, and may also be administered as an adjuvant for oral or  
 CC parenteral vaccines. The compositions may additionally be used topically  
 CC to protect against ear, nose and vaginal infections. They may further be  
 CC used to extend the viability of monocytes, thereby improving their  
 CC ability to mature into macrophages to fight infection, and may be used to  
 CC downregulate the cytotoxicity of macrophages to prevent them from  
 CC destroying normal T-cells in people with HIV infections. The composition  
 CC of the invention contains ORNs released by either harmless or pathogenic  
 CC bacteria, but is free from bacterial cells. Unlike Cpg  
 CC oligodeoxyribonucleotides (ODNs), the bacterial Cpg ORNs and compositions  
 CC containing them are non-toxic. The present sequence represents a  
 CC specifically claimed bacterial Cpg oligoribonucleotide present in  
 CC compositions of the invention.  
 CC  
 XX Sequence 20 BP; 7 A; 5 C; 6 G; 0 T; 2 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 20; DB 14; Length 20;  
 Best Local Similarity 100.0%; Pred. NO. 9.3; 0; Indels 0; Gaps 0;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGGUACAGCCGAGACUACGA 20  
 |||||  
 Db 1 AGGUACAGCCGAGACUACGA 20  
 |||||  
 RESULT 8  
 ABT40830  
 ID ABT40830 standard; DNA; 5253 BP.  
 XX  
 XX ABT40830;  
 AC  
 XX 26-JUN-2003 (first entry)  
 DT  
 XX Toxicity modelling related rat gene SEQ ID No 532.  
 DE  
 XX Toxic effect; gene expression profile; renal toxicity; toxicity marker;  
 XX database; drug screening; toxicity assay; rat; de.  
 KW  
 OS Rattus norvegicus.  
 XX  
 XX WO200295000-A2.  
 PN

XX 28-NOV-2002.  
 PD  
 XX  
 XX 22-MAY-2002; 2002WO-US016173.  
 PE  
 XX  
 XX 22-MAY-2001; 2001US-0292335P.  
 PR 13-JUN-2001; 2001US-0297523P.  
 PR 19-JUN-2001; 2001US-028925P.  
 PR 10-JUL-2001; 2001US-030807P.  
 PR 10-JUL-2001; 2001US-030808P.  
 PR 10-JUL-2001; 2001US-030810P.  
 PR 28-AUG-2001; 2001US-0315047P.  
 PR 27-SEP-2001; 2001US-0324928P.  
 PR 22-OCT-2001; 2001US-0330462P.  
 PR 01-NOV-2001; 2001US-0330867P.  
 PR 21-NOV-2001; 2001US-0331805P.  
 PR 06-DEC-2001; 2001US-0336144P.  
 PR 19-DEC-2001; 2001US-0340873P.  
 PR 21-FEB-2002; 2002US-0357842P.  
 PR 21-FEB-2002; 2002US-0357843P.  
 PR 21-FEB-2002; 2002US-0357844P.  
 PR 15-MAR-2002; 2002US-0364134P.  
 PR 08-APR-2002; 2002US-0370206P.  
 PR 08-APR-2002; 2002US-0370206P.  
 PR 17-APR-2002; 2002US-0372794P.  
 PR 21-APR-2002; 2002US-0371679P.  
 PR  
 PA (GENE-) GENE LOGIC INC.  
 PI  
 XX Mendrick D, Porter M, Johnson K, Higgs B, Caastle A, Blashoff M;  
 XX WPI: 2003-148464/14.  
 DR  
 XX Predicting at least one toxic effect of a compound, useful for toxicity  
 PT modelling, comprises preparing a gene expression profile of a tissue or  
 PT cell sample exposed to the compound, and comparing the gene expression  
 PT profile to a database.  
 PT  
 PS Example 4; Page; 446pp; English.  
 XX  
 XX The invention relates to a novel method of predicting at least one toxic  
 CC effect of a compound. The method comprises a gene expression profile of a  
 CC tissue or cell sample exposed to the compound, and comparing the gene  
 CC expression profile to a database comprising at least part of the data or  
 CC information given in the specification. The methods are useful for  
 CC predicting at least one toxic effect of a compound, predicting the  
 CC progression of a toxic effect of a compound, predicting the renal  
 CC toxicity of a compound, or identifying toxicity markers in tissues or  
 CC cells exposed to known renal toxin. The genes are useful as toxicity  
 CC markers in drug screening and toxicity assays, in monitoring disease or  
 CC physiological states, or disease progression. This polynucleotide  
 CC represents a rat DNA sequence relating to the toxic effect database  
 CC described in the specification. NOTE: The sequence data for this patent  
 CC did not form part of the printed specification, but was obtained in  
 CC electronic format directly from the World Intellectual Property  
 CC Organization  
 CC  
 XX Sequence 5253 BP; 1380 A; 1379 C; 1440 G; 1054 T; 0 U; 0 Other;  
 SQ  
 Query Match 90.0%; Score 18; DB 10; Length 5253;  
 Best Local Similarity 88.9%; Pred. NO. 1.2e+02;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GGUAACAGCCGAGACUACG 19  
 |||||  
 Db 2679 GGUAACAGCCGAGACUACG 2696  
 |||||  
 RESULT 9  
 ADV39876  
 ID ADV39876 standard; cDNA; 5253 BP.  
 XX

AC ADV39876;  
 DT 10-FEB-2005 (first entry)  
 DE Rat cardiotoxicity marker gene, SEQ ID NO:742.  
 XX Toxicology screening; drug screening; cardiotoxicity, drug-induced;  
 XX expression profile; gene expression; myocarditis; heart arrhythmia;  
 XX tachycardia; myocardial ischemia; angina; hypertension; hypotension;  
 XX dyspnea; cardiogenic shock; cardiovascular disease; gene; ss.  
 OS Rattus norvegicus.  
 XX  
 XX W02004063334-A2.  
 XX  
 XX 29-JUL-2004.  
 XX  
 XX 08-JAN-2004; 2004WO-US000240.  
 XX  
 XX 08-JAN-2003; 2003US-00338044.  
 XX  
 XX (GENE-) GENE LOGIC INC.  
 XX  
 XX Mendrick DL, Porter MW, Johnson KR, Higge B, Castle A;  
 XX Elashoff M;  
 XX WPI; 2004-561893/54.  
 XX DDBJ; AB012214.  
 DR  
 PT Predicting a toxic effect of a compound by obtaining a gene expression  
 PT profile of a tissue or cell sample exposed to the compound and comparing  
 PT the gene expression profile to a database comprising all of the data  
 PT given in the specification.  
 XX  
 XX Example 1; SEQ ID NO 742; 520pp; English.  
 PS  
 XX The invention relates to a method of predicting at least one toxic effect  
 CC of a compound by obtaining a gene expression profile of a tissue or cell  
 CC sample exposed to the compound and comparing the gene expression profile  
 CC to a database of toxicity prediction genes which are differentially  
 CC expressed on exposure to known toxins. The tissue or cell sample is  
 CC especially derived from heart tissue, and the predicted toxic effect is  
 CC especially a cardiotoxic effect such as myocarditis, arrhythmias,  
 CC tachycardia, myocardial ischemia, angina, hypertension, hypotension,  
 CC dyspnea, cardiogenic shock or other specific heart pathologies. The  
 CC invention is based on the elucidation of global changes in gene  
 CC expression in tissues or cells exposed to known toxins, particularly  
 CC cardiotoxins, and the identification of individual genes (toxicity  
 CC markers) that are differentially expressed on toxin exposure. The  
 CC invention also relates to methods for predicting the cardiotoxicity of a  
 CC compound's toxic effects, for predicting the cardiotoxicity of a  
 CC compound, for identifying an agent that modulates the onset or  
 CC progression of a toxic response, and for predicting which cellular  
 CC pathways a particular compound will modulate. The invention further  
 CC relates to sets of at least two hybridization probes specific for  
 CC toxicity prediction genes, and solid supports and kits comprising them.  
 CC The method of the invention is useful in toxicology screening for  
 CC predicting the toxic effects (especially cardiotoxic effects) of  
 CC compounds such as pharmaceutical agents or environmental pollutants.  
 CC Sequences ADV39135-ADV41830 represent cardiotoxicity marker  
 CC polynucleotides of rat origin whose expression is altered on exposure to  
 CC at least one cardiotoxin. Note: The sequence data for this patent did not  
 CC form part of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 XX Sequence 5253 BP; 1380 A; 1379 C; 1440 G; 1054 T; 0 U; 0 Other;  
 SQ  
 Query Match 90.0%; Score 18; DB 13; Length 5253;  
 Best Local Similarity 88.9%; Pred. No. 1.2e+02;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 2679 GGTACAGCCAGACTACG 2696  
 RESULT 10  
 AAZ50957  
 ID AAZ50957 standard; DNA; 720 BP.  
 XX  
 XX AAZ50957;  
 XX  
 XX 05-JUN-2000 (first entry)  
 XX  
 XX Pseudomonas aeruginosa lasR response regulator ORF.  
 XX  
 XX luxI; chemical inducer; response regulator protein; inducible promoter;  
 XX gene switch; pest control; gene therapy; transgenic plant; mango; melon;  
 XX soybean; lethal protein; treatment; cancer; lasR; ODDHL;  
 XX N-(3-oxododecanolyl)-L-homoserine lactone; ds.  
 XX  
 XX Pseudomonas aeruginosa.  
 XX  
 XX  
 XX Key Location/Qualifiers  
 XX CDS 1..720  
 XX /tag= a  
 XX /product= "lasR response regulator protein"  
 XX /note= "Induced by autoinducer, N-(3-oxododecanolyl) -L-  
 XX homoserine lactone"  
 XX  
 XX W0200009704-A1.  
 XX  
 XX 24-FEB-2000.  
 XX  
 XX 12-AUG-1999; 99WO-GB002653.  
 XX  
 XX 13-AUG-1998; 98GB-00017704.  
 XX  
 XX (ZENE ) ZENECA LTD.  
 XX  
 XX Martinez A, Jepson I, Frey RG;  
 XX WPI; 2000-224341/19.  
 XX P-PSDB; AAY70035.  
 DR  
 PT Inducing target gene expression in plants such as melons, mangoes,  
 PT soybean, via a gene switch operably linked to a foreign gene.  
 PT  
 XX  
 XX Example 3; Page 74-75; 78pp; English.  
 PS  
 XX The patent discloses a method of initiating transcription of a target  
 CC gene in a eukaryotic cell, by applying a chemical inducer capable of  
 CC binding to the response protein produced by the eukaryotic cell itself,  
 CC to form an inducing complex which binds to and induces the inducible  
 CC promoter operably linked to the target gene. The gene switch is useful  
 CC for externally regulating the target gene expression. This method is  
 CC useful for selectively controlling pests in the fields, in gene therapy  
 CC and to produce transgenic plants like melons, mangoes and soybean. It can  
 CC be used to switch on genes which produce lethal proteins, that can be  
 CC employed in the treatment of cancer. The present sequence is the  
 CC Pseudomonas aeruginosa response regulator protein, lasR encoding DNA.  
 CC LasR is a positive transcriptional activator, that responds to signals  
 CC from the lasI inducer gene, that directs the synthesis of autoinducer, N-  
 CC (3-oxododecanolyl)-L-homoserine lactone (ODDHL).  
 XX  
 XX Sequence 720 BP; 145 A; 200 C; 227 G; 148 T; 0 U; 0 Other;  
 SQ  
 Query Match 84.0%; Score 16.8; DB 3; Length 720;  
 Best Local Similarity 85.0%; Pred. No. 4e+02;  
 Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 11  
ID ABD09355 standard; DNA; 735 BP.  
XX  
XX ABD09355;  
AC  
XX  
XX 29-JUL-2004 (first entry)  
DT  
XX  
XX Pseudomonas aeruginosa polynucleotide #7959.  
DE  
XX  
XX Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;  
KM antibacterial.  
XX  
XX Pseudomonas aeruginosa.  
OS  
XX US6551795-B1.  
PN  
XX 22-APR-2003.  
PD  
XX 18-FEB-1999; 99US-00252991.  
PP  
XX 18-FEB-1998; 98US-0074788P.  
PR 27-JUL-1998; 98US-0094190P.  
XX  
XX (GENO-) GENOME THERAPEUTICS CORP.  
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
XX WPI; 2003-615309/58.  
DR P-PSDB; AB075784.  
XX  
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
PT useful as molecular targets for diagnosis, prophylaxis and treatment of  
XX pathological conditions resulting from bacterial infection.  
XX  
XX Disclosure; SEQ ID NO 7959; 455bp; English.  
XX  
XX The invention relates to Pseudomonas aeruginosa polypeptides and the  
CC polynucleotides encoding them. The sequences are useful in diagnosis and  
CC therapy of pathological conditions, as molecular targets for diagnostics,  
CC prophylaxis and treatment of pathological conditions resulting from a  
CC bacterial infection, for evaluating a compound, such as a polypeptide,  
CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
CC effective antibacterial targets, as targets for antibacterial drugs,  
CC including anti-P. aeruginosa drugs, as templates for recombinant  
CC production of P. aeruginosa-derived peptides or polypeptides, as target  
CC components for diagnosis and/or treatment of P. aeruginosa-caused  
CC infection, and in detection of P. aeruginosa sequences or other sequences  
CC of Pseudomonas species using bioclip technology. Sequences ABD01397-  
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html  
XX  
XX Sequence 735 BP; 150 A; 203 C; 232 G; 150 T; 0 U; 0 Other;  
SQ  
Query Match 84.0%; Score 16.8; DB 11; Length 735;  
Best Local Similarity 85.0%; Pred. No. 4e+02;  
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 AGGUACAGCCAGACUACGA 20  
DB 139 AAGGACAGCCAGACUACGA 158

RESULT 12  
ID ABD33090 standard; DNA; 145068 BP.  
XX  
XX ABD33090;  
AC  
XX  
XX 18-NOV-2004 (first entry)  
DT

DE Murine cancer-associated (CA) gene MD07-006.  
XX  
XX Mouse; cancer-associated protein; CAP; cancer-associated gene; CA; gene;  
KM ds; cancer; cytostatic.  
XX  
XX Mus musculus.  
OS  
XX WO2004058146-A2.  
PN  
XX 15-JUL-2004.  
PD  
XX 15-DEC-2003; 2003WO-US040081.  
PP  
XX 17-DEC-2002; 2002US-00322281.  
PR (SAGR-) SAGRES DISCOVERY INC.  
XX  
XX Morris DW, Malandro MS;  
PI WPI; 2004-499109/47.  
XX  
XX Novel human cancer associated protein encoded within open reading frame  
PT of cancer associated gene, useful as targets for diagnosing cancer.  
XX  
XX Disclosure; SEQ ID NO 33; 182bp; English.  
XX  
XX The invention relates to cancer-associated proteins (CAP) and the cancer-  
CC associated (CA) nucleic acids encoding them. The invention also relates  
CC to a method for treating cancers involving administering to a patient an  
CC inhibitor of CAP, and a method of screening for anticancer activity in a  
CC potential drug involving providing a cell that expresses a CA gene,  
CC contacting a tissue sample derived from a cancer cell with an anticancer  
CC drug candidate and monitoring the effect of the anticancer drug candidate  
CC on expression of the CA gene. The CAP proteins are useful for detecting  
CC cancer associated with expression of a CAP protein in a test cell sample  
CC and for screening for a bioactive agent capable of modulating the  
CC activity of a CAP protein. The CA nucleic acids are useful for diagnosing  
CC cancer, involving determining the expression of a CA nucleic acid in a  
CC tissue. This sequence represents a murine CA gene of the invention. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 145068 BP; 38358 A; 33586 C; 33004 G; 36708 T; 0 U; 3412 Other;  
SQ  
Query Match 84.0%; Score 16.8; DB 13; Length 145068;  
Best Local Similarity 85.0%; Pred. No. 5.7e+02;  
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 AGGUACAGCCAGACUACGA 20  
DB 50545 AGGTACTGCCAGACACGCA 50564

RESULT 13  
ID AAF10633 standard; cDNA; 246 BP.  
XX  
XX AAF10633;  
AC  
XX  
XX 13-MAR-2001 (first entry)  
DT  
XX  
XX Fusarium venenatum EST SEQ ID NO:3156.  
DE  
XX  
XX Multiple gene expression; filamentous fungal cell; EST;  
KM expressed sequence tag; Fusarium venenatum; Aspergillus niger;  
KM Aspergillus oryzae; Trichoderma reesei; identification; recombination;  
KM culture condition; environmental stress; spore morphogenesis;  
XX metabolic pathway engineering; catabolic pathway engineering; ss-  
XX Fusarium venenatum.  
OS  
XX WO200056762-A2.  
PN

XX 28-SEP-2000.  
 PD 22-MAR-2000; 2000MO-US007781.  
 XX 22-MAR-1999; 99US-00273623.  
 PR 22-MAR-1999; 99US-00273623.  
 XX (NOVO) NOVO NORDISK BIOTECH INC.  
 PA (NOVO) NOVO NORDISK AS.  
 XX Berka RM, Rey MW, Shuster JR, Kaupinen S, Clausen IG, Olsen PB;  
 PI MPI; 2000-594572/56.  
 DR Monitoring differential expression of genes in filamentous fungal cells  
 XX uses fluorescence-labeled nucleic acids isolated from the cells and a  
 PT substrate of expressed sequence tags.  
 PS Claim 86; Page 1507; 3161pp; English.  
 XX The present invention describes a method for monitoring differential  
 CC expression of genes in a first filamentous fungal (FF) cell relative to  
 CC expression of the same genes in one or more second filamentous fungal  
 CC cells. The method uses fluorescence-labeled nucleic acids isolated from  
 CC cells. The method uses a substrate of expressed sequence tags (EST). The ESTs  
 CC are used in the methods for monitoring differential expression of genes  
 CC in a first filamentous fungal (FF) cell relative to expression of the  
 CC same genes in one or more second filamentous fungal cells. Monitoring the  
 CC global expression of genes from FF cells allows the production potential  
 CC of the microorganisms to be improved. New genes may be discovered,  
 CC possible functions of unknown open reading frames can be identified and  
 CC gene copy number variation and stability can be monitored. The expression  
 CC of genes can be used to study how FF cells adapt to changes in culture  
 CC conditions, environmental stress, spore morphogenesis, recombination,  
 CC metabolic or catabolic pathway engineering. Using ESTs provides several  
 CC advantages over genomic or random cDNA clones including elimination of  
 CC redundancy as one spot on an array equals one gene or open reading frame,  
 CC and organization of the microarrays based on function of the gene  
 CC products to facilitate analysis of the results. AA07478 to AA07478  
 CC represents ESTs from *Fusarium venenatum*; AA07478 to AA07478 represents  
 CC ESTs from *Aspergillus niger*; AA07478 to AA07478 represents ESTs from  
 CC *Aspergillus oryzae*; and AA07478 to AA07478 represents ESTs from  
 CC *Trichoderma reesei*, which are all specifically claimed in the present  
 CC invention.  
 XX Sequence 246 BP; 67 A; 55 C; 64 G; 60 T; 0 U; 0 Other;  
 SQ  
 Query Match 82.0%; Score 16.4; DB 3; Length 246;  
 Best Local Similarity 83.3%; Pred. No. 5.8e+02;  
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 GUAACGCCAGACUACGA 20  
 DB 154 GTACACCGAGACTACGA 171  
 RESULT 14  
 ADU54674  
 ID ADU54674 standard; cDNA; 246 BP.  
 AC ADU54674;  
 DT 10-FEB-2005 (first entry)  
 XX  
 DE *Fusarium venenatum* CCl-3 EST, SEQ ID NO:3156.  
 XX Gene expression; biochip; microarray; hybridization; EST;  
 KW expressed sequence tag; ss.  
 XX *Fusarium venenatum*; CCl-3.  
 OS  
 XX US2004229367-A1.  
 FN

PD 18-NOV-2004.  
 XX 29-AUG-2003; 2003US-00653047.  
 XX 22-MAR-1999; 99US-00273623.  
 PR 22-MAR-2000; 2000US-00533559.  
 XX (NOVO) NOVOZYMES BIOTECH INC.  
 PA (NOVO) NOVOZYMES INC AS.  
 XX Berka RM, Rey MW, Shuster JR, Kaupinen S, Clausen IG, Olsen PB;  
 PI MPI; 2004-832481/82.  
 DR Monitoring differential expression of genes in a filamentous fungal cell  
 XX relative to expression of the genes in second filamentous fungal cells,  
 PT comprises using microarrays containing *Fusarium venenatum* expressed  
 PT sequence tags.  
 XX Claim 1; SEQ ID NO 3156; 274pp; English.  
 XX The invention relates to a method for monitoring the differential  
 CC expression of genes in a first filamentous fungal cell relative to the  
 CC same genes in one or more second filamentous fungal cells. The method  
 CC involves differentially labeling nucleic acids from the first and second  
 CC fungal cells with fluorescent reporter dyes, and adding the mixture of  
 CC fluorescently labeled polynucleotides to a substrate containing an array  
 CC of *Fusarium venenatum* expressed sequence tags (ESTs) selected from  
 CC ADU5119-ADU5288 under conditions that permit hybridization. Relative  
 CC expression of genes in the fungal cells is determined by fluorescence;  
 CC the fluorescent signal emitted when labeled nucleic acids from the first  
 CC fungal cell bind to the ESTs in the array differs in color from that  
 CC emitted when labeled nucleic acids from the second fungal cell hybridize.  
 CC When both sets of labeled nucleic acids are produced. The filamentous fungal  
 CC cells used in the method are chosen from *Acromonium*, *Aspergillus*,  
 CC *Fusarium*, *Hemicella*, *Mucor*, *Myceliophthora*, *Neurospora*, *Penicillium*,  
 CC *Thielavia*, *Tolyposcidium*, and *Trichoderma* *oryzae*. The method of the  
 CC invention is useful for monitoring the expression of the cells' protein  
 CC in filamentous fungal cells, in order to improve the cells' protein  
 CC production capacity when such organisms are used for the industrial  
 CC production of proteins (e.g., enzymes). The present sequence represents  
 CC an EST derived from *Fusarium venenatum* CCl-3 (a morphological mutant of  
 CC strain ATCC 20334) which is specifically claimed for use in the method of  
 CC the invention. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from the US patent office at  
 CC [seqdata.uspto.gov/sequence.html?docID=US20040222367](http://seqdata.uspto.gov/sequence.html?docID=US20040222367).  
 XX Sequence 246 BP; 67 A; 55 C; 64 G; 60 T; 0 U; 0 Other;  
 SQ  
 Query Match 82.0%; Score 16.4; DB 13; Length 246;  
 Best Local Similarity 83.3%; Pred. No. 5.8e+02;  
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 GUAACGCCAGACUACGA 20  
 DB 154 GTACACCGAGACTACGA 171  
 RESULT 15  
 ADZ92677  
 ID ADZ92677 standard; cDNA; 246 BP.  
 AC ADZ92677;  
 DT 11-AUG-2005 (first entry)  
 XX  
 DE *Fusarium venenatum* expressed sequence tag cDNA SEQ ID NO 3156.  
 XX differential expression; gene expression; filamentous fungus;  
 KW expressed sequence tag; EST; variation; microarray; ss.  
 XX

XX OS Fusarium venenatum.  
 XX XX US6902867-B1.  
 XX XX 07-JUN-2005.  
 XX XX 22-MAR-2000; 2000US-00533559.  
 XX XX 22-MAR-1999; 99US-00273623.  
 XX PA (NOVO ) NOVOZYMES BIOTECH INC.  
 XX PA (NOVO ) NOVOZYMES AS.  
 XX PI Berka RM, Rey MM, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;  
 XX WPI; 2005-401635/41.  
 XX DR  
 XX PT Monitoring differential expression of genes in first filamentous fungal  
 XX PT cell relative to that of genes in second fungal cells, comprises  
 XX PT hybridizing fluorescence labeled nucleic acids from the cells to an array  
 XX PT of expressed sequence tags.  
 XX PS Disclosure; SEQ ID NO 3156; 264pp; English.  
 XX CC The invention relates to a method of monitoring (M1) differential  
 XX CC expression of multiple genes in a first filamentous fungal cell relative  
 XX CC to expression of the same genes in one or more second filamentous fungal  
 XX CC cells, comprises adding fluorescence labeled nucleic acids isolated from  
 XX CC the cells to a substrate containing an array of Aspergillus oryzae  
 XX CC expressed sequence tag (EST) of AD293898-AD296922, and examining the  
 XX CC array under fluorescence excitation conditions. (M1) is useful for  
 XX CC monitoring global expression of several genes from a filamentous fungal  
 XX CC cell, discovering new genes, identifying possible functions of unknown  
 XX CC open reading frames and monitoring gene copy number variation and  
 XX CC stability. In (M1), one spot on an array equals one gene or open reading  
 XX CC frame, extensive follow-up characterization is unnecessary since sequence  
 XX CC information is available and EST microarrays can be organized based on  
 XX CC function of the gene products. This sequence corresponds to an EST  
 XX CC sequence of the invention. (Note: this sequence is not given in the  
 XX CC printed specification but can be obtained in electronic form from the  
 XX CC USPTO web site [uspto.gov/sequence.html](http://uspto.gov/sequence.html), Document ID: 6902867B1).  
 XX CC  
 XX SQ Sequence 246 BP; 67 A; 55 C; 64 G; 60 T; 0 U; 0 Other;  
 OY  
 Query Match 82.0%; Score 16.4; DB 14; Length 246;  
 Best Local Similarity 83.3%; Pred. No. 5.8e+02;  
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Db 3 GUACAGCCAGGACUACGA 20  
 154 GATACACCGAGACTACGA 171  
 RESULT 16  
 ADX13768  
 ID ADX13768 standard; cDNA; 1308 BP.  
 XX AC ADX13768;  
 XX DT 21-APR-2005 (first entry)  
 XX DE Plant full length insert polynucleotide seqid 8343.  
 XX XX plant protectant; plant growth regulator; gene therapy; plant;  
 XX KW recombinant DNA construct; physical array; plant breeding marker;  
 XX KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
 XX KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
 XX KW growth rate; cell cycle pathway; disease resistance;  
 XX KW galactomannan production; lignin production; plant growth regulator;  
 XX KW yield; plant growth; plant development; seed oil; protein yield;  
 XX KW protein content; gene; ss.

OS Unidentified.  
 XX XX US2004034888-A1.  
 XX XX 19-FEB-2004.  
 XX XX 28-APR-2003; 2003US-00425114.  
 XX XX 06-MAY-1999; 99US-00304517.  
 XX XX 05-NOV-2001; 2001US-00985678.  
 XX PA (LITU//) LIU J.  
 XX PA (ZHOU//) ZHOU Y.  
 XX PA (KOVA//) KOVALIC D K.  
 XX PA (SCRE//) SCREEN S E.  
 XX PA (TABAS//) TABASKA J E.  
 XX PA (CAOY//) CAO Y.  
 XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
 XX WPI; 2004-180133/17.  
 XX DR  
 XX XX  
 XX PT New recombinant DNA construct, useful for improving plant tolerance to  
 XX PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
 XX PT pests, for conferring increased resistance to plant disease, or for  
 XX PT improving yield.  
 XX PS Claim 1; SEQ ID NO 8343; 15pp; English.  
 XX CC The invention describes a recombinant DNA construct comprising a  
 XX CC polynucleotide consisting of a sequence encoding an amino acid sequence  
 XX CC available in electronic form from the US patent office at  
 XX CC [ftp.segdata.uspto.gov/sequence.html?DocID:2004034888](http://ftp.segdata.uspto.gov/sequence.html?DocID:2004034888). The polynucleotide  
 XX CC of the invention are also useful in physical arrays of molecules and as  
 XX CC plant breeding markers. The recombinant DNA construct is useful for  
 XX CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
 XX CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
 XX CC plant cells by modification of the cell cycle pathway, for conferring  
 XX CC increased resistance to plant disease, for producing galactomannan,  
 XX CC lignin or plant growth regulators, for increasing the rate of homologous  
 XX CC recombination in plants, for improving yield by modification of  
 XX CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
 XX CC or by providing improved plant growth and development under at least one  
 XX CC stress condition or for modifying seed oil or protein yield and/or  
 XX CC content. This sequence represents a plant full length insert  
 XX CC polynucleotide that can be used in the recombinant DNA construct of the  
 XX CC invention.  
 XX SQ Sequence 1308 BP; 376 A; 282 C; 278 G; 372 T; 0 U; 0 Other;  
 OY  
 Query Match 82.0%; Score 16.4; DB 13; Length 1308;  
 Best Local Similarity 83.3%; Pred. No. 6.5e+02;  
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Db 2 GGUACAGCCGAGGACUACG 19  
 44 GATACAGCCGAGACTACG 61  
 RESULT 17  
 ADA03035/C  
 ID ADA03035 standard; DNA; 31632 BP.  
 XX AC ADA03035;  
 XX DT 06-NOV-2003 (first entry)  
 XX DE Mouse Rorc carcinoma associated gene, SEQ ID NO:1553.  
 XX XX Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast;  
 XX KW prostate; lymphoma; leukemia; cytostatic; gene therapy; drug screening;  
 XX KW gene; ds.

OS Mus sp.  
 XX WO2003057146-A2.  
 PN 17-JUL-2003.  
 XX 26-DEC-2002; 2002WO-US041414.  
 XX 26-DEC-2001; 2001US-00035832.  
 XX (SAGR-) SAGRES DISCOVERY.  
 XX Morris DW;  
 XX WPI; 2003-587068/55.  
 XX New recombinant nucleic acid encoding carcinoma associated protein,  
 PT useful for preparing compositions for treating carcinomas.  
 XX Claim 1; SEQ ID NO 1553; 245pp; English.

CC The invention relates to recombinant carcinoma associated (CA) nucleic  
 CC acid sequences from mouse and human (ADA01482-ADA03094), and to  
 CC recombinant carcinoma associated proteins (CAP) encoded by them. The  
 CC invention also encompasses expression vectors and host cells comprising a  
 CC CA nucleic acid, a polypeptide (especially an antibody) that specifically  
 CC binds to the protein, and a block comprising CA nucleic acid or  
 CC fragments thereof. The sequences of the invention were identified using  
 CC oncogenic retroviruses, which insert into the genome of the host organism  
 CC at random. Many of these do not carry transduced host oncogenes or  
 CC pathogenic trans-acting viral genes, meaning that cancer incidence is a  
 CC direct consequence of the effects of proviral integration into host  
 CC protooncogenes. The CA nucleic acid sequences can be used to diagnose  
 CC carcinoma (especially breast cancer, prostate cancer, lymphoma or  
 CC leukemia) or a propensity to carcinoma by determination of the sequence  
 CC of a CA gene, or by determination of CA gene expression in particular  
 CC tissues. CA nucleic acids, proteins and antibodies are also useful as  
 CC therapeutic agents and in screening and evaluating drug candidates. The  
 CC present sequence represents a specifically claimed murine CA nucleic acid  
 CC sequence of the invention. Note: The complete sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 31632 BP; 7931 A; 8130 C; 7983 G; 7588 T; 0 U; 0 Other;  
 SQ

Query Match 82.0%; Score 16.4; DB 9; Length 31632;  
 Best Local Similarity 83.3%; Pred. No. 8e+02;  
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUAC 18  
 DB 26940 AGGTACAGCCAGGCTAC 26923

RESULT 18  
 ADA66319/c  
 ID ADA66319 standard; DNA; 31632 BP.  
 XX  
 XX ADA66319;  
 AC  
 XX 20-NOV-2003 (first entry)  
 DT  
 XX  
 XX Mouse Rorc gene genomic DNA sequence.  
 DE  
 XX carcinoma-associated gene; CA gene; Rorc gene; MCG15938 gene; BATT1 gene;  
 XX Igga1 gene; IGAP1 gene; Zfp29 gene; hCG27579 gene; Kcnj9 gene;  
 XX KCMJ9 gene; Pp3cc gene; Pp3cc gene; MCG9110 gene; hCG27579 gene;  
 XX cancer cell; lymphatic cell; breast cell; prostate cell; epithelial cell;  
 XX carcinoma-associated protein; CAP; cytostatic; gene therapy; anticancer;  
 XX vaccine; carcinoma; lymphoma carcinoma; lymphatic cancer; breast cancer;  
 XX prostate cancer; DNA vaccine; animal model; mouse; murine; ds; Rorc.

OS Mus sp.  
 XX WO2003053224-A2.  
 PN 03-JUL-2003.  
 XX 20-DEC-2002; 2002WO-US041776.  
 XX 20-DEC-2001; 2001US-00034650.  
 XX (SAGR-) SAGRES DISCOVERY.  
 XX Morris DW, Engelhard EK;  
 XX WPI; 2003-569168/53.  
 XX Novel recombinant carcinoma-associated nucleic acid, useful for  
 PT evaluating the effect of a candidate carcinoma drug, and for diagnosing  
 PT carcinoma.  
 XX Claim 1; Page 51-55; 229pp; English.

CC This invention relates to a novel recombinant carcinoma-associated (CA)  
 CC nucleic acid comprising a fully defined genomic, mRNA or coding sequences  
 CC of mouse Rorc gene or human RORC gene, mouse MCG15938 or human gene BATT1,  
 CC mouse Igga1 gene or human IGAP1 gene, mouse Zfp29 gene or human  
 CC mouse Kcnj9 gene, mouse MCG9110 gene or human KCMJ9 gene, mouse Pp3cc gene or  
 CC hCG27579 gene, mouse MCG15938 gene or human hCG27579 gene, as given in  
 CC the specification. CA genes are genes which are preferably expressed in  
 CC cancer cells, preferably lymphatic, breast, prostate or epithelial cells.  
 CC A compound which modifies the expression of the CA genes or bind to  
 CC carcinoma-associated proteins (CAP) may have cytostatic activity and the  
 CC sequences of the invention may enable the use of gene therapy or a  
 CC development of an anticancer vaccine. Therefore the invention may be  
 CC useful for diagnosis and treatment of carcinomas, especially lymphoma  
 CC carcinoma, breast cancer and prostate cancer. The CA genes may also be  
 CC useful as DNA vaccines and for generating animal models of carcinomas.  
 CC The present sequence is that of the mouse Rorc gene genomic DNA sequence  
 CC of the invention.

XX Sequence 31632 BP; 7931 A; 8128 C; 7985 G; 7588 T; 0 U; 0 Other;  
 SQ

Query Match 82.0%; Score 16.4; DB 9; Length 31632;  
 Best Local Similarity 83.3%; Pred. No. 8e+02;  
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUAC 18  
 DB 26940 AGGTACAGCCAGGCTAC 26923

RESULT 19  
 ADB72773/c  
 ID ADB72773 standard; DNA; 31632 BP.  
 XX  
 XX ADB72773;  
 AC  
 XX 04-DEC-2003 (first entry)  
 DT  
 XX  
 XX Mouse Rorc gene.  
 DE  
 XX mouse; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;  
 XX cancer; neoplasm; adenocarcinoma; sarcoma; gene.  
 XX  
 XX Mus sp.  
 OS  
 XX WO2003008583-A2.  
 PN 30-JAN-2003.  
 XX 26-DEC-2001; 2001WO-US051291.  
 XX 02-MAR-2001; 2001US-00798586.



PR 23-OCT-2001; 2001US-00004113.  
PR 08-NOV-2001; 2001US-00052482.  
PR 30-NOV-2001; 2001US-00997722.  
PR 20-DEC-2001; 2001US-00034650.  
PA (SAGR-) SAGRES DISCOVERY.  
XX  
XX Morris DW, Engelhard EK;  
XX WPI; 2003-239337/23.  
DR  
XX  
XX New recombinant nucleic acid, useful for treating carcinomas, lymphomas,  
PT cancers, neoplasia, adenocarcinoma, or sarcomas.  
XX  
XX  
XX Claim 1; SEQ ID NO 601; 2304bp; English.  
XX  
XX The invention relates to a novel recombinant nucleic acid comprising a  
CC nucleotide sequence selected from any of the 660 sequences fully defined  
CC in the specification. A polynucleotide of the invention has cytostatic  
CC activity, and may have a use in gene therapy, or in a vaccine. The  
CC recombinant nucleic acids and polypeptides are useful for treating  
CC carcinomas, e.g. lymphomas, cancers, neoplasia, adenocarcinoma, and  
CC sarcomas. The present sequence represents a mouse gene of the invention.  
XX  
SQ Sequence 31632 BP; 7931 A; 8130 C; 7983 G; 7588 T; 0 U; 0 Other;  
XX  
Query Match 82.0%; Score 16.4; DB 10; Length 31632;  
Best Local Similarity 83.3%; Pred. No. 8e+02;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
OY 1 AGGUAACGCCAGACUAC 18  
DB 26940 AGGTACGACGAGGCTAC 26923  
XX  
RESULT 20  
ADA02933  
ID ADA02933 standard; DNA; 96599 BP.  
XX  
AC ADA02933;  
XX  
DT 06-NOV-2003 (first entry)  
XX  
XX Mouse Braf carcinoma associated gene, SEQ ID NO:1451.  
XX  
XX Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast;  
KM prostate; lymphoma; leukemia; cytostatic; gene therapy; drug screening;  
KM gene; ds.  
XX  
XX Mus sp.  
XX  
XX WO2003057146-A2.  
XX  
XX 17-JUL-2003.  
XX  
XX 26-DEC-2002; 2002WO-US041414.  
XX  
XX 26-DEC-2001; 2001US-00035832.  
XX  
XX (SAGR-) SAGRES DISCOVERY.  
XX  
XX Morris DW;  
XX WPI; 2003-587068/55.  
XX  
XX New recombinant nucleic acid encoding carcinoma associated protein,  
PT useful for preparing compositions for treating carcinomas.  
XX  
XX Claim 1; SEQ ID NO 1451; 245bp; English.  
XX  
XX The invention relates to recombinant carcinoma associated (CA) nucleic  
CC acid sequences from mouse and human (ADA01482-ADA03094), and to  
CC recombinant carcinoma associated proteins (CAP) encoded by them. The

CC invention also encompasses expression vectors and host cells comprising a  
CC CA nucleic acid, a polypeptide (especially an antibody) that specifically  
CC binds to the protein, and a biochip comprising CA nucleic acid or  
CC fragments thereof. The sequences of the invention were identified using  
CC oncogenic retroviruses, which insert into the genome of the host organism  
CC at random. Many of these do not carry transduced host oncogenes or  
CC pathogenic trans-acting viral genes, meaning that cancer incidence is a  
CC direct consequence of the effects of proviral integration into host  
CC protooncogenes. The CA nucleic acid sequences can be used to diagnose  
CC carcinoma (especially breast cancer, prostate cancer, lymphoma or  
CC leukemia) or a propensity to carcinoma by determination of the sequence  
CC of a CA gene, or by determination of CA gene expression in particular  
CC tissues. CA nucleic acids, proteins and antibodies are also useful as  
CC therapeutic agents and in screening and evaluating drug candidates. The  
CC present sequence represents a specifically claimed murine CA nucleic acid  
CC sequence of the invention. Note: The complete sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
XX ftp://wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 96599 BP; 28457 A; 18209 C; 18968 G; 30477 T; 0 U; 488 Other;  
XX  
Query Match 82.0%; Score 16.4; DB 9; Length 96599;  
Best Local Similarity 83.3%; Pred. No. 8.6e+02;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
OY 1 AGGUAACGCCAGACUAC 18  
DB 28454 AGGTACGACGAGGCTAC 28471  
XX  
RESULT 21  
ADB72671  
ID ADB72671 standard; DNA; 96599 BP.  
XX  
AC ADB72671;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
XX Mouse Braf gene.  
XX  
XX mouse; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;  
KM cancer; neoplasia; adenocarcinoma; sarcoma; gene.  
XX  
XX Mus sp.  
XX  
XX WO2003008583-A2.  
XX  
XX 30-JAN-2003.  
XX  
XX 26-DEC-2001; 2001WO-US051291.  
XX  
XX 02-MAR-2001; 2001US-00798586.  
XX  
XX 23-OCT-2001; 2001US-00004113.  
XX  
XX 08-NOV-2001; 2001US-00052482.  
XX  
XX 30-NOV-2001; 2001US-00997722.  
XX  
XX 20-DEC-2001; 2001US-00034650.  
XX  
XX (SAGR-) SAGRES DISCOVERY.  
XX  
XX Morris DW, Engelhard EK;  
XX WPI; 2003-239337/23.  
XX  
XX New recombinant nucleic acid, useful for treating carcinomas, lymphomas,  
PT cancers, neoplasia, adenocarcinoma, or sarcomas.  
XX  
XX Claim 1; SEQ ID NO 499; 2304bp; English.  
XX  
XX The invention relates to a novel recombinant nucleic acid comprising a  
CC nucleotide sequence selected from any of the 660 sequences fully defined  
CC in the specification. A polynucleotide of the invention has cytostatic  
CC activity, and may have a use in gene therapy, or in a vaccine. The

CC recombinant nucleic acids and polypeptides are useful for treating  
 CC carcinomas, e.g. lymphomas, cancers, neoplasms, adenocarcinoma, and  
 CC sarcomas. The present sequence represents a mouse gene of the invention.  
 XX Sequence 96599 BP; 28457 A; 18209 C; 18968 G; 30477 T; 0 U; 488 Other;  
 SQ

Query Match 82.0%; Score 16.4; DB 10; Length 96599;  
 Best Local Similarity 83.3%; Pred. No. 8.6e+02;  
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGUAACAGCCAGACGACUAC 18  
 |||:|||||:|||||:|  
 Db 28454 AGGTACAGCCAGCGCTAC 28471

RESULT 22  
 ADC85413  
 ID ADC85413 standard; DNA; 96599 BP.  
 XX  
 AC ADC85413;  
 XX  
 DT 01-JAN-2004 (first entry)  
 XX  
 DE Mouse Braf genomic sequence.  
 XX  
 KM Cytostatic; gene therapy; vaccine; cancer; carcinoma-associated gene; CA;  
 KM secreted; transmembrane; intracellular; ds.  
 XX  
 OS Mus BP.  
 XX  
 PN WO2003045230-A2.  
 XX  
 PD 05-JUN-2003.  
 XX  
 PF 02-DEC-2002; 2002MO-US038582.  
 XX  
 PR 30-NOV-2001; 2001US-00997722.  
 XX  
 PA (SAGR-) SAGRES DISCOVERY.  
 XX  
 PI Morris DW, Engelhard EK;  
 XX  
 DR WPI; 2003-513603/48.  
 XX  
 PT New recombinant nucleic acid comprising a nucleotide sequence of any of  
 PT the carcinoma-associated (CA) genes, useful for screening for drug  
 PT candidates for diagnosing or treating carcinomas.  
 XX  
 PS Claim 1; SEQ ID NO 199; 983bp; English.  
 XX  
 CC The invention relates to a recombinant nucleic acid comprising a  
 CC nucleotide sequence selected from any of the fully defined carcinoma-  
 CC associated (CA) genes from the 50 tables given in the specification. The  
 CC CA proteins are secreted, transmembrane or intracellular proteins. The  
 CC recombinant nucleic acids are useful for screening for drug candidates  
 CC for diagnosing or treating carcinomas. Sequences given in ADC85215-  
 CC ADC85514 represent CA genes of the invention.  
 XX  
 SQ Sequence 96599 BP; 28457 A; 18209 C; 18968 G; 30477 T; 0 U; 488 Other;  
 XX

Query Match 82.0%; Score 16.4; DB 10; Length 96599;  
 Best Local Similarity 83.3%; Pred. No. 8.6e+02;  
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGUAACAGCCAGACGACUAC 18  
 |||:|||||:|||||:|  
 Db 28454 AGGTACAGCCAGCGCTAC 28471

RESULT 23  
 ADM74528  
 ID ADM74528 standard; DNA; 96599 BP.  
 XX

AC ADM74528;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Murine carcinoma associated (CA) nucleic acid #100.  
 XX  
 KM Mouse; carcinoma associated nucleic acid; CA nucleic acid; gene; ds;  
 KM carcinoma associated protein; CAP; carcinoma; leukemia; lymphoma;  
 KM cytostatic.  
 XX  
 OS Mus musculus.  
 XX  
 PN US2004072154-A1.  
 XX  
 PD 15-APR-2004.  
 XX  
 PF 30-NOV-2001; 2001US-00997722.  
 XX  
 PR 22-DEC-2000; 2000US-00747377.  
 PR 02-MAR-2001; 2001US-00798586.  
 XX  
 PA (MORRIS/) MORRIS D W.  
 PA (ENGELHARD/) ENGELHARD B K.  
 XX  
 PI Morris DW, Engelhard EK;  
 XX  
 DR WPI; 2004-328562/30.  
 XX  
 PT New carcinoma associated gene or protein, useful for preparing a  
 PT composition for diagnosing or treating carcinoma e.g., leukemia or  
 PT lymphoma.  
 XX  
 PS Claim 1; SEQ ID NO 199; 29pp; English.  
 XX  
 CC The invention relates to new recombinant nucleic acids. The invention  
 CC also relates to a host cell comprising a recombinant nucleic acid or  
 CC expression vector, an expression vector comprising a recombinant nucleic  
 CC acid, a recombinant protein, a method of screening for drug candidates, a  
 CC method of screening for a bioactive agent capable of binding to a  
 CC carcinoma associated protein (CAP) encoded by a nucleotide sequence, a  
 CC method of screening for a bioactive agent capable of modulating the  
 CC activity of a CAP, a method of evaluating the effect of a candidate  
 CC carcinoma drug, a method of diagnosing carcinoma, a method for inhibiting  
 CC the activity of a CAP, a method of treating carcinomas, a method of  
 CC neutralising the effect of a CAP and a method of diagnosing carcinoma or  
 CC propensity to carcinoma. A method of evaluating the effect of a candidate  
 CC carcinoma drug comprises administering the drug to a patient, removing a  
 CC cell sample from the patient and determining alterations in the  
 CC expression or activation of a gene comprising the nucleotide sequence. A  
 CC method of diagnosing carcinoma comprises determining the expression of  
 CC one or more genes comprising the nucleic acid sequence in a first tissue  
 CC type of a first individual and comparing the expression of the gene from  
 CC a second normal tissue type from the first individual or a second  
 CC unaffected individual, where a difference in the expression indicates  
 CC that the first individual has carcinoma. A method of inhibiting the  
 CC activity of a CAP comprises binding an inhibitor to the CAP. Treating  
 CC carcinomas comprises administering to a patient an inhibitor of CAP.  
 CC Neutralising the effect of a CAP comprises contacting an agent specific  
 CC for the CAP. The polypeptide specifically binds to the protein encoded by  
 CC the nucleic acid. It comprises an antibody that specifically binds to the  
 CC protein encoded by the nucleic acid. The nucleic acids are useful for  
 CC preparing a composition for diagnosing or treating carcinoma e.g.,  
 CC leukemia or lymphoma. This sequence represents a murine carcinoma  
 CC associated (CA) nucleic acid of the invention. Note: The sequence data  
 CC obtained in electronic format directly from the printed specification but was  
 CC obtained in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html.  
 XX  
 SQ Sequence 96599 BP; 28457 A; 18209 C; 18968 G; 30477 T; 0 U; 488 Other;  
 XX

Query Match 82.0%; Score 16.4; DB 12; Length 96599;  
 Best Local Similarity 83.3%; Pred. No. 8.6e+02;  
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGUACAGCCAGACUAC 18  
|||:|||||:|||||  
DB 28454 AGGTACAGCCAGGCTAC 28471

## RESULT 24

ABL20341  
ID ABL20341 standard; DNA; 2550 BP.

AC ABL20341;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 12496.

KM Drosophila; developmental biology; cell signalling; insecticide;  
pharmaceutical; gene; ds.

OS Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US009231.

PR 23-MAR-2000; 2000US-0191637P.

PR 11-JUL-2000; 2000US-00614150.

PA (PERKE ) PB CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;

PI WPI; 2001-656860/75.

PT New isolated nucleic acid detection reagent for detecting 1000 or more  
genes from Drosophila and for elucidating cell signaling and cell-cell  
interactions.

PS Claim 1; SEQ ID NO 12496; 21pp + Sequence listing; English.

CC The invention relates to an isolated nucleic acid detection reagent  
capable of detecting 1000 or more genes from Drosophila. The invention is  
useful in developmental biology and in elucidating cell signalling and  
cell-cell interactions in higher eukaryotes for the development of  
insecticides, therapeutics and pharmaceutical drugs. The invention  
discloses genomic DNA sequences (AB16176-AB130511), expressed DNA  
sequences (AB101840-AB16175) and the encoded proteins (AB57737-  
AB872072). The sequence data for this patent did not form part of the  
printed specification, but was obtained in electronic format directly  
from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

SO Sequence 2550 BP; 717 A; 651 C; 644 G; 538 T; 0 U; 0 Other;

Query Match Best Local Similarity 80.0%; Score 16; DB 4; Length 2550;

Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GUACAGCCAGACUAC 18  
|||:|||||:|||||  
DB 1447 GTACAGCCAGACTAC 1462

## RESULT 25

ABL09903  
ID ABL09903 standard; CDNA; 2668 BP.

AC ABL09903;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 24191.

KM Drosophila; developmental biology; cell signalling; insecticide;  
pharmaceutical; gene; ds.  
OS Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US009231.

PR 23-MAR-2000; 2000US-0191637P.

PR 11-JUL-2000; 2000US-00614150.

PA (PERKE ) PB CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;

PI WPI; 2001-656860/75.  
P-PSDB; ABB65800.

PT New isolated nucleic acid detection reagent for detecting 1000 or more  
genes from Drosophila and for elucidating cell signaling and cell-cell  
interactions.

PS Claim 1; SEQ ID NO 24191; 21pp + Sequence listing; English.

CC The invention relates to an isolated nucleic acid detection reagent  
capable of detecting 1000 or more genes from Drosophila. The invention is  
useful in developmental biology and in elucidating cell signalling and  
cell-cell interactions in higher eukaryotes for the development of  
insecticides, therapeutics and pharmaceutical drugs. The invention  
discloses genomic DNA sequences (AB16176-AB130511), expressed DNA  
sequences (AB101840-AB16175) and the encoded proteins (AB57737-  
AB872072). The sequence data for this patent did not form part of the  
printed specification, but was obtained in electronic format directly  
from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

SO Sequence 2668 BP; 745 A; 682 C; 665 G; 576 T; 0 U; 0 Other;

Query Match Best Local Similarity 80.0%; Score 16; DB 4; Length 2668;

Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GUACAGCCAGACUAC 18  
|||:|||||:|||||  
DB 1565 GTACAGCCAGACTAC 1580

RESULT 26  
ABL20340/c  
ID ABL20340 standard; DNA; 4972 BP.

AC ABL20340;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 12493.

KM Drosophila; developmental biology; cell signalling; insecticide;  
pharmaceutical; gene; ds.

OS Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US009231.

PR 23-MAR-2000; 2000US-0191637P.  
PR 11-JUL-2000; 2000US-00614150.

XX (PEKE ) PE CORP NY.  
 PA Venter JC, Adams M, Li PWD, Myers EW;  
 PI WPI; 2001-656860/75.  
 XX  
 DR New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signaling and cell-cell  
 PT interactions.  
 XX  
 PS Claim 1; SEQ ID NO 12493; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signaling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA  
 CC sequences (AB101840-AB16175) and the encoded proteins (AB57737-  
 CC AB82072). The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 CC  
 SQ Sequence 4972 BP; 1255 A; 1057 C; 1134 G; 1526 T; 0 U; 0 Other;  
 XX  
 Query Match 80.0%; Score 16; DB 4; Length 4972;  
 Best Local Similarity 87.5%; Pred. No. 1.1e+03;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 3 GUACAGCCAGAGACTAC 18  
 DB 2160 GTACAGCCAGAGACTAC 2145  
 XX  
 RESULT 27  
 ABL09902/c  
 ID ABL09902 standard; cDNA; 4989 BP.  
 XX  
 AC ABL09902;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 24188.  
 XX  
 KW Drosophila; developmental biology; cell signaling; insecticide;  
 KW pharmaceutical; gene; ss.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 PN WO200171042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 23-MAR-2001; 2001WO-US009231.  
 XX  
 PR 23-MAR-2000; 2000US-0191637P.  
 PR 11-JUL-2000; 2000US-00614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX  
 DR WPI; 2001-656860/75.  
 DR P-PSDB; ABB85799.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signaling and cell-cell  
 PT interactions.  
 XX  
 PS Claim 1; SEQ ID NO 24188; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signaling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA  
 CC sequences (AB101840-AB16175) and the encoded proteins (AB57737-  
 CC AB82072). The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 CC  
 SQ Sequence 4989 BP; 1258 A; 1059 C; 1140 G; 1532 T; 0 U; 0 Other;  
 XX  
 Query Match 80.0%; Score 16; DB 4; Length 4989;  
 Best Local Similarity 87.5%; Pred. No. 1.1e+03;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 3 GUACAGCCAGAGACTAC 18  
 DB 2160 GTACAGCCAGAGACTAC 2145  
 XX  
 RESULT 28  
 ADQ97596  
 ID ADQ97596 standard; DNA; 90616 BP.  
 XX  
 AC ADQ97596;  
 XX  
 DT 07-OCT-2004 (first entry)  
 XX  
 XX Mouse cancer associated sequence MD10-012, SEQ ID 573.  
 XX  
 KW Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Mouse; ds.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO2004060304-A2.  
 XX  
 PD 22-JUL-2004.  
 XX  
 PF 22-DEC-2003; 2003WO-US041389.  
 XX  
 PR 27-DEC-2002; 2002US-00330773.  
 XX  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 XX  
 PI Morris DW, Malandro MS;  
 XX  
 DR WPI; 2004-543781/52.  
 XX  
 PT New isolated cancer associated nucleic acids comprising at least 10  
 PT contiguous nucleotides, useful for diagnosing, preventing and/or treating  
 PT cancers such as leukemia and lymphoma.  
 XX  
 PS Claim 1; SEQ ID NO 573; 199pp; English.  
 XX  
 CC The present invention relates to cancer associated sequences (ADQ97025-  
 CC ADQ98004). The sequences are useful for the diagnosis, prevention and/or  
 CC treatment of cancer, such as leukemia and lymphoma. Note: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 90616 BP; 22442 A; 19414 C; 20208 G; 27923 T; 0 U; 629 Other;  
 XX  
 Query Match 80.0%; Score 16; DB 12; Length 90616;  
 Best Local Similarity 87.5%; Pred. No. 1.3e+03;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 3 GUACAGCCAGAGACTAC 18  
 DB 39970 GTACAGCCAGAGACTAC 39985

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RESULT 29
ID ADC85298
XX AD85298 standard; DNA; 96599 BP.
XX
XX
AC AD85298;
XX
XX 01-JAN-2004 (first entry)
XX
XX Human Bgr2 coding sequence.
XX
XX Cytostatic; gene therapy; vaccine; cancer; carcinoma-associated gene; CA;
XX secreted; transmembrane; intracellular; ds.
XX
XX Homo sapiens.
XX
XX WO2003045230-A2.
XX
XX 05-JUN-2003.
XX
XX 02-DEC-2002; 2002WO-US038582.
XX
XX 30-NOV-2001; 2001US-00997722.
XX
XX (SAGR-) SAGRES DISCOVERY.
XX
XX Morris DW, Engelhard EK;
XX
XX WPI; 2003-513603/48.
XX
XX New recombinant nucleic acid comprising a nucleotide sequence of any of
XX the carcinoma-associated (CA) genes, useful for screening for drug
XX candidates for diagnosing or treating carcinomas.
XX
XX Claim 1; SEQ ID NO 84; 983bp; English.
XX
XX The invention relates to a recombinant nucleic acid comprising a
XX nucleotide sequence selected from any of the fully defined carcinoma-
XX associated (CA) genes from the 50 tables given in the specification. The
XX CA proteins are secreted, transmembrane or intracellular proteins. The
XX recombinant nucleic acids are useful for screening for drug candidates
XX for diagnosing or treating carcinomas. Sequences given in ADC85215-
XX ADC85514 represent CA genes of the invention.
XX
XX Sequence 96599 BP; 27390 A; 19000 C; 20559 G; 29350 T; 0 U; 300 Other;
XX
XX Query Match 80.0%; Score 16; DB 10; Length 96599;
XX Best Local Similarity 87.5%; Pred. No. 1.3e+03;
XX Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX 3 GUACAGCCAGGACTAC 18
XX
XX Db 91765 GTACAGCCAGGACTAC 91780
XX
XX
XX RESULT 30
XX ADA02819
XX ID ADA02819 standard; DNA; 96600 BP.
XX
XX ADA02819;
XX
XX 06-NOV-2003 (first entry)
XX
XX Mouse Sos1 carcinoma associated gene, SEQ ID NO:1337.
XX
XX Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast;
XX prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
XX gene; ds.
XX
XX Mus sp.
XX
XX WO2003057146-A2.
XX
XX 17-JUL-2003.
XX

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XX
XX 26-DEC-2002; 2002WO-US041414.
XX
XX AD85298 standard; DNA; 96599 BP.
XX
XX 26-DEC-2001; 2001US-00035832.
XX
XX (SAGR-) SAGRES DISCOVERY.
XX
XX Morris DW;
XX
XX WPI; 2003-587068/55.
XX
XX New recombinant nucleic acid encoding carcinoma associated protein,
XX useful for preparing compositions for treating carcinomas.
XX
XX Claim 1; SEQ ID NO 1337; 245bp; English.
XX
XX The invention relates to recombinant carcinoma associated (CA) nucleic
XX acid sequences from mouse and human (ADA01482-ADA03094), and to
XX recombinant carcinoma associated proteins (CAP) encoded by them. The
XX invention also encompasses expression vectors and host cells comprising a
XX CA nucleic acid, a polypeptide (especially an antibody) that specifically
XX binds to the protein, and a biochip comprising CA nucleic acid or
XX fragments thereof. The sequences of the invention were identified using
XX oncogenic retroviruses, which insert into the genome of the host organism
XX at random. Many of these do not carry transduced host oncogenes or
XX pathogenic trans-acting viral genes, meaning that cancer incidence is a
XX direct consequence of the effects of proviral integration into host
XX protooncogenes. The CA nucleic acid sequences can be used to diagnose
XX carcinoma (especially breast cancer, prostate cancer, lymphoma or
XX leukaemia) or a propensity to carcinoma by determination of the sequence
XX of a CA gene, or by determination of CA gene expression in particular
XX tissues. CA nucleic acids, proteins and antibodies are also useful as
XX therapeutic agents and in screening and evaluating drug candidates. The
XX present sequence represents a specifically claimed murine CA nucleic acid
XX sequence of the invention. Note: The complete sequence data for this
XX patent did not form part of the printed sequence specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 96600 BP; 27391 A; 19001 C; 20558 G; 29350 T; 0 U; 300 Other;
XX
XX Query Match 80.0%; Score 16; DB 9; Length 96600;
XX Best Local Similarity 87.5%; Pred. No. 1.3e+03;
XX Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX 3 GUACAGCCAGGACTAC 18
XX
XX Db 91766 GTACAGCCAGGACTAC 91781
XX
XX
XX RESULT 31
XX ADB72557
XX ID ADB72557 standard; DNA; 96600 BP.
XX
XX ADB72557;
XX
XX 04-DEC-2003 (first entry)
XX
XX Mouse Sos1 gene.
XX
XX mouse; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphoma;
XX cancer; neoplasm; adenocarcinoma; sarcoma; gene.
XX
XX Mus sp.
XX
XX WO2003008583-A2.
XX
XX 30-JAN-2003.
XX
XX 26-DEC-2001; 2001WO-US051291.
XX
XX 02-MAR-2001; 2001US-00798586.
XX
XX 23-OCT-2001; 2001US-00004113.
XX

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PR 08-NOV-2001; 2001US-00052482.  
 PR 30-NOV-2001; 2001US-00997722.  
 PR 20-DEC-2001; 2001US-00034650.  
 PA (SAGR-) SAGRES DISCOVERY.  
 PI Morris DW, Engelhard EK;  
 DR WPI; 2003-239337/23.  
 PT New recombinant nucleic acid, useful for treating carcinomas, lymphomas,  
 PT cancer, neoplasm, adenocarcinoma, or sarcomas.  
 PS Claim 1; SEQ ID NO 385; 2304pp; English.  
 CC The invention relates to a novel recombinant nucleic acid comprising a  
 CC nucleotide sequence selected from any of the 660 sequences fully defined  
 CC in the specification. A polynucleotide of the invention has cytostatic  
 CC activity, and may have a use in gene therapy, or in a vaccine. The  
 CC recombinant nucleic acids and polypeptides are useful for treating  
 CC carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and  
 CC sarcomas. The present sequence represents a mouse gene of the invention.  
 SO Sequence 96600 BP; 27391 A; 19001 C; 20558 G; 29350 T; 0 U; 300 Other;  
 QY Query Match 80.0%; Score 16; DB 10; Length 96600;  
 DB Best Local Similarity 87.5%; Pred. No. 1.3e+03;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GUNACGCCAGACUAC 18  
 DB 91766 GTACAGCCAGACTAC 91781  
 RESULT 32  
 ID ADM74414 standard; DNA; 96600 BP.  
 AC ADM74414;  
 XX 01-JUL-2004 (first entry)  
 DT Murine carcinoma associated (CA) nucleic acid #43.  
 DE Mouse; carcinoma associated nucleic acid; CA nucleic acid; gene; ds;  
 KM carcinoma associated protein; CAP; carcinoma; leukaemia; lymphoma;  
 KM cytosolic.  
 XX Mus musculus.  
 OS US2004072154-A1.  
 XX 15-APR-2004.  
 PD 30-NOV-2001; 2001US-00997722.  
 PF 22-DEC-2000; 2000US-00747377.  
 PR 02-MAR-2001; 2001US-00798586.  
 XX (MORR/) MORRIS D W.  
 PA (ENGEL/) ENGELHARD E K.  
 PI Morris DW, Engelhard EK;  
 DR WPI; 2004-328562/30.  
 CC New carcinoma associated gene or protein, useful for preparing a  
 CC composition for diagnosing or treating carcinoma e.g., leukemia or  
 CC lymphoma.  
 PS Claim 1; SEQ ID NO 85; 29pp; English.  
 CC The invention relates to new recombinant nucleic acids. The invention

CC also relates to a host cell comprising a recombinant nucleic acid or  
 CC expression vector, an expression vector comprising a recombinant nucleic  
 CC acid, a recombinant protein, a method of screening for drug candidates, a  
 CC method of screening for a bioactive agent capable of binding to a  
 CC carcinoma associated protein (CAP) encoded by a nucleotide sequence, a  
 CC method of screening for a bioactive agent capable of modulating the  
 CC activity of a CAP, a method of evaluating the effect of a candidate  
 CC carcinoma drug, a method of diagnosing carcinoma, a method for inhibiting  
 CC the activity of a CAP, a method of treating carcinomas, a method of  
 CC neutralizing the effect of a CAP and a method of diagnosing carcinoma or  
 CC propensity to carcinoma. A method of evaluating the effect of a candidate  
 CC carcinoma drug comprises administering the drug to a patient, removing a  
 CC cell sample from the patient and determining alterations in the  
 CC expression or activation of a gene comprising the nucleotide sequence. A  
 CC method of diagnosing carcinoma comprises determining the expression of  
 CC one or more genes comprising the nucleic acid sequence in a first tissue  
 CC type of a first individual and comparing the expression of the gene from  
 CC a second normal tissue type from the first individual or a second  
 CC unaffected individual, where a difference in the expression indicates  
 CC that the first individual has carcinoma. A method of inhibiting the  
 CC activity of a CAP comprises binding an inhibitor to the CAP. Treating  
 CC carcinomas comprises administering to a patient an inhibitor of CAP.  
 CC Neutralising the effect of a CAP comprises contacting an agent specific  
 CC for the CAP. The polypeptide specifically binds to the protein encoded by  
 CC the nucleic acid. It comprises an antibody that specifically binds to the  
 CC protein encoded by the nucleic acid. The nucleic acids are useful for  
 CC preparing a composition for diagnosing or treating carcinoma e.g.,  
 CC leukaemia or lymphoma. This sequence represents a murine carcinoma  
 CC associated (CA) nucleic acid of the invention. Note: The sequence data  
 CC for this patent did not form part of the printed specification but was  
 CC obtained in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html.  
 SO Sequence 96600 BP; 27391 A; 19001 C; 20558 G; 29350 T; 0 U; 300 Other;  
 QY Query Match 80.0%; Score 16; DB 12; Length 96600;  
 DB Best Local Similarity 87.5%; Pred. No. 1.3e+03;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GUNACGCCAGACUAC 18  
 DB 91766 GTACAGCCAGACTAC 91781  
 RESULT 33  
 ID ADP74214/C  
 ADP74214 standard; DNA; 144411 BP.  
 AC ADP74214;  
 XX 26-AUG-2004 (first entry)  
 DT Equine herpesvirus 4 genome gm deletion mutant #2.  
 DE Equine herpesvirus 4 genome gm deletion mutant #2.  
 KM virucide; vaccine; Equine Herpes Virus; EHV; gm; vaccine;  
 KM EHV-associated condition; Equine herpesvirus 4; EHV4; ds; mutant; mutein.  
 XX Equine herpesvirus 4.  
 OS Synthetic.  
 OS US2004109873-A1.  
 XX 10-JUN-2004.  
 PD 21-JUL-2003; 2003US-00624149.  
 PF 19-JUL-2002; 2002US-01033064.  
 PR 14-AUG-2002; 2002US-0403282P.  
 PR 11-APR-2003; 2003DS-01017008.  
 XX (BOEH ) BOEHRINGER INGELHEIM VETMEDICA GMBH.  
 PA Neubauer A, Ziegler C;  
 PI

XX WPI; 2004-440311/41.  
 XX  
 XX New recombinant equine herpes (EHV) virus free of heterologous elements,  
 PT and where protein gm has been deleted, useful as a vaccine for treating  
 PT or preventing EHV infections.  
 XX  
 XX Claim 18; Page; 156pp; English.  
 XX  
 CC The invention describes a new recombinant Equine Herpes Virus (EHV) where  
 CC the protein gm is absent, and the EHV is free of heterologous elements.  
 CC Also described are: a nucleic acid coding for an EHV defined above; a  
 CC vaccine preparation comprising the EHV or nucleic acid; obtaining a  
 CC recombinant EHV; and a cell line for use in the method, where the gene  
 CC encoding the protein gm is transfected into the cell line, and the cell  
 CC line expresses gm. The vaccine comprising the EHV or nucleic acid  
 CC encoding EHV is useful for treating and/or preventing EHV-associated  
 CC condition, and for monitoring the therapeutic success. The recombinant  
 CC EHV is useful as a vaccine against EHV infections. This sequence  
 CC represents an Equine herpesvirus 4 genome in which nucleotides 92681-  
 CC 93865, comprising regions of the gm gene, have been deleted.  
 CC  
 SQ Sequence 144411 BP; 35893 A; 36645 C; 36246 G; 35627 T; 0 U; 0 Other;  
 Query Match 80.0%; Score 16; DB 12; Length 144411;  
 Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GGUACAGCCAGACTA 17  
 DB 76346 GGTACAGCCAGACTA 76331  
 ID ADF74213 standard; DNA; 144486 BP.  
 AC ADF74215;  
 XX 26-AUG-2004 (first entry)  
 DT  
 DE Equine herpesvirus 4 genome gm deletion mutant #3.  
 XX  
 XX virucide; vaccine; Equine Herpes Virus; EHV; gm; vaccine;  
 KM EHV-associated condition; Equine herpesvirus 4; EHV4; ds; mutant; mutein.  
 XX  
 OS Equine herpesvirus 4.  
 OS Synthetic.  
 XX US2004109873-A1.  
 XX 10-JUN-2004.  
 PD  
 PF 21-JUN-2003; 2003US-00624149.  
 XX  
 XX 19-JUL-2002; 2002DE-01033064.  
 PR 14-AUG-2002; 2002US-0403282P.  
 PR 11-APR-2003; 2003DE-01017008.  
 XX  
 PA (BOEHR) BOEHRINGER INGELHEIM VETMEDICA GMBH.  
 XX  
 XX Neubauer A, Ziegler C;  
 PI  
 DR WPI; 2004-440311/41.  
 XX  
 PT New recombinant equine herpes (EHV) virus free of heterologous elements,  
 PT and where protein gm has been deleted, useful as a vaccine for treating  
 PT or preventing EHV infections.  
 XX  
 PS Claim 19; Page; 156pp; English.  
 XX  
 CC The invention describes a new recombinant Equine Herpes Virus (EHV) where  
 CC the protein gm is absent, and the EHV is free of heterologous elements.

CC Also described are: a nucleic acid coding for an EHV defined above; a  
 CC vaccine preparation comprising the EHV or nucleic acid; obtaining a  
 CC recombinant EHV; and a cell line for use in the method, where the gene  
 CC encoding the protein gm is transfected into the cell line, and the cell  
 CC line expresses gm. The vaccine comprising the EHV or nucleic acid  
 CC encoding EHV is useful for treating and/or preventing EHV-associated  
 CC condition, and for monitoring the therapeutic success. The recombinant  
 CC EHV is useful as a vaccine against EHV infections. This sequence  
 CC represents an Equine herpesvirus 4 genome in which nucleotides 92715-  
 CC 93824, comprising regions of the gm gene, have been deleted.  
 CC  
 SQ Sequence 144486 BP; 35916 A; 36662 C; 36259 G; 35649 T; 0 U; 0 Other;  
 Query Match 80.0%; Score 16; DB 12; Length 144486;  
 Best Local Similarity 87.5%; Pred. No. 1.4e+03;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GGUACAGCCAGACTA 17  
 DB 76346 GGTACAGCCAGACTA 76331  
 ID ADF74213 standard; DNA; 145444 BP.  
 AC ADF74213;  
 XX 26-AUG-2004 (first entry)  
 DT  
 DE Equine herpesvirus 4 genome gm deletion mutant #1.  
 XX  
 XX virucide; vaccine; Equine Herpes Virus; EHV; gm; vaccine;  
 KM EHV-associated condition; Equine herpesvirus 4; EHV4; ds; mutant; mutein.  
 XX  
 OS Equine herpesvirus 4.  
 OS Synthetic.  
 XX US2004109873-A1.  
 XX 10-JUN-2004.  
 PD  
 PF 21-JUN-2003; 2003US-00624149.  
 XX  
 XX 19-JUL-2002; 2002DE-01033064.  
 PR 14-AUG-2002; 2002US-0403282P.  
 PR 11-APR-2003; 2003DE-01017008.  
 XX  
 PA (BOEHR) BOEHRINGER INGELHEIM VETMEDICA GMBH.  
 XX  
 XX Neubauer A, Ziegler C;  
 PI  
 DR WPI; 2004-440311/41.  
 XX  
 PT New recombinant equine herpes (EHV) virus free of heterologous elements,  
 PT and where protein gm has been deleted, useful as a vaccine for treating  
 PT or preventing EHV infections.  
 XX  
 PS Claim 17; Page; 156pp; English.  
 XX  
 CC The invention describes a new recombinant Equine Herpes Virus (EHV) where  
 CC the protein gm is absent, and the EHV is free of heterologous elements.  
 CC Also described are: a nucleic acid coding for an EHV defined above; a  
 CC vaccine preparation comprising the EHV or nucleic acid; obtaining a  
 CC recombinant EHV; and a cell line for use in the method, where the gene  
 CC encoding the protein gm is transfected into the cell line, and the cell  
 CC line expresses gm. The vaccine comprising the EHV or nucleic acid  
 CC encoding EHV is useful for treating and/or preventing EHV-associated  
 CC condition, and for monitoring the therapeutic success. The recombinant  
 CC EHV is useful as a vaccine against EHV infections. This sequence  
 CC represents an Equine herpesvirus 4 genome in which nucleotides 92681-  
 CC 92731 and 93765-93865, comprising regions of the gm gene, have been  
 CC deleted.



```
XX Sequence 145444 BP; 36178 A; 36893 C; 36497 G; 35876 T; 0 U; 0 Other;
SQ
Query Match 80.0%; Score 16; DB 12; Length 145444;
Best Local Similarity 87.5%; Pred. NO. 1.4e+03;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGACUA 17
DB 76346 GTTACAGCCAGACTA 76331

RESULT 36
ADP74202/c
ID ADP74202 standard; DNA; 145596 BP.
XX
AC ADP74202;
XX
DT 26-AUG-2004 (first entry)
XX
DE Equine herpesvirus 4 genome segid 2.
XX
XX virucide; vaccine; Equine Herpes Virus; EHV; gm; vaccine;
XX EHV-associated condition; Equine herpesvirus 4; EHV4; ds.
XX
OS Equine herpesvirus 4.
XX
XX US2004109873-A1.
XX
XX 10-JUN-2004.
XX
XX 21-JUL-2003; 2003US-00624149.
XX
XX 19-JUL-2002; 2002DE-01033064.
XX 14-AUG-2002; 2002US-0403282P.
XX 11-APR-2003; 2003DE-01017008.
XX
PA (BOEH ) BOEHRINGER INGELHEIM VETMEDICA GMBH.
XX
PI Neuberger A, Ziegler C;
XX
DR WPI; 2004-440311/41.
XX
XX New recombinant equine herpes (EHV) virus free of heterologous elements,
PT and where protein gm has been deleted, useful as a vaccine for treating
PT or preventing EHV infections.
XX
XX Disclosure; SEQ ID NO 2; 156pp; English.
XX
XX The invention describes a new recombinant Equine Herpes Virus (EHV) where
XX the protein gm is absent, and the EHV is free of heterologous elements.
XX Also described are: a nucleic acid coding for an EHV defined above; a
XX vaccine preparation comprising the EHV or nucleic acid; obtaining a
XX recombinant EHV; and a cell line for use in the method, where the cell
XX encoding the protein gm is transfected into the cell line, and the cell
XX line expresses gm. The vaccine comprising the EHV or nucleic acid
XX encoding EHV is useful for treating and/or preventing EHV-associated
XX condition, and for monitoring the therapeutic success. The recombinant
XX EHV is useful as a vaccine against EHV infections. This sequence
XX represents the Equine herpesvirus 4 genome.
XX
SQ Sequence 145596 BP; 36213 A; 36932 C; 36529 G; 35922 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 12; Length 145596;
Best Local Similarity 87.5%; Pred. NO. 1.4e+03;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGACUA 17
DB 76346 GTTACAGCCAGACTA 76331

RESULT 37
```

```
ADZ13116/c
ID ADZ13116 standard; DNA; 241748 BP.
XX
AC ADZ13116;
XX
DT 16-JUN-2005 (first entry)
XX
DE Murine cancer-associated genomic DNA #54.
XX
XX Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;
XX cytosolic; gene; ds.
XX
XX Mus sp.
XX
XX WO2005031001-A2.
XX
XX 07-APR-2005.
XX
XX 23-SEP-2004; 2004WO-US031617.
XX
XX 23-SEP-2003; 2003US-00669920.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Morris DW, Malandro MS;
XX
XX WPI; 2005-273395/28.
XX
XX Nucleic acid array useful for detecting cancer associated nucleic acid,
XX comprises two or more nucleic acid probes.
XX
XX Disclosure; SEQ ID NO 636; 198pp; English.
XX
XX The invention relates to a nucleic acid array for detecting a cancer
XX associated (CA) nucleic acid, comprising two or more nucleic acid probes.
XX The invention also relates to a peptide array comprising two or more
XX isolated polypeptides encoded by a CA nucleic acid sequence, a compound
XX that binds to a polypeptide, an isolated antibody or its fragment which
XX binds to a polypeptide, which is prepared by immunizing a host animal
XX with a composition comprising the polypeptide or its antigen binding
XX fragment and collecting cells from the host expressing antibodies against
XX the antigen or its antigen binding fragment, a composition comprising the
XX antibody and a carrier, a method of screening for anticancer activity, a
XX method of detecting a CA nucleic acid, a method of inhibiting expression of a CA
XX nucleic acid in a cell. The CA nucleic acid are useful for detecting CA
XX absence of cancer cells in an individual which involves contacting cells
XX from the individual with the antibody and detecting a complex of a CA
XX protein from the cancer cells and the antibody, where the detection of
XX the complex correlates with the presence of cancer cells in the
XX individual. The composition is useful for inhibiting growth of cancer
XX cells in an individual or for delivering a therapeutic agent to cancer
XX cells in an individual. The invention is also useful for diagnosing
XX cancer, for treating cancer and for inhibiting expression of a CA gene in
XX a cell. This sequence represents murine cancer-associated genomic DNA of
XX the invention.
XX
SQ Sequence 241748 BP; 59664 A; 56662 C; 57444 G; 61211 T; 0 U; 6767 Other;

Query Match 80.0%; Score 16; DB 14; Length 241748;
Best Local Similarity 87.5%; Pred. NO. 1.4e+03;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGUACAGCCAGACUAC 18
DB 42387 GTTACAGCCAGACTAC 42372

RESULT 38
ABD15945/c
ID ABD15945 standard; DNA; 411 BP.
XX
```

AC ABD15945;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Pseudomonas aeruginosa polynucleotide #14549.  
 XX  
 KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;  
 XX antibacterial.  
 OS Pseudomonas aeruginosa.  
 XX  
 PN US6551795-B1.  
 XX  
 PD 22-APR-2003.  
 XX  
 PF 18-FEB-1999; 99US-00252991.  
 XX  
 PR 18-FEB-1998; 98US-0074788P.  
 XX  
 PR 27-JUL-1998; 98US-0094190P.  
 XX  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 XX  
 PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
 DR WPI; 2003-615309/58.  
 DR P-PSDB; ABO82374.  
 XX  
 PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
 PT pathological conditions resulting from bacterial infection.  
 XX  
 PS Disclosure; SEQ ID NO 14549; 455pp; English.  
 XX  
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the  
 CC polynucleotides encoding them. The sequences are useful in diagnosis and  
 CC therapy of pathological conditions, as molecular targets for diagnostics,  
 CC prophylaxis and treatment of pathological conditions resulting from a  
 CC bacterial infection, for evaluating a compound, such as a polypeptide,  
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
 CC effective antibacterial targets, as targets for antibacterial drugs,  
 CC including anti-P. aeruginosa drugs, as templates for recombinant  
 CC production of P. aeruginosa-derived peptides or polypeptides, as target  
 CC components for diagnosis and/or treatment of P. aeruginosa-caused  
 CC infection, and in detection of P. aeruginosa sequences or other sequences  
 CC of Pseudomonas species using biochip technology. Sequences ABD01397-  
 CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html  
 CC  
 XX  
 SQ Sequence 411 BP; 56 A; 128 C; 170 G; 57 T; 0 U; 0 Other;  
 SO

Query Match 79.0%; Score 15.8; DB 11; Length 411;  
 Best Local Similarity 78.9%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGUNCAGCCGAGACTUAG 19  
 ||:|||||:|||||  
 Db 346 AGCTACAGCCTGAGACTACG 328

RESULT 39  
 ABD16211  
 ID ABD16211 standard; DNA; 537 BP.  
 XX  
 AC ABD16211;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Pseudomonas aeruginosa polynucleotide #14815.  
 XX  
 KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;  
 KW antibacterial.

XX  
 OS Pseudomonas aeruginosa.  
 XX  
 PN US6551795-B1.  
 XX  
 PD 22-APR-2003.  
 XX  
 PF 18-FEB-1999; 99US-00252991.  
 XX  
 PR 18-FEB-1998; 98US-0074788P.  
 XX  
 PR 27-JUL-1998; 98US-0094190P.  
 XX  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 XX  
 PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
 DR WPI; 2003-615309/58.  
 DR P-PSDB; ABO82640.  
 XX  
 PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
 PT pathological conditions resulting from bacterial infection.  
 XX  
 PS Disclosure; SEQ ID NO 14815; 455pp; English.  
 XX  
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the  
 CC polynucleotides encoding them. The sequences are useful in diagnosis and  
 CC therapy of pathological conditions, as molecular targets for diagnostics,  
 CC prophylaxis and treatment of pathological conditions resulting from a  
 CC bacterial infection, for evaluating a compound, such as a polypeptide,  
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
 CC effective antibacterial targets, as targets for antibacterial drugs,  
 CC including anti-P. aeruginosa drugs, as templates for recombinant  
 CC production of P. aeruginosa-derived peptides or polypeptides, as target  
 CC components for diagnosis and/or treatment of P. aeruginosa-caused  
 CC infection, and in detection of P. aeruginosa sequences or other sequences  
 CC of Pseudomonas species using biochip technology. Sequences ABD01397-  
 CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html  
 CC  
 XX  
 SQ Sequence 537 BP; 76 A; 226 C; 160 G; 75 T; 0 U; 0 Other;  
 SO

Query Match 79.0%; Score 15.8; DB 11; Length 537;  
 Best Local Similarity 78.9%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGUNCAGCCGAGACTUAG 19  
 ||:|||||:|||||  
 Db 162 AGCTACAGCCTGAGACTACG 180

RESULT 40  
 ABV15922/C  
 ID ABV15922 standard; cDNA; 542 BP.  
 XX  
 AC ABV15922;  
 XX  
 DT 13-SEP-2002 (first entry)  
 XX  
 DE Human prostate expression marker cDNA 15913.  
 XX  
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 KW pharmacogenomic marker; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200160860-A2.  
 XX  
 PD 23-AUG-2001.  
 XX  
 PR 20-FEB-2001; 2001WO-US005171.

```
XX 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JB;
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1; Page 2668; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for: (a) assessing whether
XX a patient is afflicted with prostate cancer; (b) monitoring the efficacy
XX of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX determining whether prostate cancer has metastasized in a patient; (h)
XX assessing the aggressiveness or indolence of prostate cancer in a patient
XX ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
XX Sequence 542 BP; 130 A; 111 C; 124 G; 173 T; 0 U; 4 Other;
XX
XX Query Match 79.0%; Score 15.8; DB 5; Length 542;
XX Best Local Similarity 78.9%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 AGGUAACGCCAGACUACG 19
XX |||:|||||||:|
XX 90 AGGTAGCCAGACTATG 72
XX
XX
XX RESULT 41
XX ABV45722/c
XX ID ABV45722 standard; cDNA; 592 BP.
XX
XX ABV45722;
XX
XX 16-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 45713.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US005171.
XX
XX 17-FEB-2000; 2000US-0183319P.
XX 16-MAR-2000; 2000US-0189862P.
XX 25-MAY-2000; 2000US-0207454P.
XX 09-JUN-2000; 2000US-0211314P.
XX 18-JUL-2000; 2000US-0219007P.
XX 13-DEC-2000; 2000US-0255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
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XX Schlegel R, Endege WO, Monahan JB;
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1; Page 9040; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for: (a) assessing whether
XX a patient is afflicted with prostate cancer; (b) monitoring the efficacy
XX of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX determining whether prostate cancer has metastasized in a patient; (h)
XX assessing the aggressiveness or indolence of prostate cancer in a patient
XX ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
XX Sequence 592 BP; 141 A; 124 C; 142 G; 185 T; 0 U; 0 Other;
XX
XX Query Match 79.0%; Score 15.8; DB 5; Length 592;
XX Best Local Similarity 78.9%; Pred. No. 1.2e+03;
XX Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 AGGUAACGCCAGACUACG 19
XX |||:|||||||:|
XX 136 AGGTAGCCAGACTATG 118
XX
XX
XX RESULT 42
XX AAS89740/c
XX ID AAS89740 standard; cDNA; 693 BP.
XX
XX AAS89740;
XX
XX 13-FEB-2002 (first entry)
XX
XX DNA encoding novel human diagnostic protein #25544.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX 31-MAR-2000; 2000US-00540217.
XX 23-AUG-2000; 2000US-00649167.
XX
XX (HYSB-) HYSBQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX P-PSDB; ABG25553.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 1; SEQ ID NO 25544; 103pp; English.
XX
```

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping.  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS6197-AAS94564 represent novel human diagnostic  
CC coding sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
CC  
SQ Sequence 693 BP, 141 A, 192 C, 218 G, 142 T, 0 U, 0 Other;  
Query Match 79.0%; Score 15.8; DB 5; Length 693;  
Best Local Similarity 84.2%; Pred. No. 1.2e+03;  
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
OY 2 GGUACAGCCAGGACTUACGA 20  
DB 186 GGCACAGCCAGGACTUACGA 168  
RESULT 43  
ABL04139/c  
ID ABL04139 standard; cDNA, 978 BP.  
XX  
AC ABL04139;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 6899.  
XX  
KW Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical; gene; SS.  
XX  
OS Drosophila melanogaster.  
XX  
PN WO200171042-A2.  
XX  
PD 27-SEP-2001.  
XX  
PF 23-MAR-2001; 2001WO-US009231.  
XX  
PR 23-MAR-2000; 2000US-0191637P.  
PR 11-JUL-2000; 2000US-00614150.  
XX  
PA (PERKE ) PE CORP NY.  
XX  
PI Venter JC, Adams M, Li PWD, Myers EW;  
XX  
DR WPI; 2001-656860/75.  
DR P-PDB; ABB60036.  
XX  
PT New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions.  
XX  
PS Claim 1; SEQ ID NO 6899; 21pp + Sequence listing; English.  
XX  
CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and

CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
CC  
SQ Sequence 978 BP, 213 A, 253 C, 234 G, 278 T, 0 U, 0 Other;  
Query Match 79.0%; Score 15.8; DB 4; Length 978;  
Best Local Similarity 78.9%; Pred. No. 1.2e+03;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
OY 1 AGUACAGCCAGGACTUACG 19  
DB 236 AGGTATGCGCAGGACTUACG 218  
RESULT 44  
ADS14617  
ID ADS14617 standard; DNA, 1023 BP.  
XX  
AC ADS14617;  
XX  
DT 16-DEC-2004 (first entry)  
XX  
DE Pseudomonas aeruginosa quorum sensing controlled gene PA2514, SEQ ID 172.  
XX  
KW Cytostratic; Anti-HIV; Antimicrobial; Immunosuppressive;  
KW quorum sensing signalling; bacterium; quorum sensing controlled gene;  
KW biofilm-associated disease; cystic fibrosis; AIDS; middle ear infection;  
KW acne; periodontal disease; gene; ds; PA2514.  
XX  
OS Pseudomonas aeruginosa.  
XX  
PN WO2004083385-A2.  
XX  
PD 30-SEP-2004.  
XX  
PF 11-MAR-2004; 2004WO-US007467.  
XX  
PR 14-MAR-2003; 2003US-00389647.  
XX  
PA (IOWA ) UNIV IOWA RES FOUND.  
XX  
PI Greenberg EP, Schuster M, Lostroh C;  
XX  
DR WPI; 2004-709932/69.  
XX  
PT Identifying a modulator of quorum sensing signalling in bacteria, useful  
PT for treating a biofilm-associated disorder, comprises contacting the cell  
PT with a quorum sensing signal molecule in the presence and absence of a  
PT test compound.  
XX  
PS Disclosure; SEQ ID NO 172; 23pp; English.  
XX  
CC The present invention relates to a method for identifying a modulator of  
CC quorum sensing signalling in bacteria. The method comprises: providing a  
CC cell that comprises a quorum sensing controlled gene (ADS1446-ADS14798),  
CC where the cell is responsive to a quorum sensing signal molecule such  
CC that a detectable signal is generated; contacting the cell with a quorum  
CC sensing signal molecule in the presence and absence of a test compound;  
CC and detecting a change in the detectable signal. The method and modulator  
CC identified by the method are useful for treating a biofilm-associated  
CC disease or disorder, e.g. cystic fibrosis, AIDS, middle ear infections,  
CC acne, periodontal disease, catheter-associated infections, and medical  
CC device-associated infections. Note: The sequence data for this patent was  
CC obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
CC  
SQ Sequence 1023 BP, 142 A, 392 C, 329 G, 160 T, 0 U, 0 Other;

Query Match 79.0%; Score 15.8; DB 13; Length 1023;  
 Best Local Similarity 78.9%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGUAACCCGAGACUACG 19  
 ||:|||||  
 DB 166 AGCTACAGCTGTGACTACG 184

## RESULT 45

ABD16472 standard; DNA; 1044 BP.

AC ABD16472;

DT 29-JUL-2004 (first entry)

DE Pseudomonas aeruginosa polynucleotide #15076.

KM Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;  
 anti-bacterial.

OS Pseudomonas aeruginosa.

PN US6551795-B1.

PD 22-APR-2003.

PF 18-FEB-1999; 99US-00252991.

PR 18-FEB-1998; 98US-0074788P.

PT 27-JUL-1998; 98US-0094190P.

PA (GENE-) GENOME THERAPEUTICS CORP.

PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;

DR WPI; 2003-615309/58.

DR P-PSDB; ABO82901.

PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
 useful as molecular targets for diagnostics, prophylaxis and treatment of  
 pathological conditions resulting from bacterial infection.

PS Disclosure; SEQ ID NO 15076; 455bp; English.

XX The invention relates to Pseudomonas aeruginosa polypeptides and the  
 CC polynucleotides encoding them. The sequences are useful in diagnosis and  
 CC therapy of pathological conditions, as molecular targets for diagnostics,  
 CC prophylaxis and treatment of pathological conditions resulting from a  
 CC bacterial infection, for evaluating a compound, such as a polypeptide,  
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
 CC effective antibacterial targets, as targets for antibacterial drugs,  
 CC including anti-P. aeruginosa-derived peptides or polypeptides, as target  
 CC components for diagnosis and/or treatment of P. aeruginosa-caused  
 CC infection, and in detection of P. aeruginosa sequences or other sequences  
 CC of Pseudomonas species using biochip technology. Sequences ABD01397-  
 CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html

XX Sequence 1044 BP; 142 A; 404 C; 336 G; 162 T; 0 U; 0 Other;

QY Query Match 79.0%; Score 15.8; DB 11; Length 1044;  
 Best Local Similarity 78.9%; Pred. No. 1.2e+03;  
 Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGUAACCCGAGACUACG 19  
 ||:|||||  
 DB 184 AGCTACAGCTGTGACTACG 202

RESULT 46  
 AAZ61623 standard; cDNA; 1057 BP.

XX AAZ61623;

DT 27-MAR-2000 (first entry)

DE cDNA encoding rat skin cell secreted protein, SEQ ID NO:18.

KM Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;  
 KM embryonic skin cell; keratinocyte stem cell; transit amplifying cell;  
 KM secreted; transmembrane; inflammation; cancer; neurological disease;  
 KM angiogenesis; tumour vascularisation; growth disorder;  
 KM developmental disorder; skin wound; hair follicle disorder;  
 KM anti-inflammatory; cytostatic; neuroprotective; vulnery; se.

OS Rattus sp.

PN WO9955865-A1.

PD 04-NOV-1999.

PF 29-APR-1999; 99WO-NZ000051.

PR 29-APR-1998; 98US-00069726.

PT 09-NOV-1998; 98US-00188930.

PA (GENE-) GENESIS RES & DEV CORP LTD.

PI Strachan L, Sleeman M, Watson JD, Onrust R, Kumble A, Murlison JG;

DR WPI; 2000-072177/06.

PT Novel polynucleotides useful for the treatment of various conditions  
 including wounds and cancer.

PS Claim 1; Page 69-70; 235bp; English.

XX The invention relates to novel nucleic acid sequences derived from rat  
 CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,  
 CC and mouse embryonic skin, keratinocyte stem cells and transit amplifying  
 CC cells. Polypeptides of the invention may be used to treat inflammation,  
 CC cancer and neurological diseases. The proteins may be used to stimulate  
 CC the growth and motility of keratinocytes, to inhibit the growth of cancer  
 CC cells, to modulate angiogenesis and tumour vascularisation, to modulate  
 CC skin inflammation, to modulate epithelial cell growth and to inhibit  
 CC binding of HIV-1 to leukocytes. The invention may also be used to treat  
 CC growth and developmental defects, skin wounds and hair follicle  
 CC disorders. Sequences AAZ61606-261832 represent cDNA sequences derived  
 CC from several mouse, rat or human skin cell types. Sequences AAZ61606-  
 CC 261649, AAZ61725-261765, AAZ61802-261811 and AAZ61826 encode proteins  
 CC with an N-terminal signal sequence, indicating that the proteins are  
 CC secreted. Sequences AAZ61650-261668, AAZ61766-261780, AAZ61812-261817 and  
 CC AAZ61827-261829 encode proteins with one or more putative transmembrane  
 CC domains

XX Sequence 1057 BP; 223 A; 315 C; 295 G; 224 T; 0 U; 0 Other;

QY Query Match 79.0%; Score 15.8; DB 3; Length 1057;  
 Best Local Similarity 84.2%; Pred. No. 1.2e+03;  
 Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGUAACCCGAGACUACGA 20  
 ||:|||||  
 DB 1022 GCTACAGCCGAGCAACGA 1040

RESULT 47  
 AAC99556 standard; cDNA; 1057 BP.  
 XX AAC99556  
 XX

AC AAC99556;  
XX  
DN 08-MAR-2001 (first entry)  
XX  
DE Skin cell cDNA, SEQ ID NO: 18.  
XX  
XX Rat; skin cell; cytostatic; anti-inflammatory; anti-HIV; nootropic;  
KM neuroprotective; vulnary; immunomodulatory; vaccine;  
KM keratinocyte growth stimulation; cancer; angiogenesis inhibition;  
XX inflammation; neurological disease; ss.  
OS Rattus sp.  
XX  
PN WO20069884-A2.  
XX  
PD 23-NOV-2000.  
XX  
PF 15-MAY-2000; 2000MO-NZ000075.  
XX  
PR 14-MAY-1999; 99US-00312283.  
XX  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
XX  
PI Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD;  
PI Murison JG;  
XX  
DR WPI: 2001-007495/01.  
DR P-PSDB; AAB55898.  
XX  
PT New isolated polynucleotide used in the identification of genetic  
PT disorders and encoding polypeptides used for treating inflammatory  
XX disease, cancer and neurological diseases.  
XX  
PS Claim 1; Page 81; 352pp; English.  
XX  
XX The present polynucleotide encodes a polypeptide which is expressed in  
CC mammalian skin cells. The polypeptide is useful for stimulating  
CC keratinocyte growth and motility, inhibiting the growth of cancer cells,  
CC modulating angiogenesis, inhibiting angiogenesis and vascularisation of  
CC tumours, modulating skin inflammation, stimulating the growth of  
CC epithelial cells, inhibiting the binding of human immunodeficiency virus  
CC (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and  
CC neurological diseases. The polynucleotide can be used as a marker, in the  
CC identification of genetic disorders, and for the design of  
CC oligonucleotides for examining expression patterns  
XX  
SQ Sequence 1057 BP; 223 A; 315 C; 295 G; 224 T; 0 U; 0 Other;  
XX  
Query Match 79.0%; Score 15.8; DB 4; Length 1057;  
Best Local Similarity 84.2%; Pred. No. 1.2e+03;  
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 GGUACAGCCAGACUACGA 20  
DB 1022 GCTACAGCCAGACGAACA 1040  
XX  
RESULT 48  
ABL34708  
ID ABL34708 standard; cDNA; 1057 BP.  
XX  
AC ABL34708;  
XX  
DT 04-APR-2002 (first entry)  
XX  
DE Rat cDNA isolated from skin cells SEQ ID NO: 18.  
XX  
XX Human; rat; mouse; skin cell; skin wound; cancer; growth defect;  
KM developmental defect; inflammatory disease; dermatological; vulnary;  
KM immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;  
XX ss.  
XX Rattus sp.  
OS

XX  
PN WO200190357-A1.  
XX  
PD 29-NOV-2001.  
XX  
PF 24-MAY-2001; 2001WO-NZ000099.  
XX  
PR 24-MAY-2000; 2000US-0206650P.  
PR 25-JUL-2000; 2000US-0221232P.  
XX  
XX (GENE-) GENESIS RES & DEV CORP LTD.  
XX  
PI Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG;  
PI Kumble KD;  
XX  
DR WPI: 2002-122020/16.  
XX  
PT New polynucleotides and polypeptides encoded by the polynucleotides  
PT isolated from skin cells, useful for treating skin wounds, cancers,  
PT growth and developmental defects, inflammatory diseases, or for  
PT modulating immune responses.  
XX  
PS Claim 1; Page 83; 466pp; English.  
XX  
XX The present invention provides the protein and coding sequences of cDNAs  
CC isolated from human, murine and rat skin cell libraries. The sequences  
CC can be used in the development of therapeutic agents useful in the  
CC treatment of skin diseases, including skin wounds, cancer, growth  
CC defects, developmental defects and inflammatory diseases. The proteins  
CC have important roles in the induction of hair growth, cell proliferation  
CC and cell-cell interaction, in maintaining tissue integrity, in wound  
CC healing and in modulating immune responses. The present sequence is a  
CC cDNA of the invention  
XX  
SQ Sequence 1057 BP; 223 A; 315 C; 295 G; 224 T; 0 U; 0 Other;  
XX  
Query Match 79.0%; Score 15.8; DB 6; Length 1057;  
Best Local Similarity 84.2%; Pred. No. 1.2e+03;  
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 GGUACAGCCAGACUACGA 20  
DB 1022 GCTACAGCCAGACGAACA 1040  
XX  
RESULT 49  
ABD16075/C  
ID ABD16075 standard; DNA; 1452 BP.  
XX  
AC ABD16075;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Pseudomonas aeruginosa polynucleotide #14679.  
XX  
XX Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;  
KM antibacterial.  
XX  
XX Pseudomonas aeruginosa.  
OS  
XX US6551795-B1.  
XX  
PN 22-APR-2003.  
XX  
PD 18-FEB-1999; 99US-00252891.  
XX  
PF 18-FEB-1998; 98US-0074788P.  
PR 27-JUL-1998; 98US-0094190P.  
XX  
XX (GENE-) GENOME THERAPEUTICS CORP.  
XX  
PI Rubenfeld MJ, Nollig J, Deloughery C, Bush D,  
XX

DR WPI; 2003-615309/58.  
 DR P-PSDB; ABO82504.  
 XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
 PT useful as molecular targets for diagnosis, prophylaxis and treatment of  
 PT pathological conditions resulting from bacterial infection.  
 XX  
 PS Disclosure; SEQ ID NO 14679; 455bp; English.  
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the  
 CC polynucleotides encoding them. The sequences are useful in diagnosis and  
 CC therapy of pathological conditions, as molecular targets for diagnostics,  
 CC prophylaxis and treatment of pathological conditions resulting from a  
 CC bacterial infection, for evaluating a compound, such as a polypeptide,  
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
 CC effective antibacterial targets, as targets for antibacterial drugs,  
 CC including anti-P. aeruginosa drugs, as templates for recombinant  
 CC production of P. aeruginosa-derived peptides or polypeptides, as target  
 CC components for diagnosis and/or treatment of P. aeruginosa-caused  
 CC infection, and in detection of P. aeruginosa sequences or other sequences  
 CC of Pseudomonas species using biochip technology. Sequences ABD01397-  
 CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html  
 XX  
 SQ Sequence 1452 BP; 220 A; 453 C; 559 G; 220 T; 0 U; 0 Other;  
 Query Match 79.0%; Score 15.8; DB 11; Length 1452;  
 Best Local Similarity 78.9%; Pred. No. 1.3e+03;  
 Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 AGGUACAGCCAGACUACG 19  
 ||:|||||:|||||  
 Db 693 AGCTACAGCCTGACTACG 675  
 RESULT 50  
 AAC99799  
 ID AAC99799 standard; cDNA; 1890 BP.  
 XX AAC99799;  
 AC  
 XX 08-MAR-2001 (first entry)  
 DT  
 XX  
 DE Skin cell cDNA, SEQ ID NO: 447.  
 XX  
 KM Rat; skin cell; cytostatic; antiinflammatory; anti-HIV; nootropic;  
 KM neuroprotective; vulnery; immunomodulatory; vaccine;  
 KM keratinocyte growth stimulation; cancer; angiogenesis inhibition;  
 KM inflammation; neurological disease; ss.  
 XX  
 OS Rattus sp.  
 XX  
 PN WO200069884-A2.  
 XX  
 PD 23-NOV-2000.  
 XX  
 PF 15-MAY-2000; 2000WO-NZ000075.  
 XX  
 PR 14-MAY-1999; 99US-00312283.  
 XX  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 XX  
 PI Watson JD, Strachan L, Omrust R, Sleeman M, Kumble KD,  
 PI Murlison JG;  
 XX  
 DR WPI; 2001-007495/01.  
 XX  
 PT New isolated polynucleotide used in the identification of genetic  
 PT disorders and encoding polypeptides used for treating inflammatory  
 PT disease, cancer and neurological diseases.  
 XX

PS Claim 1; Page 338-339; 352bp; English.  
 XX The present polynucleotide encodes a polypeptide which is expressed in  
 CC mammalian skin cells. The polypeptide is useful for stimulating  
 CC keratinocyte growth and motility, inhibiting the growth of cancer cells,  
 CC modulating angiogenesis, inhibiting angiogenesis and vascularisation of  
 CC tumours, modulating skin inflammation, stimulating the growth of  
 CC epithelial cells, inhibiting the binding of human immunodeficiency virus  
 CC (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and  
 CC neurological diseases. The polynucleotide can be used as a marker, in the  
 CC identification of genetic disorders, and for the design of  
 CC oligonucleotides for examining expression patterns  
 XX  
 SQ Sequence 1890 BP; 388 A; 611 C; 463 G; 428 T; 0 U; 0 Other;  
 Query Match 79.0%; Score 15.8; DB 4; Length 1890;  
 Best Local Similarity 84.2%; Pred. No. 1.3e+03;  
 Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 GGUACAGCCAGACUACGA 20  
 ||:|||||:|||||  
 Db 881 GCTACAGCCAGACUACGA 899  
 Search completed: March 18, 2006, 18:55:40  
 Job time : 463.923 secs





[illegible]

242	15.8	79.0	487	5	BK469160	BK469160	315	15.8	79.0	847	7	CO398269	CO398269
243	15.8	79.0	490	5	CF750369	CF750369	316	15.8	79.0	849	7	CV264133	CV264133
244	15.8	79.0	504	10	CG608885	CG608885	317	15.8	79.0	853	10	CZ320781	CZ320781
245	15.8	79.0	517	2	BD607163	BD607163	318	15.8	79.0	861	7	CO389710	CO389710
246	15.8	79.0	521	3	BI564259	BI564259	319	15.8	79.0	874	10	CO709565	CO709565
247	15.8	79.0	523	10	CM595084	CM595084	320	15.8	79.0	881	10	DU052797	DU052797
248	15.8	79.0	530	9	AZ680085	AZ680085	321	15.8	79.0	883	10	CNS02NXT	CNS02NXT
249	15.8	79.0	536	6	CA427013	CA427013	322	15.8	79.0	898	10	CZ309832	CZ309832
250	15.8	79.0	548	10	CM348442	CM348442	323	15.8	79.0	916	10	CC327826	CC327826
251	15.8	79.0	558	7	BW516073	BW516073	324	15.8	79.0	963	7	CO544698	CO544698
252	15.8	79.0	560	7	CO188771	CO188771	325	15.8	79.0	966	10	CG329405	CG329405
253	15.8	79.0	561	9	CC8009	CC8009	326	15.8	79.0	997	10	CNS00130	CNS00130
254	15.8	79.0	561	9	CC315209	CC315209	327	15.8	79.0	1001	10	CL127709	CL127709
255	15.8	79.0	564	5	BW512743	BW512743	328	15.8	79.0	1006	11	CNS03438	CNS03438
256	15.8	79.0	564	5	BW524883	BW524883	329	15.8	79.0	1022	9	B2561209	B2561209
257	15.8	79.0	568	2	BI170224	BI170224	330	15.8	79.0	1101	3	BI689036	BI689036
258	15.8	79.0	569	6	CD331205	CD331205	331	15.8	79.0	1139	8	DN733399	DN733399
259	15.8	79.0	574	2	BI164186	BI164186	332	15.8	79.0	1150	8	DN721655	DN721655
260	15.8	79.0	577	5	CG5351	CG5351	333	15.8	79.0	1195	8	DN706868	DN706868
261	15.8	79.0	584	3	CV934022	CV934022	334	15.8	79.0	1236	8	DN713207	DN713207
262	15.8	79.0	584	3	BI674686	BI674686	335	15.8	79.0	1241	8	DN731737	DN731737
263	15.8	79.0	585	10	CL189480	CL189480	336	15.8	79.0	1252	8	DN730147	DN730147
264	15.8	79.0	592	2	BF478383	BF478383	337	15.8	79.0	1266	8	DN714494	DN714494
265	15.8	79.0	595	1	AA567128	AA567128	338	15.8	79.0	1373	10	CG757669	CG757669
266	15.8	79.0	601	2	BG963412	BG963412	339	15.8	79.0	1443	9	CC289415	CC289415
267	15.8	79.0	603	5	BW080989	BW080989	340	15.8	79.0	1487	8	DN720251	DN720251
268	15.8	79.0	603	5	BW709047	BW709047	341	15.8	79.0	1543	4	AK051724	AK051724
269	15.8	79.0	607	3	BI674441	BI674441	342	15.8	79.0	3347	8	H27186	H27186
270	15.8	79.0	610	3	BI697524	BI697524	343	15.4	77.0	170	9	AZ381479	AZ381479
271	15.8	79.0	627	5	BW517201	BW517201	344	15.4	77.0	180	9	AZ398452	AZ398452
272	15.8	79.0	628	6	CA333958	CA333958	345	15.4	77.0	206	8	TI2785	TI2785
273	15.8	79.0	628	6	CA333958	CA333958	346	15.4	77.0	228	2	BB378756	BB378756
274	15.8	79.0	628	11	DR21K22T	DR21K22T	347	15.4	77.0	242	2	BB459281	BB459281
275	15.8	79.0	633	11	CR150798	CR150798	348	15.4	77.0	242	1	BI159788	BI159788
276	15.8	79.0	634	10	CM576388	CM576388	349	15.4	77.0	247	2	BB371268	BB371268
277	15.8	79.0	635	3	BI277434	BI277434	350	15.4	77.0	255	8	CV827016	CV827016
278	15.8	79.0	642	10	CM315751	CM315751	351	15.4	77.0	267	9	AZ242692	AZ242692
279	15.8	79.0	648	6	CA588912	CA588912	352	15.4	77.0	267	9	BH174232	BH174232
280	15.8	79.0	648	6	CD470960	CD470960	353	15.4	77.0	280	2	AA964793	AA964793
281	15.8	79.0	650	3	BI282622	BI282622	354	15.4	77.0	282	1	BB200657	BB200657
282	15.8	79.0	650	3	BI677720	BI677720	355	15.4	77.0	287	1	BI156596	BI156596
283	15.8	79.0	654	2	BB460629	BB460629	356	15.4	77.0	289	1	AM335750	AM335750
284	15.8	79.0	656	1	BB020150	BB020150	357	15.4	77.0	290	1	BB032437	BB032437
285	15.8	79.0	656	3	BI695756	BI695756	358	15.4	77.0	301	2	BE474679	BE474679
286	15.8	79.0	656	9	CC413225	CC413225	359	15.4	77.0	304	1	AI548289	AI548289
287	15.8	79.0	656	10	CM167983	CM167983	360	15.4	77.0	307	2	BF399895	BF399895
288	15.8	79.0	657	2	BB634508	BB634508	361	15.4	77.0	310	1	AM561160	AM561160
289	15.8	79.0	660	6	CD866713	CD866713	362	15.4	77.0	312	1	AM561160	AM561160
290	15.8	79.0	661	2	BG067931	BG067931	363	15.4	77.0	318	10	CM117050	CM117050
291	15.8	79.0	662	10	CE621874	CE621874	364	15.4	77.0	319	9	AO515892	AO515892
292	15.8	79.0	662	3	BI628999	BI628999	365	15.4	77.0	319	8	CV879206	CV879206
293	15.8	79.0	663	10	CM895792	CM895792	366	15.4	77.0	336	8	AA668023	AA668023
294	15.8	79.0	679	9	AZ994739	AZ994739	367	15.4	77.0	338	1	AA668023	AA668023
295	15.8	79.0	680	10	CM315750	CM315750	368	15.4	77.0	343	3	BQ312024	BQ312024
296	15.8	79.0	682	8	CK694848	CK694848	369	15.4	77.0	349	1	AM535128	AM535128
297	15.8	79.0	686	2	BI217544	BI217544	370	15.4	77.0	369	2	BF556900	BF556900
298	15.8	79.0	703	2	BF525855	BF525855	371	15.4	77.0	380	10	CG594842	CG594842
299	15.8	79.0	715	6	CF435611	CF435611	372	15.4	77.0	382	9	BH052630	BH052630
300	15.8	79.0	720	11	CNS03CBM	CNS03CBM	373	15.4	77.0	383	6	CA871200	CA871200
301	15.8	79.0	725	9	BZ204158	BZ204158	374	15.4	77.0	390	5	BY611150	BY611150
302	15.8	79.0	725	10	CMW57589	CMW57589	375	15.4	77.0	393	3	BZ505462	BZ505462
303	15.8	79.0	736	10	AG461042	AG461042	376	15.4	77.0	399	1	AW327174	AW327174
304	15.8	79.0	740	10	CL633673	CL633673	377	15.4	77.0	404	7	BI201831	BI201831
305	15.8	79.0	745	11	CR916574	CR916574	378	15.4	77.0	404	4	CR459710	CR459710
306	15.8	79.0	753	7	CO561094	CO561094	379	15.4	77.0	406	8	BY678881	BY678881
307	15.8	79.0	753	7	CO567779	CO567779	380	15.4	77.0	406	5	CV784936	CV784936
308	15.8	79.0	763	10	AG548590	AG548590	381	15.4	77.0	409	9	BH062782	BH062782
309	15.8	79.0	766	10	BI186771	BI186771	382	15.4	77.0	417	6	CF798693	CF798693
310	15.8	79.0	791	10	CG045789	CG045789	383	15.4	77.0	418	9	AO338710	AO338710
311	15.8	79.0	830	7	CK202209	CK202209	384	15.4	77.0	420	5	BO467993	BO467993
312	15.8	79.0	835	7	CO564356	CO564356	385	15.4	77.0	438	7	CN801139	CN801139
313	15.8	79.0	840	10	CM703269	CM703269	386	15.4	77.0	431	7	CK341514	CK341514
314	15.8	79.0	846	9	BH096346	BH096346	387	15.4	77.0	432	1	AM596672	AM596672



534	15.4	77.0	744	10	AG412255	AG412255 Mus muscu	607	15.2	76.0	182	1	AV257143	AV257143
535	15.4	77.0	747	10	AG572677	AG572677 Mus muscu	608	15.2	76.0	201	7	CP935303	CP935303 TREST-B20
536	15.4	77.0	752	8	CG077326	CG077326 UCRS08_5	609	15.2	76.0	208	7	BG641140	BG641140
537	15.4	77.0	752	10	AG404098	AG404098 Mus muscu	610	15.2	76.0	220	8	R22448	R22448 yq08d07.81
538	15.4	77.0	755	6	CP402893	CP402893 RTW1_23	611	15.2	76.0	231	10	CG653475	CG653475 OST418877
539	15.4	77.0	755	10	AG322563	AG322563 Mus muscu	612	15.2	76.0	235	7	CP932859	CP932859 TREST-B21
540	15.4	77.0	759	9	CC580601	CC580601 CH240_375	613	15.2	76.0	237	1	AW315728	AW315728 NAR
541	15.4	77.0	759	10	AG409260	AG409260 Mus muscu	614	15.2	76.0	237	3	BO292194	BO292194 PM2-AN008
542	15.4	77.0	765	6	CF931855	CF931855 RTDR3_10	615	15.2	76.0	244	1	BI159744	BI159744
543	15.4	77.0	769	6	CA752464	CA752464 UI-M-FOO-	616	15.2	76.0	245	8	W70831	W70831 me44h04.t1
544	15.4	77.0	770	8	CK638568	CK638568 UCRPT02_3	617	15.2	76.0	255	8	W17406	W17406 mb58a12.t1
545	15.4	77.0	772	8	DR688987	DR688987 EST107907	618	15.2	76.0	262	2	BF880530	BF880530 QV3-BT019
546	15.4	77.0	774	8	CK638567	CK638567 UCRPT02_3	619	15.2	76.0	265	1	AJ757553	AJ757553 AJ757553
547	15.4	77.0	778	7	CN784348	CN784348 EST783039	620	15.2	76.0	265	1	AJ757554	AJ757554 AJ757554
548	15.4	77.0	778	7	BN121301	BN121301 RRC1-24-2	621	15.2	76.0	270	11	TA275801P	TA275801P
549	15.4	77.0	788	10	AG474418	AG474418 Mus muscu	622	15.2	76.0	274	7	CN436627	CN436627 BE04101A1
550	15.4	77.0	790	11	CR031132	CR031132 Reverse b	623	15.2	76.0	281	5	BQ485968	BQ485968 3524_1_22
551	15.4	77.0	791	9	B2144150	B2144150 CH230-266	624	15.2	76.0	288	7	CK494839	CK494839 rwbD0_00
552	15.4	77.0	798	3	BP464869	BP464869 BP464869	625	15.2	76.0	301	2	BI170981	BI170981 RE1621_5
553	15.4	77.0	800	8	DR492310	DR492310 MS02919_C	626	15.2	76.0	303	5	BM858839	BM858839 BM858839
554	15.4	77.0	807	8	DR498984	DR498984 MS02919_C	627	15.2	76.0	315	10	AG966007	AG966007 Dioboph11
555	15.4	77.0	811	7	CV704540	CV704540 UCRPT01_0	628	15.2	76.0	327	8	DN274847	DN274847 1153892_M
556	15.4	77.0	811	9	BZ262449	BZ262449 CH230-409	629	15.2	76.0	331	1	A1986929	A1986929 rsl9d02.Y
557	15.4	77.0	819	8	DR465931	DR465931 MS00936_B	630	15.2	76.0	331	1	AM888182	AM888182 NKNV_105
558	15.4	77.0	826	8	DR674937	DR674937 EST106505	631	15.2	76.0	333	11	CR054076	CR054076 Reverse b
559	15.4	77.0	830	9	B2749748	B2749748 PUPBD307D	632	15.2	76.0	337	8	CK111786	CK111786 R1055C11
560	15.4	77.0	836	10	CZ547811	CZ547811 SRRA-Bad7	633	15.2	76.0	338	9	AQ066882	AQ066882 HS_2227_B
561	15.4	77.0	838	11	CR822576	CR822576 GROMA52B	634	15.2	76.0	339	5	BY306312	BY306312
562	15.4	77.0	840	8	DR555370	DR555370 MS0325_C2	635	15.2	76.0	344	10	CE305047	CE305047 t1gr-g9b-
563	15.4	77.0	846	8	CK641319	CK641319 UCRPT02_5	636	15.2	76.0	345	1	A1824274	A1824274 w10b01.x
564	15.4	77.0	851	8	DR553449	DR553449 MS03226_C	637	15.2	76.0	347	1	A1388450	A1388450 A139370.5
565	15.4	77.0	857	7	CV291062	CV291062 aof01-13m	638	15.2	76.0	357	8	DN874889	DN874889 na035h12
566	15.4	77.0	861	8	DR564409	DR564409 MS02630_C	639	15.2	76.0	356	9	AZ355180	AZ355180 IM0094E19
567	15.4	77.0	862	8	CK668397	CK668397 UCRCP01_0	640	15.2	76.0	358	10	CE533480	CE533480
568	15.4	77.0	862	8	DR393501	DR393501 EST113104	641	15.2	76.0	360	7	CO263755	CO263755 EK089537
569	15.4	77.0	864	8	CK667108	CK667108 UCRCP01_0	642	15.2	76.0	366	5	BY064429	BY064429
570	15.4	77.0	866	8	DN527076	DN527076 1271895_M	643	15.2	76.0	366	10	CL335785	CL335785 RPT44_25
571	15.4	77.0	872	8	DN937321	DN937321 AGENCOURT	644	15.2	76.0	368	1	AM681297	AM681297 EST00015
572	15.4	77.0	877	7	CK936416	CK936416 GCP100438	645	15.2	76.0	369	1	AM681609	AM681609
573	15.4	77.0	880	3	BI950061	BI950061 HVSMEL001	646	15.2	76.0	372	2	BG635564	BG635564 SD1015.5
574	15.4	77.0	891	8	CK641689	CK641689 UCRPT02_5	647	15.2	76.0	373	9	AZ644140	AZ644140 IM0507P21
575	15.4	77.0	902	8	DR692635	DR692635 EST108272	648	15.2	76.0	374	2	BB870259	BB870259 BB870259
576	15.4	77.0	907	7	CK187465	CK187465 EST776780	649	15.2	76.0	374	7	CP944686	CP944686 TREST-A02
577	15.4	77.0	912	2	BE534457	BE534457 601232772	650	15.2	76.0	376	2	BB840855	BB840855
578	15.4	77.0	912	8	CK641289	CK641289 UCRPT02_5	651	15.2	76.0	377	5	BY022208	BY022208
579	15.4	77.0	915	8	DR580007	DR580007 WS00753_C	652	15.2	76.0	379	8	CP932464	CP932464 TREST-B20
580	15.4	77.0	919	9	BZ569738	BZ569738 pac82-164	653	15.2	76.0	381	2	BR904645	BR904645 MEM03873
581	15.4	77.0	925	10	DU035737	DU035737 18096_Tom	654	15.2	76.0	384	5	BK630425	BK630425 CM3-MT022
582	15.4	77.0	925	9	CC382787	CC382787 PUDI5037D	655	15.2	76.0	384	5	BK630425	BK630425
583	15.4	77.0	938	10	AG365415	AG365415 Mus muscu	656	15.2	76.0	386	1	AJ671460	AJ671460
584	15.4	77.0	1023	5	BX340647	BX340647 BX340647	657	15.2	76.0	387	7	BP644948	BP644948
585	15.4	77.0	1033	10	CL286324	CL286324 ZMMBB063	658	15.2	76.0	389	7	CK495061	CK495061 rwbD0_00
586	15.4	77.0	1074	4	AK085314	AK085314 Mus muscu	659	15.2	76.0	393	1	AA085110	AA085110 z14d05.x
587	15.4	77.0	1085	11	CNS06NOX	AL407047 T3 end of	660	15.2	76.0	393	3	BO338406	BO338406
588	15.4	77.0	1100	6	CB236105	CB236105 AGENCOURT	661	15.2	76.0	394	1	A1514554	A1514554
589	15.4	77.0	1128	10	AG324118	AG324118 Mus muscu	662	15.2	76.0	394	7	CO336422	CO336422
590	15.4	77.0	1186	10	AG324118	AG324118 Mus muscu	663	15.2	76.0	400	2	BB639312	BB639312
591	15.4	77.0	1218	3	BM416338	BM416338 OPI2419_M	664	15.2	76.0	401	6	CFP092222	CFP092222
592	15.4	77.0	1302	3	BZ553393	BZ553393 pac81-60	665	15.2	76.0	410	5	BY201817	BY201817
593	15.4	77.0	1340	9	BZ569737	BZ569737 pac82-164	666	15.2	76.0	410	8	W62028	W62028 m883h01.t1
594	15.4	77.0	1440	11	DQ037941	DQ037941 Pac82-164	667	15.2	76.0	411	8	CK212498	CK212498 MNS16121
595	15.4	77.0	1536	11	DQ037940	DQ037940 Homo sapi	668	15.2	76.0	412	7	CO288575	CO288575
596	15.4	77.0	1597	4	AK086409	AK086409 Mus muscu	669	15.2	76.0	412	5	BI271995	BI271995
597	15.4	77.0	2203	4	AK045461	AK045461 Mus muscu	670	15.2	76.0	415	2	BF019596	BF019596
598	15.4	77.0	2252	4	AK037215	AK037215 Mus muscu	671	15.2	76.0	415	9	CP932658	CP932658 TREST-B11
599	15.4	77.0	2612	4	AK028554	AK028554 Mus muscu	672	15.2	76.0	415	9	B422778	B422778 HS-1056-B1-
600	15.4	77.0	2755	4	AK079717	AK079717 Mus muscu	673	15.2	76.0	416	2	BF552988	BF552988 UI-R-A0-b
601	15.4	77.0	2836	4	AK084636	AK084636 Mus muscu	674	15.2	76.0	416	3	BI466262	BI466262
602	15.2	76.0	69	10	CL436985	CL436985 PST4264-N	675	15.2	76.0	419	3	BO375010	BO375010
603	15.2	76.0	91	1	A1096562	A1096562 q889g04.x	676	15.2	76.0	420	1	AM165642	AM165642
604	15.2	76.0	118	10	CL706313	CL706313 CMD-GT_1	677	15.2	76.0	422	1	BE990872	BE990872 UI-M-B21-
605	15.2	76.0	166	2	BG557321	BG557321 BML_42_BO	678	15.2	76.0	422	3	BI734816	BI734816
606	15.2	76.0	179	1	AA084790	AA084790 znl3a05.x	679	15.2	76.0	423	1	AM366090	AM366090 QVO-HT009

C 680	15.2	76.0	423	1	AW459923	AW459923	B106C04.Y	C 753	15.2	76.0	523	2	BE067955	BE067955	CM0-BT036
681	15.2	76.0	424	1	AA819372	AA819372	UT-R-A0-B	C 754	15.2	76.0	524	2	BG632607	BG632607	GHI1267.3
682	15.2	76.0	426	1	AW871608	AW871608	ra79h12.Y	C 755	15.2	76.0	524	5	BW884283	BW884283	BW884283
683	15.2	76.0	426	3	BT734650	BT734650	603356505	C 756	15.2	76.0	524	7	CO303933	CO303933	CR432309.
684	15.2	76.0	426	3	BP586060	BP586060	BP586060	C 757	15.2	76.0	525	10	CL628993	CL628993	CR432309.
685	15.2	76.0	428	1	AV762253	AV762253	AV762253	C 758	15.2	76.0	528	5	BU968747	BU968747	H808H10r
686	15.2	76.0	428	7	CO328040	CO328040	BP08453.3	C 759	15.2	76.0	529	6	BY472374	BY472374	BY472374
687	15.2	76.0	429	1	AM172108	AM172108	618049H04	C 760	15.2	76.0	529	6	CD555677	CD555677	BY472374
688	15.2	76.0	429	1	AA409116	AA409116	BY26601.1	C 761	15.2	76.0	530	10	AG970859	AG970859	DOBOH11
689	15.2	76.0	430	5	BY266011	BY266011	BY26601.1	C 762	15.2	76.0	532	1	AV607764	AV607764	AV607764
690	15.2	76.0	431	1	AA032339	AA032339	mi42C10.X	C 763	15.2	76.0	532	5	BO577329	BO577329	3524.1.29
691	15.2	76.0	435	1	AA978922	AA978922	LD33127.5	C 764	15.2	76.0	532	7	CK498134	CK498134	rwBDO_00
692	15.2	76.0	440	1	AI550042	AI550042	mm99906.Y	C 765	15.2	76.0	533	1	AM652953	AM652953	101414.MA
693	15.2	76.0	441	3	BI502238	BI502238	IP1-69_E0	C 766	15.2	76.0	533	3	BI566807	BI566807	RH3636.5
694	15.2	76.0	443	3	BI51072	BI51072	IP1-R-DL0	C 767	15.2	76.0	533	8	DN277392	DN277392	1156639.M
695	15.2	76.0	443	1	AA073950	AA073950	mm99906.X	C 768	15.2	76.0	533	8	DR806342	DR806342	ZM-BFDO03
696	15.2	76.0	443	2	BB862494	BB862494	BB862494	C 769	15.2	76.0	537	2	BB639327	BB639327	BB639327
697	15.2	76.0	446	1	AM052272	AM052272	rs33f03.Y	C 770	15.2	76.0	537	5	BO578256	BO578256	3524.1.56
698	15.2	76.0	446	1	AA624285	AA624285	vm1f01.X	C 771	15.2	76.0	537	9	BO578256	BO578256	3524.1.56
699	15.2	76.0	447	6	CA399844	CA399844	EL01N0326	C 772	15.2	76.0	537	9	BO578256	BO578256	3524.1.56
700	15.2	76.0	448	1	AI594327	AI594327	vm1f01.Y	C 773	15.2	76.0	539	7	BO578256	BO578256	3524.1.56
701	15.2	76.0	449	5	BU763286	BU763286	sa840a12.	C 774	15.2	76.0	540	9	AV477053	AV477053	1M0573K23
702	15.2	76.0	450	1	AA070397	AA070397	zm69h10.8	C 775	15.2	76.0	541	6	CA431391	CA431391	UI-H-PG1-
703	15.2	76.0	451	1	AA270616	AA270616	va66c02.X	C 776	15.2	76.0	542	5	BO551474	BO551474	rwBDO_01
704	15.2	76.0	452	7	CO607046	CO607046	DG8-59F13	C 777	15.2	76.0	542	10	CE744287	CE744287	4597987-
705	15.2	76.0	454	3	BI734718	BI734718	603356582	C 778	15.2	76.0	543	3	BI170932	BI170932	RE12564.5
706	15.2	76.0	454	8	DN191141	DN191141	ACL5_1380	C 779	15.2	76.0	543	2	BI170932	BI170932	RE12564.5
707	15.2	76.0	454	10	CG993375	CG993375	ZMMBB037	C 780	15.2	76.0	546	9	AO496075	AO496075	HS_5075.A
708	15.2	76.0	459	10	CG465202	CG465202	KRIEB_2D-	C 781	15.2	76.0	547	9	AO496075	AO496075	HS_5075.A
709	15.2	76.0	463	8	DR033058	DR033058	bda020280	C 782	15.2	76.0	548	3	BI580984	BI580984	PH_LMX0_52
710	15.2	76.0	465	7	CK499893	CK499893	rwBDO_01	C 783	15.2	76.0	549	8	DR397549	DR397549	PH_LMX0_52
711	15.2	76.0	469	1	AM267668	AM267668	zm69h10.X	C 784	15.2	76.0	550	5	BM801414	BM801414	BM801414
712	15.2	76.0	470	1	AL906288	AL906288	AL906288	C 785	15.2	76.0	551	1	BI378051	BI378051	BM801414
713	15.2	76.0	471	1	AL906288	AL906288	AL906288	C 786	15.2	76.0	554	1	AM601586	AM601586	BM801414
714	15.2	76.0	472	9	AO526053	AO526053	HS_5309.B	C 787	15.2	76.0	554	7	CV353869	CV353869	BM801414
715	15.2	76.0	476	1	AJ760475	AJ760475	AJ760475	C 788	15.2	76.0	555	7	CK501010	CK501010	BM801414
716	15.2	76.0	476	1	BO133573	BO133573	sa840a10.	C 789	15.2	76.0	557	2	BI239025	BI239025	BM330420
717	15.2	76.0	478	7	CR362112	CR362112	CR362112	C 790	15.2	76.0	557	7	CK495385	CK495385	rwBDO_00
718	15.2	76.0	478	9	AZ898026	AZ898026	RPCI-24-1	C 791	15.2	76.0	557	7	CK495385	CK495385	rwBDO_00
719	15.2	76.0	480	1	AA339054	AA339054	LD08792.5	C 792	15.2	76.0	559	5	BO577613	BO577613	BM330420
720	15.2	76.0	480	3	BO373559	BO373559	RCO-FY007	C 793	15.2	76.0	559	5	BO577613	BO577613	BM330420
721	15.2	76.0	482	5	BU973241	BU973241	HB24D22x	C 794	15.2	76.0	559	7	CK495385	CK495385	rwBDO_00
722	15.2	76.0	482	5	BU973241	BU973241	HB24D22x	C 795	15.2	76.0	560	8	DN190737	DN190737	BM330420
723	15.2	76.0	482	7	BN245976	BN245976	BN245976	C 796	15.2	76.0	561	2	BI228137	BI228137	BM330420
724	15.2	76.0	485	2	BF023600	BF023600	ux09h11.Y	C 797	15.2	76.0	562	7	CR442580	CR442580	BM330420
725	15.2	76.0	487	1	AI591092	AI591092	tw91B05.X	C 798	15.2	76.0	563	2	BI228137	BI228137	BM330420
726	15.2	76.0	491	2	BF732968	BF732968	tw91B05.X	C 799	15.2	76.0	564	1	AM178615	AM178615	BM330420
727	15.2	76.0	493	7	CK496920	CK496920	rwBDO_00	C 800	15.2	76.0	564	2	BI228137	BI228137	BM330420
728	15.2	76.0	494	7	CP941326	CP941326	NCBSTRdb8	C 801	15.2	76.0	565	2	BI228137	BI228137	BM330420
729	15.2	76.0	494	7	CP941326	CP941326	NCBSTRdb8	C 802	15.2	76.0	566	2	BI228137	BI228137	BM330420
730	15.2	76.0	495	6	CB522618	CB522618	UI-M-GK0-	C 803	15.2	76.0	568	2	BI228137	BI228137	BM330420
731	15.2	76.0	495	6	CB522618	CB522618	UI-M-GK0-	C 804	15.2	76.0	569	3	BI228137	BI228137	BM330420
732	15.2	76.0	496	1	AA867049	AA867049	vm22907.X	C 805	15.2	76.0	569	3	BI228137	BI228137	BM330420
733	15.2	76.0	497	1	AA867049	AA867049	vm22907.X	C 806	15.2	76.0	570	3	BI228137	BI228137	BM330420
734	15.2	76.0	497	6	CA856923	CA856923	NCBSTRdb1	C 807	15.2	76.0	572	6	CA618174	CA618174	BM330420
735	15.2	76.0	502	6	CP423018	CP423018	NCBSTRdb3	C 808	15.2	76.0	572	6	CA618174	CA618174	BM330420
736	15.2	76.0	502	6	CP798394	CP798394	NCBSTRdb4	C 809	15.2	76.0	574	1	AO764037	AO764037	BM330420
737	15.2	76.0	503	6	BN953568	BN953568	UI-M-CCL-	C 810	15.2	76.0	574	1	AO764037	AO764037	BM330420
738	15.2	76.0	504	8	DN191363	DN191363	ACL5_15H0	C 811	15.2	76.0	575	5	BU263468	BU263468	BM330420
739	15.2	76.0	505	1	AJ682367	AJ682367	AJ682367	C 812	15.2	76.0	575	5	BU263468	BU263468	BM330420
740	15.2	76.0	506	3	BM086580	BM086580	sbh30f02.	C 813	15.2	76.0	576	5	BU263468	BU263468	BM330420
741	15.2	76.0	510	9	AO294880	AO294880	HS_3046.A	C 814	15.2	76.0	577	3	BM077113	BM077113	BM330420
742	15.2	76.0	512	1	AM178504	AM178504	CM0-HT011	C 815	15.2	76.0	578	6	CA827713	CA827713	BM330420
743	15.2	76.0	512	5	BU829878	BU829878	T001B10.P	C 816	15.2	76.0	578	6	CA827713	CA827713	BM330420
744	15.2	76.0	516	2	BI172156	BI172156	RE14431.5	C 817	15.2	76.0	579	3	BM077113	BM077113	BM330420
745	15.2	76.0	517	10	CL371101	CL371101	RPCI44.30	C 818	15.2	76.0	579	3	BM077113	BM077113	BM330420
746	15.2	76.0	518	2	BA462533	BA462533	BA462533	C 819	15.2	76.0	580	10	CA801871	CA801871	BM330420
747	15.2	76.0	518	6	CF797874	CF797874	NCBSTRdb6	C 820	15.2	76.0	580	10	CA801871	CA801871	BM330420
748	15.2	76.0	521	6	CK605289	CK605289	GM1491.3	C 821	15.2	76.0	581	1	AA246465	AA246465	BM330420
749	15.2	76.0	522	1	AA803753	AA803753	GM1491.5	C 822	15.2	76.0	581	6	CB568825	CB568825	BM330420
750	15.2	76.0	522	3	BI374080	BI374080	RE61591.5	C 823	15.2	76.0	581	6	CB568825	CB568825	BM330420
751	15.2	76.0	522	7	CM706533	CM706533	E0518B08-	C 824	15.2	76.0	582	11	LA8F063E03	LA8F063E03	BM330420
752	15.2	76.0	522	7	CM715993	CM715993	E0717H09-	C 825	15.2	76.0	582	1	AI989264	AI989264	BM330420



826	15.2	76.0	582	3	BP215796	BP215796	BP215796	899	15.2	76.0	638	6	CB336985	CB336985	TC025C02R	
827	15.2	76.0	582	7	CK499830	rsmb00_01	CK499830	c	900	15.2	76.0	638	8	DN190392	ACLS_0301	DN190392
828	15.2	76.0	583	1	AM613381	MR3-ST019	AM613381	901	15.2	76.0	639	10	AG950349	AG950349	AG950349	
829	15.2	76.0	583	2	BI239698	RE36267.5	BI239698	902	15.2	76.0	639	10	CL7722189	CL7722189	CL7722189	
830	15.2	76.0	586	6	CA119460	UI-M-PV0	CA119460	903	15.2	76.0	642	6	CP260581	NCBET3407	CP260581	
831	15.2	76.0	587	3	BI358616	GM27181.5	BI358616	904	15.2	76.0	644	6	CP365892	641169 NC	CP365892	
832	15.2	76.0	588	7	CK497187	rsmb00_00	CK497187	c	905	15.2	76.0	645	7	CC008424	PUDN80TD	CC008424
833	15.2	76.0	589	9	BZ311960	ldlBgl2_b	BZ311960	906	15.2	76.0	647	1	AI533183	AI533183	AI533183	
834	15.2	76.0	590	5	BO57632	3524_1.39	BO57632	907	15.2	76.0	647	7	CK499802	SD04924.5	CK499802	
835	15.2	76.0	590	10	CM852428	OG_BBA008	CM852428	908	15.2	76.0	647	7	CK499802	rsmb00_00	CK499802	
836	15.2	76.0	591	6	CP620012	NCBET3C20	CP620012	909	15.2	76.0	648	2	BB612157	BB612157	BB612157	
837	15.2	76.0	591	9	AQ282012	RPC111-81	AQ282012	910	15.2	76.0	649	1	AI513433	AI513433	AI513433	
838	15.2	76.0	593	8	DR028426	rsmb00_01	DR028426	911	15.2	76.0	651	7	CP847746	CP847746	CP847746	
839	15.2	76.0	593	8	DR028426	bda010051	DR028426	912	15.2	76.0	651	7	CK494741	CK494741	CK494741	
840	15.2	76.0	595	3	BI068877	BI068877	BI068877	c	913	15.2	76.0	652	10	CM418882	CM418882	CM418882
841	15.2	76.0	595	7	CU034926	CU034926	CU034926	914	15.2	76.0	652	10	AG11964	AG11964	AG11964	
842	15.2	76.0	596	1	AI102672	AI102672	AI102672	c	915	15.2	76.0	652	10	CL311375	CL311375	CL311375
843	15.2	76.0	596	2	BE640320	BE640320	BE640320	916	15.2	76.0	654	8	CK498476	CK498476	CK498476	
844	15.2	76.0	596	10	CL193087	CL193087	CL193087	c	917	15.2	76.0	654	8	DN190559	DN190559	DN190559
845	15.2	76.0	596	1	CK4343013	K0527G06-	CK4343013	c	918	15.2	76.0	655	2	CG674923	CG674923	CG674923
846	15.2	76.0	599	1	AJ750909	AJ750909	AJ750909	919	15.2	76.0	655	2	CG480171	CG480171	CG480171	
847	15.2	76.0	599	1	AM506713	AM506713	AM506713	920	15.2	76.0	655	9	AQ156121	AQ156121	AQ156121	
848	15.2	76.0	599	5	BO528915	3524_1.43	BO528915	c	921	15.2	76.0	655	3	BQ132844	BQ132844	BQ132844
849	15.2	76.0	599	7	CK496960	rsmb00_00	CK496960	c	922	15.2	76.0	656	8	DN191285	DN191285	DN191285
850	15.2	76.0	600	1	AV616101	AV616101	AV616101	c	923	15.2	76.0	657	8	DN103121	DN103121	DN103121
851	15.2	76.0	600	9	BZ327057	ldlBgl2_9	BZ327057	c	924	15.2	76.0	658	10	AG060655	AG060655	AG060655
852	15.2	76.0	600	9	BZ895107	Hg7_0133	BZ895107	925	15.2	76.0	659	2	BB610540	BB610540	BB610540	
853	15.2	76.0	601	6	CB336984	TC025C02F	CB336984	c	926	15.2	76.0	659	10	AG033180	AG033180	AG033180
854	15.2	76.0	601	7	CK434361	K0547F05-	CK434361	c	927	15.2	76.0	661	7	CP843377	CP843377	CP843377
855	15.2	76.0	602	6	CD741071	UI-M-A00-	CD741071	c	928	15.2	76.0	662	11	CR873013	CR873013	CR873013
856	15.2	76.0	602	7	CV353888	MR3-ST019	CV353888	c	929	15.2	76.0	663	5	BU064423	BU064423	BU064423
857	15.2	76.0	604	5	BM731655	BM731655	BM731655	930	15.2	76.0	665	5	BI544518	BI544518	BI544518	
858	15.2	76.0	604	7	CM251989	CM251989	CM251989	931	15.2	76.0	665	5	BY749097	BY749097	BY749097	
859	15.2	76.0	605	2	BB661701	BB661701	BB661701	932	15.2	76.0	666	3	BI354233	BI354233	BI354233	
860	15.2	76.0	605	3	BP148300	BP148300	BP148300	933	15.2	76.0	666	6	CB620230	CB620230	CB620230	
861	15.2	76.0	606	7	CR997381	CR997381	CR997381	934	15.2	76.0	667	6	CV516696	CV516696	CV516696	
862	15.2	76.0	608	3	BJ032129	BJ032129	BJ032129	c	935	15.2	76.0	667	6	CA190546	CA190546	CA190546
863	15.2	76.0	608	8	AD190728	AD190728	AD190728	c	936	15.2	76.0	667	9	BH180267	BH180267	BH180267
864	15.2	76.0	608	9	A2179343	SP_0165_A	A2179343	c	937	15.2	76.0	667	11	CNS07MST	CNS07MST	CNS07MST
865	15.2	76.0	609	6	CF275268	NGEST3d14	CF275268	938	15.2	76.0	668	5	BM269565	BM269565	BM269565	
866	15.2	76.0	611	5	CA055200	rsmb00_00	CA055200	939	15.2	76.0	668	5	BM968325	BM968325	BM968325	
867	15.2	76.0	611	5	CA055200	rsmb00_00	CA055200	940	15.2	76.0	669	9	BZ336374	BZ336374	BZ336374	
868	15.2	76.0	611	8	DR047410	Ph_mx0_50	DR047410	941	15.2	76.0	670	8	DN869010	DN869010	DN869010	
869	15.2	76.0	612	2	BF397009	UI-R-BB2-	BF397009	c	942	15.2	76.0	670	9	BZ011039	BZ011039	BZ011039
870	15.2	76.0	612	7	CP945300	CP945300	CP945300	c	943	15.2	76.0	670	9	BZ941124	BZ941124	BZ941124
871	15.2	76.0	612	8	DR046670	Ph_mx0_40	DR046670	944	15.2	76.0	671	10	CL802504	CL802504	CL802504	
872	15.2	76.0	612	10	CM499002	CM499002	CM499002	945	15.2	76.0	671	1	AI518481	AI518481	AI518481	
873	15.2	76.0	613	2	BG739295	EMI_81_C0	BG739295	c	946	15.2	76.0	672	8	DN890357	DN890357	DN890357
874	15.2	76.0	613	7	CK496003	rsmb00_00	CK496003	c	947	15.2	76.0	672	8	DT110711	DT110711	DT110711
875	15.2	76.0	614	7	CKS01172	rsmb00_01	CKS01172	c	948	15.2	76.0	672	10	CM687218	CM687218	CM687218
876	15.2	76.0	615	8	CK104845	BI104MT2	CK104845	c	949	15.2	76.0	674	6	CD708184	CD708184	CD708184
877	15.2	76.0	616	7	CK495013	rsmb00_00	CK495013	c	950	15.2	76.0	674	6	DN586709	DN586709	DN586709
878	15.2	76.0	616	8	DN191280	ACLS_14G0	DN191280	951	15.2	76.0	676	2	BI214314	BI214314	BI214314	
879	15.2	76.0	619	3	BQ290943	NXRV051_F	BQ290943	952	15.2	76.0	677	5	BX079104	BX079104	BX079104	
880	15.2	76.0	620	9	CP944025	TREBT-A02	CP944025	c	953	15.2	76.0	678	1	AJ752100	AJ752100	AJ752100
881	15.2	76.0	620	9	BZ787114	PURDJ62TB	BZ787114	954	15.2	76.0	678	1	AQ689554	AQ689554	AQ689554	
882	15.2	76.0	621	8	DR063243	iq27d05_9	DR063243	955	15.2	76.0	680	2	BF505653	BF505653	BF505653	
883	15.2	76.0	622	3	BP451761	BP451761	BP451761	c	956	15.2	76.0	680	9	CC620616	CC620616	CC620616
884	15.2	76.0	623	3	CK434926	CK434926	CK434926	957	15.2	76.0	680	10	AG172479	AG172479	AG172479	
885	15.2	76.0	623	10	CM381499	CM381499	CM381499	c	958	15.2	76.0	681	8	DN190504	DN190504	DN190504
886	15.2	76.0	626	5	BO578068	3524_1.52	BO578068	959	15.2	76.0	682	7	CK971955	CK971955	CK971955	
887	15.2	76.0	626	6	AY986238	AY986238	AY986238	c	960	15.2	76.0	683	9	AZ133339	AZ133339	AZ133339
888	15.2	76.0	629	6	CD547129	BO279C11-	CD547129	961	15.2	76.0	684	5	BX084212	BX084212	BX084212	
889	15.2	76.0	629	9	AZ339341	IM0070H14	AZ339341	962	15.2	76.0	685	5	CF468976	CF468976	CF468976	
890	15.2	76.0	631	7	CK496645	rsmb00_00	CK496645	963	15.2	76.0	685	6	CP892304	CP892304	CP892304	
891	15.2	76.0	633	7	CK527593	rsmb00_00	CK527593	964	15.2	76.0	685	7	DT090451	DT090451	DT090451	
892	15.2	76.0	633	7	CM283874	170004551	CM283874	c	965	15.2	76.0	688	8	CG304005	CG304005	CG304005
893	15.2	76.0	634	1	AI456135	AI456135	AI456135	966	15.2	76.0	689	2	BX673019	BX673019	BX673019	
894	15.2	76.0	634	6	CM404565	EL0100520	CM404565	c	967	15.2	76.0	690	5	BN351499	BN351499	BN351499
895	15.2	76.0	634	10	CM894153	CM894153	CM894153	968	15.2	76.0	692	8	DN190388	DN190388	DN190388	
896	15.2	76.0	635	8	DT087821	JGI_ANNK1	DT087821	c	969	15.2	76.0	693	8	DN191325	DN191325	DN191325
897	15.2	76.0	635	10	CM775256	OG_BBA009	CM775256	c	970	15.2	76.0	693	8	DN191325	DN191325	DN191325
898	15.2	76.0	637	8	DN191277	ACLS_14G0	DN191277	c	971	15.2	76.0	694	5	BU138788	BU138788	BU138788



C 972 15.2 76.0 694 10 CW002144  
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 974 15.2 76.0 698 6 CB620278  
 975 15.2 76.0 699 5 BM485981  
 976 15.2 76.0 702 7 CM270366  
 977 15.2 76.0 703 5 BM258660  
 978 15.2 76.0 703 5 BM4847824  
 979 15.2 76.0 703 9 CC971392  
 980 15.2 76.0 704 3 B1640898  
 981 15.2 76.0 704 9 CC636479  
 982 15.2 76.0 704 10 C2779238  
 983 15.2 76.0 705 8 DN263841  
 984 15.2 76.0 706 10 AG281534  
 985 15.2 76.0 707 2 BG631938  
 986 15.2 76.0 709 2 BF492519  
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 988 15.2 76.0 709 3 B1386781  
 989 15.2 76.0 710 8 DR690050  
 990 15.2 76.0 714 6 CR679766  
 991 15.2 76.0 715 9 AZ098631  
 992 15.2 76.0 717 10 AG550929  
 993 15.2 76.0 718 7 CK446426  
 994 15.2 76.0 719 6 CD636053  
 995 15.2 76.0 719 6 DN426666  
 996 15.2 76.0 719 8 DN426666  
 997 15.2 76.0 719 8 DR692424  
 998 15.2 76.0 720 8 BU560241  
 999 15.2 76.0 722 8 DT086197  
 C1000 15.2 76.0 723 1 AM128196

## ALIGNMENTS

RESULT 1  
 BU280879 60359710P1 CSBOCHN54 Gallus gallus CDNA clone CHEST572d4 5', mRNA  
 LOCUS  
 DEFINITION  
 sequence.  
 BU280879  
 VERSION  
 BU280879.1 GI:25730333  
 KEYWORDS  
 EST.  
 SOURCE  
 Gallus gallus (chicken)  
 ORGANISM  
 Gallus gallus  
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 864)  
 REFERENCE  
 1 (bases 1 to 864)  
 AUTHORS  
 Boardman, P.R., Sanz-Bizquerro, J., Overton, I.M., Burt, D.W., Bosch, R.,  
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
 TITLE  
 A Comprehensive Collection of Chicken CDNAs  
 JOURNAL  
 Curr. Biol. 12 (22), 1965-1969 (2002)  
 PUBMED  
 12445392  
 COMMENT  
 Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.  
 Location/Qualifiers  
 1..864  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="Compton Line 151"  
 /db\_xref="taxon:9031"  
 /clone="CHEST572d4"  
 /sex="Female"  
 /issue\_type="not cerebrum or cerebellum"  
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## ORIGIN

Query Match 95.0%; Score 19; DB 5; Length 864;  
 Best Local Similarity 89.5%; Pred. No. 1; 9e+02;  
 Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AGGTACAGCCAGACGACG 19  
 Db 186 AGGTACAGCCAGACGACG 204

## RESULT 2

AGS09048 747 bp DNA linear GSS 22-DEC-2004  
 LOCUS  
 DEFINITION  
 Mus musculus molossinus DNA, clone:MSMg01-412D14.TU, genomic survey  
 sequence.  
 AGS09048  
 VERSION  
 AGS09048.1 GI:48216461

KEYWORDS  
 GSS.  
 SOURCE  
 Mus musculus molossinus (Japanese wild mouse)  
 ORGANISM  
 Mus musculus molossinus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Mus.

REFERENCE  
 1 Abe, K., Noguchi, H., Tagawa, K., Yuzuriba, M., Toyoda, A., Kojima, T.,  
 Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriwaiki, K. and  
 Shirolahi, T.

TITLE  
 Contribution of Asian mouse subspecies Mus musculus molossinus to  
 genomic constitution of strain C57BL/6J, as defined by BAC-end

JOURNAL  
 PUBMED  
 15574823  
 2 (bases 1 to 747)

REFERENCE  
 2 (bases 1 to 747)  
 AUTHORS  
 Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.  
 TITLE  
 Direct Substitution  
 Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Japan  
 1-7-22 Suenho-chou, Tsukuba, Iku, Yokohama, Kanagawa, 230-0045, Japan  
 (E-mail: hattori@psc.riken.jp, URL: http://hgp.gsc.riken.go.jp/  
 Tel: 81-45-503-9111, Fax: 81-45-503-9170)

## COMMENT

Clones are derived from the mouse BAC library MSMg01. For BAC  
 library availability, please contact Kunya Abe (abe@tc.riken.jp).  
 Tsukuba Institute, Bio Resource Center,  
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1  
 Koyada, Tsukuba, 305-0074 Japan  
 phone: 81-298-36-9189, fax: 81-298-36-9199  
 e-mail: abe@tc.riken.jp

## PRIMERS

Sequencing : TU  
 LIBRARY  
 Vector : DBACE3.6  
 R Site 1 : BcORI  
 R Site 2 : BcORI.

## FEATURES

1..747  
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## ORIGIN

/db\_xref="taxon:57486"  
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/sex="male"  
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Query Match 90.0%; Score 18; DB 10; Length 747;  
Best Local Similarity 88.9%; Pred. No. 5.9e+02;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GUACAGCCGAGACUACGA 20  
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432 GTACAGCCGAGACTACGA 449

RESULT 3  
AA855258 331 bp mRNA linear EST 06-MAR-1998  
LOCUS vW70a11.r1 StrataGene mouse heart (#937316) Mus musculus cDNA clone

DEFINITION IMAGE:1260284 5', mRNA sequence.

ACCESSION AA855258  
VERSION AA855258.1 GI:2942796  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 331)  
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Schellenberg, K., Steptoe, M., Tan, P., Underwood, K., Moore, B.,  
Theising, B., Wylie, T., Lemon, G., Soares, B., Wilson, R., and  
Waterston, R.

TITLE The WashU-HMNI Mouse EST Project  
JOURNAL Unpublished (1996)  
COMMENT Contact: Maria M/Mouse EST Project  
WashU-HMNI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu

This clone is available royalty-free through LML; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:662836  
Putative full length read  
vector to vector length is 332  
Seq primer: -28m13 rev1 ET from Amersham.

## FEATURES

## SOURCE

1..331  
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/lab\_host="SOLR (kanamycin resistant)"  
/note="Organ: heart; Vector: pBluescript SK-; Site 1:  
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:  
Oligo dt. 93 pooled NIH/Swiss 13 day embryo hearts.  
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'  
adaptor sequence: 5' GAATTCGCGACGAG 3' -3' adaptor  
sequence: 5' CTCGAGTTT TTT TTT TTT TTT TTT 3' "

## ORIGIN

Query Match 87.0%; Score 17.4; DB 1; Length 331;  
Best Local Similarity 89.5%; Pred. No. 1.1e+03;  
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1..AGGUAACGACGAGACUACG 19  
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267 AGGAACGACGAGACTACG 285

RESULT 4  
A1463924 332 bp mRNA linear EST 09-MAR-1999  
LOCUS vW70a11.y1 StrataGene mouse heart (#937316) Mus musculus cDNA clone  
DEFINITION IMAGE:1260284 5', mRNA sequence.

ACCESSION A1463924  
VERSION A1463924.1 GI:4317954  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 332)  
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,  
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowles, M.,  
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,  
Ritter, B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,  
Waterston, R., and Wilson, R.  
The WashU-NCI Mouse EST Project 1999  
Unpublished (1999)  
Contact: Maria M/WashU-NCI Mouse EST Project 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu

## COMMENT

This clone is available royalty-free through LML; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:662836  
This read is a RESEQUENCE of a previously sequenced mouse clone  
correct orientation)  
Putative full length read  
vector to vector length is 333  
Seq primer: -40RP from Gibco.

## FEATURES

## SOURCE

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/dev\_stage="13 day embryos"  
/lab\_host="SOLR (kanamycin resistant)"  
/note="Organ: heart; Vector: pBluescript SK-; Site 1:  
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:  
Oligo dt. 93 pooled NIH/Swiss 13 day embryo hearts.  
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'  
adaptor sequence: 5' GAATTCGCGACGAG 3' -3' adaptor  
sequence: 5' CTCGAGTTT TTT TTT TTT TTT TTT 3' "

## ORIGIN

Query Match 87.0%; Score 17.4; DB 1; Length 332;  
Best Local Similarity 89.5%; Pred. No. 1.1e+03;  
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1..AGGUAACGACGAGACUACG 19  
|||  
268 AGGAACGACGAGACTACG 286

RESULT 5  
CE251666/c

LOCUS CE251666 632 bp DNA linear GSS 26-SEP-2003  
 DEFINITION tigr-gss-dog-17000335911441 dog library Canis familiaris genomic,  
 genomic survey sequence.  
 ACCESSION CE251666  
 VERSION CE251666.1 GI:35948584  
 KEYWORDS GSS.  
 SOURCE  
 ORGANISM Canis familiaris (dog)  
 Canis familiaris  
 Bacteria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Pisipedia; Canidae;  
 Canis.  
 REFERENCE 1 (bases 1 to 632)  
 AUTHORS Kirkness,B.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
 Ruesch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
 Venter,J.C.  
 TITLE The dog genome: survey sequencing and comparative analysis  
 JOURNAL Science 301 (5641), 1898-1903 (2003)  
 PubMed 14512627  
 COMMENT Contact: Kirkness EF  
 The Institute for Genomic Research  
 Department of Bacteriologic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirknes@tigr.org  
 Class: shotgun.  
 FEATURES  
 source Location/Qualifiers  
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 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
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 /note="Site 1: BstXI; Libraries were prepared from  
 peripheral blood"  
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 Query Match 87.0%; Score 17.4; DB 9; Length 632;  
 Best Local Similarity 84.2%; Pred. No. 1.1e+03;  
 Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 AGGACGACGACGACGACG 19  
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 Db 530 AGGTACGACGACGACGACTAG 512  
 RESULT 6  
 BH898697 706 bp DNA linear GSS 31-OCT-2002  
 BH898697/c  
 LOCUS MB6110C9 Mission Bay (San Diego, CA) uncultured virus community  
 DEFINITION uncultured marine virus genomic clone MB6110C9, genomic survey  
 sequence.  
 ACCESSION BH898697  
 VERSION BH898697.1 GI:24432823  
 KEYWORDS GSS.  
 SOURCE uncultured marine virus  
 ORGANISM uncultured marine virus  
 Viruses; environmental samples.  
 REFERENCE 1 (bases 1 to 706)  
 AUTHORS Breitbart,M., Salamon,P., Andresen,B., Mahaffy,J.M., Segall,A.M.,  
 Mead,D., Azam,F. and Rohwer,F.  
 TITLE Genomic analysis of uncultured marine viral communities  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (22), 14250-14255 (2002)  
 PubMed 12384570  
 COMMENT Contact: Rohwer F  
 Biology Dept.  
 San Diego State University  
 5500 Campanile Dr, San Diego, CA 92102, USA  
 Tel: 6195941336  
 Fax: 619595676  
 Email: forest@sunstroke.sdsu.edu  
 Class: shotgun.  
 FEATURES  
 Location/Qualifiers

source  
 1..706  
 /organism="uncultured marine virus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:186617"  
 /clone="MB6110C9"  
 /clone\_lib="Mission Bay (San Diego, CA) uncultured virus  
 community"  
 /note="Vector: pSMART; Sample from Mission Bay (San Diego,  
 CA). Marine viruses were isolated from 200 liters of  
 surface seawater using a combination of differential  
 filtration and density-dependent gradient centrifugation.  
 Linker-amplified shotgun libraries were constructed by  
 randomly shearing the total marine viral community DNA,  
 end-repeating, ligating dsDNA linkers to the ends, and  
 amplifying the fragments using Vent DNA polymerase. The  
 resulting fragments were ligated into the pSMART vector  
 and electroporated into MC12 cells (Lucigen, Middleton,  
 WI)."  
 ORIGIN  
 Query Match 87.0%; Score 17.4; DB 9; Length 706;  
 Best Local Similarity 84.2%; Pred. No. 1.2e+03;  
 Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 AGGACGACGACGACGACG 19  
 |||:|||||:|||||:  
 Db 664 AGGTACGACGACGACGACTAG 646  
 RESULT 7  
 CG307131 847 bp DNA linear GSS 26-AUG-2003  
 CG307131  
 LOCUS OG2BX53TH ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMA0759110,  
 DEFINITION genomic survey sequence.  
 ACCESSION CG307131  
 VERSION CG307131.1 GI:34224291  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACMAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 847)  
 AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utechtack,T.,  
 Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,  
 Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.  
 TITLE Consortium for Maize Genomics  
 JOURNAL Unpublished (2002)  
 COMMENT Other GSSs: OG2BX53TV  
 Contact: Cathy Whitelaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whitelaw@tigr.org  
 Seq primer: TR  
 Class: methylation filtered.  
 FEATURES  
 source Location/Qualifiers  
 1..847  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="ZMMBMA0759110"  
 /clone\_lib="ZM\_0.7-1.5\_KB"  
 /note="Vector: pBSC-K-7 Site 1: HincII; 0.7-1.5 kb  
 methylation filtered genomic DNA library"  
 ORIGIN  
 Query Match 87.0%; Score 17.4; DB 10; Length 847;  
 Best Local Similarity 84.2%; Pred. No. 1.2e+03;  
 Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;



```

/mol_type="mRNA"
/db_xref="taxon.9606"
/clone="IMAGS.3608974"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NH MGC 44"
/note="Organ: uterus; Vector: pORF7; Site: 1; XhoI; EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCGCAGGAG (g). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA Synthesis Kit (Stratagene) and Superscript II RT (Life Technologies)."

```

## ORIGIN

Query Match	87.0%	Score 17.4;	DB 2;	Length 1016;
Best Local Similarity	89.5%	Pred. No.1.2e+03;		
Matches 17; Conservative	1;	Mismatches 1;	Indels 0;	Gaps 0

```

QY      1 AGGUACAGCCAGGACTUACG 19
          ||| ||||| ||||| : |||
Db      830 AGGCACAGCCAGGACTACG 848

```

RESULT 11						
LOCUS	AI757758	437 bp	mRNA	linear	EST 18-JAN-2000	
DEFINITION	BTSTSTea34A03.y1 Bimertia S5-2 Sporozoite stage Bimertia tenella CDNA 5', mRNA sequence.					

REFERENCE  
AUTHORS  
1 (bases 1 to 427)  
Liberator, P., Diaz, C., Tang, K., Marra, M., Hillier, L., Kucaba, T.,

TITLE	JOURNAL	COMMENT
WashU-Merck Eimeria tenella project	Unpublished (1999)	Contact: David Sibley, Ph.D.

(Strtagene). Clones were converted to phagemids by mass excision using Exsist helper phage and SOLR cells (Strtagene ). Insert sizes range from 1.2-2.9 Kb."

**ORIGIN**

Query Match	85.0%	Score 17	DB 1	Length 427
Best Local Similarity	88.2%	Pred. No. 1.7e+03		
Matches 15	Conservative 2	Mismatches 0	Indels 0	Gaps 0

```

QY      1 AGGUACAGCCAGGACTUA 17
         |||:|||||||:|
Db     33 AGGTACAGCCAGGACTA 17

```

RESULT 12	CEI09731	488 bp	DNA	linear	GSS 24-SEP-2003
LOCUS	CEI09731				
DEFINITION	CEI09731	488 bp	DNA	linear	GSS 24-SEP-2003
	t45r-gss-dog-17000324505919	Dog	Library	Canis familiaris	genomic,
	genomic survey sequence.				

REFERENCE	AUTHORS	TITLE	JOURNAL
1 (bases 1 to 488)	Kirkness, B.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Frazer, C.M. and Venter, J.C.	The dog genome: survey sequencing and comparative analysis	Science 301 (5641), 1898-1903 (2003)
			14512627

FEATURES	Location/Qualifiers
source	1. .488

**ORIGIN**

Query Match	85.04	Score 17	DB 9	Length 488
Best Local Similarity	88.24	Pred. No. 1.7e+03		
Matches 15	Conservative 2	Mismatches 0	Indels 0	Gaps 0

```

QY      1 AGTUA CAGCCAGGACTUA 17
          |||:|||||||:|
Db      226 AGTACAGCCAGGACTA 242

```

RESULT 13			
BG336492			
LOCUS	BG336492	1097 bp	mRNA
DEFINITION	60240537661 NIH_MGC_21 Homo sapiens CDNA clone IMAGE:4543146 5',	linear	EST 27-FEB-2001
	mRNA sequence.		

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
1 (bases 1 to 1097)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: ATCC

CDNA library preparation: Ling Hong/Rubin Laboratory  
CDNA library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILNL at:  
<http://image.llnl.gov>  
Plate: L10C1224 row: 9 column: 19  
High quality sequence stop: 460.  
Location/Qualifiers

FEATURES  
source

1. 1097  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGR:4543146"  
/tissue\_type="choriocarcinoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_11b="NIH MGC 21"  
/note="Organ: Placenta; Vector: pOTB7; Site\_1: XhoI;  
Site\_2: EcoRI; cDNA made by oligo-OT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCGACGAG(G). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

Query Match 85.0%; Score 17; DB 2; Length 1097;  
Best Local Similarity 88.2%; Pred. NO. 2e+03;  
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 UACAGCCAGACGACUACGA 20  
:|||||||:|||||  
501 TACAGCCAGACGACTACGA 517

RESULT 14  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AO515870 320 bp DNA linear GSS 05-MAY-1999  
HS\_5235\_A2\_C05\_SP6E\_RPCI-11 Human Male BAC Library Homo sapiens  
genomic clone Plate=811 Col=10 Row=E, genomic survey sequence.  
AO515870  
AO515870.1 GI:4748128  
GSS.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
1 (bases 1 to 320)  
Mahairas,G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,  
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and  
Hood,L.  
Sequence-tagged connectors: A sequence approach to mapping and  
scanning the human genome  
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
10449764  
Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: [jwallace@u.washington.edu](mailto:jwallace@u.washington.edu)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
COMMENT

High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: [jwallace@u.washington.edu](mailto:jwallace@u.washington.edu)

Clones are derived from the human BAC library RPCI-11. For BAC  
library availability, please contact Pieter de Jong  
([pieter@dejong.med.buffalo.edu](mailto:pieter@dejong.med.buffalo.edu)). Clones may be purchased from  
BACPAC Resources ([http://bacpac.med.buffalo.edu/ordering\\_bac.htm](http://bacpac.med.buffalo.edu/ordering_bac.htm))  
or from Research Genetics (<http://www.resgen.com>). BAC end web server:  
<http://www.htsc.washington.edu>  
Plate: 811 row: E column: 10  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 320.  
Location/Qualifiers

FEATURES  
source

1. 320  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="Plate=811 Col=10 Row=E"  
/sex="male"  
/clone\_11b="RPCI-11 Human Male BAC Library"  
/note="Vector: pBACe3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
Male blood DNA was isolated from one randomly chosen donor  
and partially digested with a combination of EcoRI and  
EcoRI Methylase. Size selected DNA was cloned into the  
pBACe3.6 vector at EcoRI sites"

## ORIGIN

Query Match 84.0%; Score 16.8; DB 9; Length 320;  
Best Local Similarity 85.0%; Pred. NO. 2.1e+03;  
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGUNACGACGACGACUACGA 20  
||| ||||| ||||| |||||  
128 AGGACGACGACGACGACTACGA 147

## RESULT 15

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AO377301 427 bp DNA linear GSS 29-JUN-1999  
RPCI-11-162H24.TV RPCI-11 Homo sapiens genomic clone  
RPCI-11-162H24, genomic survey sequence.  
AO377301  
AO377301.1 GI:4348324  
GSS.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
1 (bases 1 to 427)  
Zhao,S., Adams,M.D., Nieman,W., Malek,J., de Jong,P. and  
Venter,J.C.  
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready  
Map Building  
Unpublished (1997)  
Other GSSs: RPCI-11-162H24.TJ  
Contact: Shaying Zhao, William Nieman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: [hbe@tigr.org](mailto:hbe@tigr.org)  
Clones are derived from the human BAC library RPCI-11. For BAC  
library availability, please contact Pieter de Jong  
([pieter@dejong.med.buffalo.edu](mailto:pieter@dejong.med.buffalo.edu)). Clones may be purchased from  
BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from  
Research Genetics (<http://www.resgen.com>). BAC end search page:  
[http://www.tigr.org/tcdb/humgen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tcdb/humgen/bac_end_search/bac_end_search.html)  
Seq primer: T7  
Class: BAC ends.  
Location/Qualifiers

1. 427  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"

```

/db_xref="GDB:7562015"
/db_xref="taxon:9606"
/clone="RPCI-11-162H24"
/sex="Male"
/cell_type="Lymphocytes"
/clone_1db="RPCI-11"
/notes="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC111 Human Male BAC Library"

ORIGIN

Query Match      84.0%; Score 16.8; DB 9; Length 427;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY
1 AGGATACAGCCAGGACTACGA 20
|||||:|||||:|||||
Db      104 AGGTATACGACGAGATACGA 123

RESULT 16
LOCUS      AJ691440      432 bp      mRNA      linear      EST 29-JUN-2004
ACCESSION  AJ691440      KN261 Bos taurus cDNA clone KN261-024_H05, mRNA sequence.
VERSION     AJ691440.1      GI:49424048
KEYWORDS
SOURCE      Bos taurus (cow)
ORGANISM    Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Bovidae; Bovinae; Bos.
1 (bases 1 to 432)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector:pBluescriptII(SK+) R. Site1: EcoRI;
R. Site2: SmaI 5' Seq Primer T3 Normalised library constructed from
bovine ovary. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK.
EH25 9PS, www.arkgenomics.org.
Location/Qualifiers
1..432
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="KN261-024_H05"
/tissue_type="ovary"
/clone_1db="KN261"
/notes="Vector: pBluescriptII(SK+); Site_1: EcoRI; Site_2:
SmaI; Single pass sequencing. Normalised library
constructed from bovine ovary."

ORIGIN

Query Match      84.0%; Score 16.8; DB 1; Length 432;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY
1 AGGATACAGCCAGGACTACGA 20
|||||:|||||:|||||
Db      341 AGGTATACGACGAGATACGA 360

RESULT 17
LOCUS      BY471445      527 bp      mRNA      linear      EST 02-JAN-2003
ACCESSION  BY471445      RIKEN full-length enriched, melanocyte mus musculus cDNA
DEFINITION
```

ACCESSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS
Clone G270099g11 3', mRNA sequence.				
BY474475				
BY474475.1 GI:26805854				
EST.				
Mus musculus (house mouse)				
Mus musculus				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murineae; Mus.				
1 (bases 1 to 527)				
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikiado, I., Oaso, T., Saito, R., Suzuki, H., Yanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quickbush, J., Schirral, L. M., Kanapin, A., Matsuda, H., Batalov, S., Betzel, K. W., Blake, J. A., Brad, D., Brusic, V., Chothia, C., Corbani, L. E., Cousin, S., Datta, E., Dragan, T. A., Fletcher, C. F., Forrest, A., Frazier, K. S., Gaasterland, T., Gerbould, M., Glessi, C., Godzik, A., Gough, J., Grimmond, S., Gustinch, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kani, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lehman, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numa, K., Okido, T., Pavan, W. J., Pettes, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramchandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sennell, A., Schneider, C., Semp, C. A., Setou, M., Shimada, K., Sultana, R., Takemura, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wyshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-ken, T., Kono, H., Nakamura, M., Sakemura, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Aizawa, T., Fukuda, S., Hara, A., Hashizume, M., Imotani, K., Ishi, Y., Itoh, M., Kigawa, I., Miyazaki, A., Sakai, K., Saeki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterson, R., Landier, R. S., Rogers, J., Birney, E. and Hayashizaki, Y.				
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs				
Nature 420, 563-573 (2002)				
12466851				
Contact: Yoshihide Hayashizaki				
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute				
The Institute of Physical and Chemical Research (RIKEN)				
1-7-22 Suenho-cho, Tsunumi-Ku, Yokohama, Kanagawa 230-0045, Japan				
Tel: 81-45-503-9222				
Fax: 81-45-503-9216				
Email: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/				
Hirozane, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Kono, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numata, K., Ohno, M., Sakai, K., Sakemura, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y.				
Direct Submission				
Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)				
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)				
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)				
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)				
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.				
Cells were provided by Drs. William J Pavan, Stacie Loftus, and Denise Larson (Division of Intramural Research Genetic Disease				



Research Branch National Human Genome Research Institute, National Institutes of Health (NIH) Building: 49, Room 4A82 49 Convent Drive MSC 4472 Bethesda, Maryland U.S.A) whose assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

# FEATURES

## source

Location/Qualifiers  
1..527  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="G270099G11"  
/cell\_type="melanocyte"  
/clone\_lib="RIKEN full-length enriched, melanocyte"

## ORIGIN

Query Match 84.0%; Score 16.8; DB 5; Length 527;  
Best Local Similarity 85.0%; Pred. No. 2.2e+03;  
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 AGGUAACAGCAGACUACGA 20  
213 AGGAACAGCAGCAGACTACGA 194

## RESULT 18

LOCUS BF825833 644 bp mRNA linear EST 13-JAN-2001  
DEFINITION MR2-HN0036-171100-002-a01 HN0036 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF825833  
VERSION BF825833.1 GI:12168549  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo

## REFERENCE

1 (bases 1 to 644)  
Dies Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Mateukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?c1=MR2&c2=MR2-HN0036-171100-002-a01&c3=2000-11-17&c4=1>)  
Seq primer: puc 18 forward  
High quality sequence start: 3  
High quality sequence stop: 618.  
Location/Qualifiers  
1..644  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="HN0036"  
/note="Organ: head normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products

## FEATURES

## source

Location/Qualifiers  
1..644  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="HN0036"  
/note="Organ: head normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products

## ORIGIN

Query Match 84.0%; Score 16.8; DB 2; Length 644;  
Best Local Similarity 80.0%; Pred. No. 2.3e+03;  
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 1 AGGUAACAGCAGACUACGA 20  
407 AGGUAACAGCAGCAGACTACGA 426

## RESULT 19

LOCUS AZ941856/c 644 bp DNA linear GSS 26-APR-2001  
DEFINITION 2M0201G17R Mouse 10kb plasmid U06C2M library Mus musculus genomic clone U06C2M0201G17 R, genomic survey sequence.  
ACCESSION AZ941856  
VERSION AZ941856.1 GI:13804673  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Scurionath, Muridae; Muridae; Murinae; Mus

## REFERENCE

1 (bases 1 to 644)  
Dunn,P., Aoyagi,A., Barber,M., Baecorn,T., Duval,B., Hamli,C., Isiam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0201 row: G column: 17  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 644.  
Location/Qualifiers  
1..644  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="U06C2M0201G17"  
/sex="Female"  
/lab\_host="B. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid U06C2M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number

## FEATURES

## source

Location/Qualifiers  
1..644  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="U06C2M0201G17"  
/sex="Female"  
/lab\_host="B. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid U06C2M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number



FEATURES  
source  
Fax: 301-838-0208  
Email: whitelaw@icr.org  
Seq primer: TR  
Class: methylation filtered.  
Location/Qualifiers  
1..728

ORIGIN  
Query Match 84.0%; Score 16.8; DB 9; Length 728;  
Best Local Similarity 85.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
1 AGGACAGCCAGACGACGA 20  
|||:|||||:|||||  
153 AGGTACAGCCAGACGACGA 172

RESULT 23  
AG463520/c 762 bp DNA linear GSS 22-DEC-2004  
LOCUS Mus musculus molossinus DNA, clone:MSM901-352G01.TU, genomic survey  
DEFINITION  
ACCESSION AG463520  
VERSION AG463520.1 GI:4816076  
KEYWORDS GSS.  
SOURCE Mus musculus molossinus (Japanese wild mouse)  
ORGANISM Mus musculus molossinus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
1  
Abe,K., Noguchi,H., Tagawa,K., Yuzurika,M., Toyoda,A., Kojima,T.,  
Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and  
Shiotohshi,T.  
Contribution of Asian mouse subspecies Mus musculus molossinus to  
genomic constitution of strain C57BL/6J, as defined by BAC-end  
sequence-SNP analysis  
Genome Res. 14 (12), 2439-2447 (2004)  
15574823  
2 (bases 1 to 762)  
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.  
Direct Submission  
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-chou,Tsukuba-shi, Yokohama, Kanagawa, 230-0045, Japan  
(E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,  
Tel:81-45-503-9111, Fax:81-45-503-9170)  
Clones are derived from the mouse BAC library MSM901. For BAC  
library availability, please contact Kunihisa Abe (abe@rtc.riken.jp).  
The Institute of Physical and Chemical Research (RIKEN) 3-1-1  
Koyadai, Tsukuba, 305-0074 Japan  
phone: 81-298-36-9189, fax: 81-298-36-9199  
e-mail: abe@rtc.riken.jp  
PRIMERS  
Sequencing : TU  
LIBRARY : PBACE3.6  
Vector : EcoRI  
R.site 1 : EcoRI  
R.site 2 : EcoRI  
Location/Qualifiers  
1..762  
/organism="Mus musculus molossinus"  
/mol\_type="genomic DNA"  
/sub\_species="molossinus"

/db\_xref="taxon:57486"  
/clone="MSM901-352G01.TU"  
/sex="male"  
/tissue\_type="mixture of kidney and spleen"  
/clone\_id="MSM901 Mouse Male BAC Library"

ORIGIN  
Query Match 84.0%; Score 16.8; DB 10; Length 762;  
Best Local Similarity 80.0%; Pred. No. 2.3e+03;  
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
1 AGGACAGCCAGACGACGA 20  
|||:|||||:|||||  
210 AAGTACAGCCAGACGACGA 191

RESULT 24  
CB620270 773 bp mRNA linear EST 08-APR-2003  
LOCUS OSl1Ba05F15 f OSl1Ba Oryza sativa (indica cultivar-group) cDNA  
DEFINITION  
ACCESSION CB620270  
VERSION CB620270.1 GI:29615258  
KEYWORDS EST.  
SOURCE Oryza sativa (indica cultivar-group)  
ORGANISM Oryza sativa (indica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Erbartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 773)  
Jantaauriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,  
Seahberg,B., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,  
Soderlund,C. and Wang,G.L.  
Large-scale identification of expressed sequence tags involved in  
rice and rice blast fungus interaction  
Plant Physiol. 138 (1), 105-115 (2005)  
15886863  
Contact: Rod Wing  
Arizona Genomics Institute  
University of Arizona  
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ  
85721-0088, USA  
Tel: 520 626 3967  
Fax: 520 621 9288  
Email: rwing@genome.arizona.edu  
PCR Primers  
FORWARD: gta aac cga cgg cca gtc  
BACKWARD: gga aac agc tat gac cat g  
Plate: 05 row: F column: 15  
Seq primer: gta aac cga cgg cca gtc.  
Location/Qualifiers  
1..773  
/organism="Oryza sativa (indica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="IR36"  
/db\_xref="taxon:39946"  
/clone="OS11Ba05F15"  
/tissue\_type="leaf"  
/dev\_stage="3 week"  
/lab\_host="DH10B"  
/clone\_id="OS11Ba"  
/note="Vector: Bluescript II KS +, Site\_1: EcoRI, Site\_2:  
XhoI, Lesion Mimic SPL 11"

FEATURES  
source  
Query Match 84.0%; Score 16.8; DB 6; Length 773;  
Best Local Similarity 85.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
1 AGGACAGCCAGACGACGA 20  
|||:|||||:|||||  
22 AGGTACAGCCAGACGACGA 41

## ORIGIN

Query Match 84.0%; Score 16.8; DB 6; Length 773;  
Best Local Similarity 85.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
1 AGGACAGCCAGACGACGA 20  
|||:|||||:|||||  
22 AGGTACAGCCAGACGACGA 41

FEATURES  
source  
1..762  
/organism="Mus musculus molossinus"  
/mol\_type="genomic DNA"  
/sub\_species="molossinus"

RESULT 25  
CG269100/c 784 bp DNA linear GSS 25-AUG-2003  
LOCUS OGAJK40TH ZM 0.7-1.5\_KB Zea mays genomic clone ZMMBMA0586H07,  
DEFINITION genomic survey sequence.  
ACCESSION CG269100  
VERSION CG269100.1 GI:34181241  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 784)  
Whiteclaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,  
Reinick, A., Frazer, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,  
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Other\_GSSs: OGAJK40TV  
COMMENT Contact: Cathy Whiteclaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteclaw@cigr.org  
Seq primer: TF  
Classes: methylation filtered.  
Location/Qualifiers  
1..784  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone\_id="ZMMBMA0586H07"  
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb  
methylation filtered genomic DNA library"

ORIGIN  
Query Match 84.0%; Score 16.8; DB 10; Length 784;  
Best Local Similarity 85.0%; Pred. No. 2.3e+03;  
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 AGGUACAGCCAGACUACGA 20  
|||||  
DB 468 AGGTACAGCCAGAACGCA 449

RESULT 26  
CG269110 865 bp DNA linear GSS 25-AUG-2003  
LOCUS OGAJK40TV ZM 0.7-1.5\_KB Zea mays genomic clone ZMMBMA0586H07,  
DEFINITION genomic survey sequence.  
ACCESSION CG269110  
VERSION CG269110.1 GI:34181251  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 865)  
Whiteclaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,  
Reinick, A., Frazer, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,  
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Other\_GSSs: OGAJK40TH  
COMMENT Contact: Cathy Whiteclaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteclaw@cigr.org  
Seq primer: TF  
Classes: methylation filtered.  
Location/Qualifiers  
1..865  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone\_id="ZMMBMA0586H07"  
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb  
methylation filtered genomic DNA library"

ORIGIN  
Query Match 84.0%; Score 16.8; DB 10; Length 865;  
Best Local Similarity 85.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 AGGUACAGCCAGACUACGA 20  
|||||  
DB 844 AGGTACAGCCAGAACGCA 863

RESULT 27  
CG252727 936 bp DNA linear GSS 25-AUG-2003  
LOCUS OGMHE23TV ZM 0.7-1.5\_KB Zea mays genomic clone ZMMBMA0577D21,  
DEFINITION genomic survey sequence.  
ACCESSION CG252727  
VERSION CG252727.1 GI:34154817  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 936)  
Whiteclaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,  
Reinick, A., Frazer, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,  
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Other\_GSSs: OGMHE23TH  
COMMENT Contact: Cathy Whiteclaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteclaw@cigr.org  
Seq primer: TF  
Classes: methylation filtered.  
Location/Qualifiers  
1..936  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone\_id="ZMMBMA0577D21"  
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb  
methylation filtered genomic DNA library"

ORIGIN  
Query Match 84.0%; Score 16.8; DB 10; Length 936;  
Best Local Similarity 85.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 AGGUACAGCCAGACUACGA 20  
|||||  
DB 366 AGGTACAGCCAGAACGCA 385

RESULT 28  
BZ553930/c 940 bp DNA linear GSS 17-DEC-2002  
LOCUS pacal-60\_4436.xl pacal-60 Pseudomonas aeruginosa genomic clone  
DEFINITION pacal-60\_4436, genomic survey sequence.  
ACCESSION BZ553930  
VERSION BZ553930.1 GI:27160619  
KEYWORDS GSS.  
SOURCE Pseudomonas aeruginosa  
ORGANISM Pseudomonas aeruginosa  
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
Pseudomonadaceae; Pseudomonas.  
REFERENCE 1 (bases 1 to 940)  
AUTHORS Spencer, D.H., Raymond, C.K., Smith, E.B., Sims, E.B., Hastings, M.,  
Burns, J.L., Kaul, R. and Olsen, M.V.  
TITLE Whole-Genome-Sequence Variation among multiple Isolates of  
Pseudomonas aeruginosa library  
J. Bacteriol. (2002) In press  
COMMENT Contact: Chris K. Raymond  
Genome Center  
University of Washington  
Box 352145, Seattle, WA 98105-2145, USA  
Tel: 2062216954  
Fax: 2066857244  
Email: craymond@u.washington.edu  
Class: shotgun.

FEATURES  
source  
1..940  
Location/Qualifiers  
/organism="Pseudomonas aeruginosa"  
/mol\_type="genomic DNA"  
/strain="1-60"  
/db\_xref="taxon:287"  
/clone="pacal-60\_4436"  
/clone\_lib="pacal-60"  
/note="Clinical isolate 1-60 Whole genomic shotgun  
library."

ORIGIN  
Query Match 84.0%; Score 16.8; DB 9; Length 940;  
Best Local Similarity 85.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACAGCCGAGCTACGA 20  
Db 240 AAGGACAGCCGAGCTACGA 221

RESULT 29  
BZ214228/c 965 bp mRNA linear EST 06-NOV-2000  
LOCUS BZ214228  
DEFINITION 601848401F1 NIH\_MGC\_55 Homo sapiens cDNA clone IMAGE:4079137 5',  
mRNA sequence.  
ACCESSION BZ214228  
VERSION BZ214228.1 GI:1107814  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 965)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@b-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA library Preparation: CLONTECH Laboratories, Inc.  
cDNA library Arrayed by: The I.M.A.G.E. Consortium (ILM)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/ILM at:  
<http://image.lnl.gov>  
Plate: LHC937 row: b column: 02  
High quality sequence stop: 8.  
Location/Qualifiers  
1..965  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4079137"  
/issue\_type="from acute myelogenous leukemia"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH MGC 55"  
/note="Organ: bone marrow; Vector: pDMR-LIB (Clontech);  
Site 1: SfiI (ggccctcgcc); Site 2: SfiI  
(ggccatcgcc); Double-stranded cDNA was prepared from  
cell line RNA. 5' and 3' adaptors were used in cloning as  
follows: 5' adaptor sequence: 5'-CACGCCATTATGCGC-3' and  
3' adaptor sequence:  
5'-ATTCTAGAGCCGAGCGCGCGGACATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size  
1.65 kb (range 0.9-4.0 kb). 14/15 colonies contained  
inserts by PCR. This library was enriched for full-length  
clones and was constructed by Clontech Laboratories (Palo  
Alto, CA)."

ORIGIN  
Query Match 84.0%; Score 16.8; DB 2; Length 965;  
Best Local Similarity 85.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACAGCCGAGCTACGA 20  
Db 631 AAGTACAGCCGAGCGAGA 612

RESULT 30  
BZ563339 1062 bp DNA linear GSS 17-DEC-2002  
LOCUS BZ563339  
DEFINITION pac82-164\_4207.y2 pac82-164 Pseudomonas aeruginosa genomic clone  
ACCESSION BZ563339  
VERSION BZ563339.1 GI:27166999  
KEYWORDS GSS.  
SOURCE Pseudomonas aeruginosa  
ORGANISM Pseudomonas aeruginosa  
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
Pseudomonadaceae; Pseudomonas.  
REFERENCE 1 (bases 1 to 1062)  
AUTHORS Spencer, D.H., Raymond, C.K., Smith, E.B., Sims, E.B., Hastings, M.,  
Burns, J.L., Kaul, R. and Olsen, M.V.  
TITLE Whole-Genome-Sequence Variation among multiple Isolates of  
Pseudomonas aeruginosa library  
J. Bacteriol. (2002) In press  
COMMENT Contact: Chris K. Raymond  
Genome Center  
University of Washington  
Box 352145, Seattle, WA 98105-2145, USA  
Tel: 2062216954  
Fax: 2066857244  
Email: craymond@u.washington.edu  
Class: shotgun.

FEATURES  
source  
1..1062  
Location/Qualifiers  
/organism="Pseudomonas aeruginosa"  
/mol\_type="genomic DNA"  
/strain="2-164"  
/db\_xref="taxon:287"  
/clone="pac82-164\_4207"  
/clone\_lib="pac82-164"  
/note="Clinical isolate 2-164 Whole genomic shotgun  
library."

ORIGIN

Query Match	84.0%: Score 16.8; DB 9; Length 1062;
Best Local Similarity	85.0%: Pred. No. 2.4e+03;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
QY 1 AGGUAACAGCCAGAGCUACGA 20	
Db 120 AAGGACAGCCAGAGCTACGA 139	
RESULT 31	
LOCUS CL023089	
DEFINITION CH216-15N1_RN1.1 CH216 Xenopus tropicalis genomic clone CH216-15N1,	
ACCESSION CL023089	1210 bp DNA linear GSS 31-DEC-2003
VERSION CL023089.1	GI:40464902
KEYWORDS GSS.	
SOURCE Xenopus tropicalis (western clawed frog)	
ORGANISM Xenopus tropicalis	
Bukariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;	
Xenopodinae; Xenopus; Silurana.	
1 (bases 1 to 1210)	
Kremliak, C., Carter, J., McPherson, J., Warren, W., Graves, T.,	
Mardis, E. and Wilson, R.	
A physical map of the xenopus tropicalis genome	
unpublished (2003)	
CONTACT: Richard K Wilson	
Genome Sequencing Center	
Washington University School of Medicine	
Email: submissions@watson.wustl.edu	
Insert Length: 175000 Std Error: 0.00	
Seq primer: RN1 TAGAGTCACTATAGGAGA	
Class: BAC ends	
High quality sequence start: 147	
High quality sequence stop: 495.	
Location/Qualifiers	
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/organism="Xenopus tropicalis"	
/mol_type="genomic DNA"	
/strain="Nigerian frog"	
/db_xref="taxon:8364"	
/clone="CH216-15N1"	
/sex="male"	
/cell_line="Stock 248 P7A2, inbred N7"	
/clone_1lb="CH216"	
/note="Vector: pTRABAC2.1; CHOKI-216 Xenopus tropicalis	
BAC library"	
ORIGIN	
Query Match	84.0%: Score 16.8; DB 10; Length 1210;
Best Local Similarity	80.0%: Pred. No. 2.5e+03;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;	
QY 1 AGGUAACAGCCAGAGCUACGA 20	
Db 212 AGGTACAGCCAGAGCTACGA 231	
RESULT 32	
LOCUS DN675670	
DEFINITION CFM67-H01_Y1d-s SHGC-CFw Gasterosteus aculeatus cDNA clone	
ACCESSION DN675670	1217 bp mRNA linear EST 29-MAR-2005
VERSION DN675670.1	GI:61995849
KEYWORDS EST.	
Gasterosteus aculeatus (three spined stickleback)	
Gasterosteus aculeatus	
Bukariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Actinopterygii; Neopterygii; Teleostei; Butelosteii; Neoteleostei;	
Acantomorphae; Acantopterygii; Percomorphae; Gasterosteiformes;	

REFERENCE 1 (bases 1 to 1217)  
AUTHORS Kingstaley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M., Schmutz,J. and Myers,R.M.  
TITLE Expressed sequence tags from *Gasterosteus aculeatus*  
JOURNAL Unpublished (2003)  
COMMENT Contact: Grimwood, Jane  
Stanford Human Genome Center  
Stanford University School of Medicine  
975 S California Ave, Palo Alto, CA 94304, USA  
Tel: 650 320 5917  
Fax: 650 320 5801  
Email: jane@shgc.stanford.edu  
Plate: 87  
High quality sequence stop: 855.  
Location/Qualifiers  
1. 1217  
/organism="Gasterosteus aculeatus"  
/mol\_type="mRNA"  
/strain="Conner Creek sticklebacks, WA USA"  
/db\_xref="taxon:69293"  
/clone="CFW87-H01"  
/sex="mixed male and female"  
/tissue\_type="gills"  
/dev\_stage="adult"  
/lab\_host="DH10B (T1 phage resistant)"  
/clone\_11b="SHGC-CFW"  
/note="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: 5'-GACTAGTCTGATGCGGAGCGGCCGCTT)25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form '...xxxAATC' (where 1s AATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at: [http://www.openbiosystems.com/cdna\\_library\\_construction\\_fa\\_q.php#8](http://www.openbiosystems.com/cdna_library_construction_fa_q.php#8) The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria. Clones available from Open Biosystems: <http://www.openbiosystems.com/stickleback>"

ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 1217;  
Best Local Similarity 80.0%; Pred. No. 2.5e+03;  
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGUAAGCCGAGACUACGA 20  
|||:|||||:|||||:  
Db 446 AAGTACAGCCAGACTACAA 465

RESULT 33  
AK050767/c LOCUS  
DEFINITION AK050767 3033 bp mRNA linear HTC 03-APR-2004  
MUS musculus 9 days embryo whole body cDNA, RIKEN full-length  
enriched library, clone:ID030018D22 Product:unclassified, full  
insert sequence.  
ACCESSION AK050767  
VERSION AK050767.1 GI:26094105  
KEYWORDS HTC, CAP trapper.  
SOURCE MUS musculus (house mouse)  
ORGANISM Mus musculus; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1

AUTHORS Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 PUBLISHED 10349636  
 REFERENCE  
 AUTHORS  
 2  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
 JOURNAL prepare full-length cDNA libraries for rapid discovery of new genes  
 PUBLISHED Genome Res. 10 (10), 1617-1630 (2000)  
 REFERENCE 11042159  
 AUTHORS  
 3  
 Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,  
 Komno, H., Akiyama, J., Nishi, K., Kitsuami, T., Teshitro, H., Itoh, M.,  
 Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,  
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasai, Y.,  
 Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,  
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format  
 JOURNAL sequencing pipeline with 384 multicapillary sequencer  
 PUBLISHED Genome Res. 10 (11), 1757-1771 (2000)  
 REFERENCE 11076861  
 AUTHORS  
 4  
 The RIKEN Genome Exploration Research Group Phase II Team and the  
 JOURNAL Functional Consortium.  
 PUBLISHED Functional annotation of a full-length mouse cDNA collection  
 REFERENCE Nature 409, 685-690 (2001)  
 AUTHORS  
 5  
 The PANTOM Genome Exploration and the RIKEN Genome Exploration Research  
 JOURNAL Group Phase I & II Team.  
 PUBLISHED Analysis of the mouse transcriptome based on functional annotation  
 REFERENCE of 60,770 full-length cDNAs  
 JOURNAL Nature 420, 563-573 (2002)  
 REFERENCE 5 (bases 1 to 3033)  
 AUTHORS  
 Adachi, J., Aizawa, K., Akiyama, T., Arahawa, T., Bono, H., Carninci, P.,  
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,  
 Hoti, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komno, H., Kouda, M.,  
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,  
 Okazaki, Y., Saito, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
 Muramatsu, M. and Hayashizaki, Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-UTB-2001) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration and Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute; 1-7-22 Suicho-cho, Tsunrumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,  
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
 Fax: 81-45-503-9216)  
 COMMENT  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.jp/  
 URL: http://pantom.gsc.riken.jp/  
 location/Qualifiers  
 1. 3033  
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 /moi\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="PANTOM\_DB:D030018D22"  
 /db\_xref="taxon:10090"  
 /clone="D030018D22"  
 /tissue\_type="whole body"  
 /clone\_Tib="RIKEN full-length enriched mouse cDNA library"

```

/dev stage="9 days embryo"
1..3033
/note="unclassifiable"

misc_feature
Query Match      84.0%; Score 16.8; DB 4; Length 3033;
Best Local Similarity 85.0%; Pred. No. 2.8e+03;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0

ORIGIN
1 AGGACAGCCAGGACUACGA 20
|||||
2232 AGGACAGCCAGGACTACAA 2213

RESULT 34
A2106943 176 bp DNA linear GSS 09-MAY-2000
A2106943
LOCUS
DEFINITION
RPCI-23-453P19.TV RPCI-23 Mus musculus genomic clone
RPCI-23-453P19, genomic survey sequence.
ACCESSION
A2106943
VERSION
A2106943.1 GI:7759999
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Butharyota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 176)
Zhao,S., Niemann,W., Feldblum,T., Malek,J., Shatman,S.,
Akuret,B., Levins,M., McGann,S., Teegaye,G., Geer,K., Krol,M., de
Jong,P. and Frazer,C.M.,
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSSs: RPCI-23-453P19.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel.: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pjeter@tigr.org, med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Reses ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tcdb/bac_end/mouse/bac_end_intro.html
Page: 453 row: P column: 19
Seq primer: SP6
Class: BAC ends.

FEATURES
source
Location/Qualifiers
1..176
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-453P19"
/sex="Female"
/lab_host="DH10B"
/clone_id="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site 1:
EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI methylase. Size
selected DNA was cloned into the pBAC3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
ORIGIN
Query Match      82.0%; Score 16.4; DB 9; Length 176;
Best Local Similarity 83.3%; Pred. No. 3e+03;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```



```

Db          120 AGGTACAGCCAGCGCTTC 137

RESULT 35
LOCUS       AM599118
DEFINITION  225 bp mRNA linear EST 22-MAR-2000
            pgi01e10_v1 Moss EST library PPN Physcomitrella patens cDNA clone
            per SOURCE_ID:PPN090319 5' similar to SW:RS_ONYSA P49199 40S
            RIBOSOMAL PROTEIN 58.7, mRNA sequence.

ACCESSION   AM599118
VERSION     AM599118
KEYWORDS    EST.
SOURCE      Physcomitrella patens
            Bryophyta; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
            Bryopsida; Funariaceae; Funariidae; Funariaceae; Physcomitrella.

REFERENCE   1 (bases 1 to 225)
AUTHORS     Quatraro, R., Bashirades, S., Cove, D., Cumins, A., Knight, C.,
            Clifton, S., Marra, M., Hillier, L., Page, D., Martin, J., Wyllie, T.,
            Underwood, K., Theising, B., Allen, M., Bowers, Y., Peterson, B.,
            Swaller, T., Septeoe, M., Gibbons, M., Harvey, N., Ritter, S.,
            Jackson, Y., McCann, R., Mearns, R., and Wilson, R.
            Leeds/Wash U Moss EST Project
            Leeds/Wash U Moss EST Project
            Unpublished (1999)
            Contact: Ralph Quatraro
            Leeds/Wash U Moss EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@washington.wustl.edu
            Libraries were constructed by Dr. Stavros Bashirades as part of the
            Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
            Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
            University Genome Sequencing Center For information on obtaining a
            clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
            Seg primer: -40RP from Gldco.
            Location/Qualifiers
                1..225
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                /mol_type="mRNA"
                /db_xref="taxon:3218"
                /clone="PEP_SOURCE_ID:PPN090319"
                /isue_type="Protonemata: 7 day old tissue auxin treated"
                /lab_host="DH10B"
                /clone_lib="Moss EST library PPN"
                /notes="vector: pBluescript SK-; Site 1: EcoRI; Site 2:
                XhoI; Construction of the cDNA library was carried out
                using Stratagene's 'UniZAP' - cDNA synthesis kit'. cDNA was
                constructed using an oligo dt primer/linker that contains
                a XhoI site within it. Following ds cDNA synthesis,
                EcoRI adapters were ligated to the blunt ends and sample
                was digested with XhoI. The result is cDNA with an EcoRI
                sticky end on one side and a XhoI sticky end on the other.
                This cDNA was ligated directionally in UniZAP arms. The
                vector is designed containing the pBluescript sequence as
                well as lambda DNA and cDNA is cloned within this
                pBluescript sequence. The vector was then packaged using
                Gold gigaPackaging extracts. Library was grown in XL1Blue
                MRP cells and amplified. The library was excised by mass
                excision using Stratagene's 'Mass excision kit' that uses
                exasist as a helper phage that releases the pBluescript
                sequence and circularises it as single stranded plasmids
                that are then packaged (by helper phage) and secreted out
                of the host cell as phagemide. SOLR cells were transformed
                with phagemids and the library was plated out on LB-amp
                plates to select for transformants. Approximately
                1,000,000 colonies were grown and recovered. The double
                stranded plasmid library was recovered by using Qulagen
                Midl prep kit 2 micro grams of each library were used to
                transform DH10B cells by electroporation."

```

Query Match	82.0%	Score 16.4	DB 1	Length 225
Best Local Similarity	83.3%	Pred. No. 3.1e+03		
Matches	15	Conservative	2	Mismatches 1, Indels 0, Gaps 0
Db	158	GGTACGCGCAGCACTACG	175	
QY	2	GGUACAGCCGAGACUACG	19	
RESULT 36				
LOCUS	AM753512	305 bp	mRNA	linear EST 28-APR-2000
DEFINITION	PMO-CT0263-051199-005-H09 CT0263	Homo sapiens	CDNA, mRNA	sequence.
ACCESSION	AM753512			
VERSION	AM753512.1	GI:7668444		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
REFERENCE	Homnidae; Homo			
AUTHORS	1 (bases 1 to 305)			
	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Stimpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Stimpson, A.J.			
	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags			
	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)			
TITLE	10737800			
JOURNAL	Contact: Stimpson A.J.G.			
PUBMED	Laboratory of Cancer Genetics			
COMMENT	Ludwig Institute for Cancer Research			
	Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil			
	Tel: +55-11-2704922			
	Fax: +55-11-2707001			
	Email: astimpson@ludwig.org.br			
	This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL			
	(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM0ct2-PMO-CT0263-051199-005-H09ct3-1999-11-05ct4=1)			
	Seq primer: puc 18 forward			
	High quality sequence start: 12			
	High quality sequence stop: 38.			
	Location/Qualifiers			
FEATURES	1.305			
SOURCE	/organism="Homo sapiens"			
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	/dev_stage="Adult"			
	/clone_lib="CT0263"			
	/note="Organ: colon; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORSSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."			
ORIGIN				
Query Match	82.0%	Score 16.4	DB 1	Length 305
Best Local Similarity	88.9%	Pred. No. 3.2e+03		
Matches	16	Conservative	1	Indels 0, Gaps 0
QY	1	AGGACGCGCAGCACTAC	18	
Db	52	AGGACGCGCAGCACTAC	35	

RESULT 37  
BG408882 307 bp mRNA linear EST 13-MAR-2001  
LOCUS 981c06.y1 Moss EST library PPG Physcomitrella patens cDNA clone  
DEFINITION PEP SOURCE ID: PPG CopyA-100612 5' similar to TR:081361 081361 40S  
RIBOSOMAL PROTEIN S8. ; mRNA sequence.  
ACCESSION BG408882  
VERSION BG408882.1 GI:13315227  
KEYWORDS EST.  
SOURCE Physcomitrella patens  
ORGANISM Physcomitrella patens  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;  
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.  
REFERENCE Quatrano, R., Bashardes, S., Cove, D., Cuming, A., Knight, C.,  
AUTHORS Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T.,  
Underwood, K., Theising, B., Allen, M., Bowers, Y., Person, B.,  
Swaller, T., Stepien, M., Gibbons, M., Harvey, N., Rittner, E.,  
Jackson, Y., McCann, R., Waterson, R. and Wilson, R.  
Leeds/Wash U Moss EST Project  
Unpublished (1999)  
TITLE Contact: Ralph Quatrano  
JOURNAL Leeds/Wash U Moss EST Project  
COMMENT Leeds/Wash U Moss EST Project  
Leeds/Wash U Moss EST Project  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Libraries were constructed by Dr. Stavros Bashardes as part of the  
Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and  
Washington Univ. in St. Louis (USA) DNA sequencing by Washington  
University Genome Sequencing Center For information on obtaining a  
trace please contact: Celia Knight (c.d.knight@leeds.ac.uk)  
Seq primer: -40RP from Gibco  
High quality sequence scop: 1.  
Location/Qualifiers  
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/csize\_type="gametophore: 30 day old tissue,  
ammonium-grown"  
/lab\_host="DH10B"  
/clone\_lib="Moss EST library PPG"  
/note="Vector: PAMPI; Construction of the cDNA library was  
performed by Dr. W. Gregg Clark using a modification of  
the cDNA synthesis protocol developed in the laboratory of  
Dr. Michael Lovett by Dr. Yulia Korshunova (personal  
communication). First polyA + RNA was isolated from total  
gametophore RNA using oligo dT magnetic beads. Following  
this, first strand cDNA synthesis was performed on the  
bead-bound polyA + RNA, during which an oligonucleotide  
anchor sequence was incorporated onto the 5'-ends of the  
cDNA. PCR amplification was then used to synthesize the  
second strand, to amplify the double stranded DNA, and to  
incorporate dntp containing sequences into the ends of the  
double stranded cDNA. This DNA was size selected and  
cloned into PAMPI using the CloneAMP PAMPI System (Life  
Technologies, GibcoBRL) for cloning amplification products  
by a non-restriction site dependant process. The cloning  
was directional based on sequence asymmetry introduced at  
the ends during PCR amplification. The 3' cDNA ends are  
proximal to the NotI site of the multiple cloning site in  
PAMPI. This annealing mixture was transformed into  
ampicillin competent DH10B cells and selected for  
330,000 were pooled to make the library."

82.0%; Score 16.4; DB 2; Length 307;

ORIGIN  
Query Match

Best Local Similarity 83.3%; Pred. No. 3.3e+03;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Qy 2 GGUACAGCCAGGACTUAC 19  
||:|||||:|||||  
Db 84 GGTACAGCCAGGACTACTAC 101  
RESULT 38  
BP427629 308 bp mRNA linear EST 24-MAY-2004  
LOCUS BP427629 Mus musculus cerebellum E18-P56 Mus musculus cDNA clone  
DEFINITION FD1374. mRNA sequence.  
ACCESSION BP427629  
VERSION BP427629.1 GI:47589653  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE Furuchi, T. and Sato, A.  
AUTHORS Gene expression during the postnatal cerebellar development  
JOURNAL Unpublished (2004)  
COMMENT Contact: Teiichi Furuchi  
Laboratory for Molecular Neurogenesis  
RIKEN Brain Science Institute  
2-1 Hirotsawa, Wako, Saitama 351-0198, Japan  
Tel: 81-48-467-5906  
Fax: 81-48-467-6079  
Email: mol-neurogenes@brain.riken.go.jp, URL:  
http://www.brain.riken.go.jp/labs/lmn/index.html.  
Location/Qualifiers  
1..308  
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/clone="FD1374"  
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/dev\_stage="E18-P56"  
/clone\_lib="Mus musculus cerebellum E18-P56"  
ORIGIN  
Query Match 82.0%; Score 16.4; DB 3; Length 308;  
Best Local Similarity 83.3%; Pred. No. 3.3e+03;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 AGTACAGCCAGGACTUAC 18  
||:|||||:|||||  
Db 74 AGTACAGCCAGGACTACTAC 91  
RESULT 39  
C2689611 341 bp DNA linear GSS 14-JUN-2005  
LOCUS OA\_BBA0160P02.r OA\_BBA Oryza alta genomic clone OA\_BBA0160P02 3'  
DEFINITION genomic survey sequence.  
ACCESSION C2689611  
VERSION C2689611.1 GI:70810763  
KEYWORDS GSS.  
SOURCE Oryza alta  
ORGANISM Oryza alta  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoidae; Oryzaceae; Oryza.  
REFERENCE Samtuguel, P., Westerman, R., Kim, H., Yu, Y., Watsotaki, M., Yost, D.,  
AUTHORS Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C.,  
Haffield, J., Soderlund, C., Wing, R. and Jackson, S.A.  
OMAP (Oryza Map Alignment Project) - Purdue University  
Unpublished (2004)

## COMMENT

Contact: Scott A. Jackson  
Jackson Laboratory  
Purdue University  
915 W. State St., West Lafayette, IN 47907, USA  
Tel: 7654963621  
Fax: 7654967255

Email: sjackson@purdue.edu  
Basecalling by phred version 0.020425.c. This sequence was derived from the raw sequence read by clipping with Lucy version 1.198.  
Bases 108-448 of the raw sequence (length 1010) were retained after clipping.

Plate: 0160 row: F column: 02  
Seq primer: CAC TCA TTA GGC ACC CCA  
Class: BAC ends.

## FEATURES

## source

Location/Qualifiers  
1..341  
/organism="Oryza sativa"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:52545"  
/clone="OA\_BBA0160P02"  
/issue\_type="Young leaves"  
/lab\_host="DH10B-T1 phage resistant"  
/clone\_11b="OA\_BBA"  
/note="Vector: pAG1BAC1, Site\_1: HindIII, Site\_2: HindIII"

## ORIGIN

Query Match 82.0%; Score 16.4; DB 1; Length 341;  
Best Local Similarity 83.3%; Pred. No. 3.3e+03;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
1 AGGACAGCCAGACGACGAC 18  
|||:|||||:|||||:|||||:  
269 AGGTACAGCAGACGACGAC 286

RESULT 40  
AM598793 373 bp mRNA linear EST 22-MAR-2000  
LOCUS ga88b10.y1 Mose EST library PPU Physcomitrella patens cDNA clone  
DEFINITION PPU\_SOURCE ID:PPU61320 5' similar to SW\_RS8\_ORFSA P49199 408  
RIBOSOMAL PROTEIN 88.; mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AM598793  
AM598793.1 GI:7286306  
EST.  
Physcomitrella patens  
Physcomitrella patens  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;  
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.

REFERENCE  
AUTHORS

1 (bases 1 to 373)  
Quatrano, R., Bashirades, S., Cove, D., Cumling, A., Knight, C.,  
Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T.,  
Underwood, K., Theising, B., Allen, M., Bowers, Y., Person, B.,  
Swaller, T., Steptoe, M., Gibbons, M., Harvey, N., Ritter, E.,  
Jackson, Y., McCann, R., Waterston, R. and Wilson, R.

TITLE  
JOURNAL  
COMMENT

Unpublished (1999)  
Contact: Ralph Quatrano  
Leeds/Mash U Mose EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@wustl.wustl.edu  
Libraries were constructed by Dr. Stavros Bashirades as part of the  
Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and  
Washington Univ. in St. Louis (USA) DNA sequencing by: Washington  
University Genome Sequencing Center for information on obtaining a  
clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)  
Seq primer: -40RP from Gibco  
High quality sequence atop: 262.

FEATURES  
source

Location/Qualifiers  
1..373  
/organism="Physcomitrella patens"

/mol\_type="mRNA"  
/db\_xref="taxon:3218"  
/clone="PPU\_SOURCE\_ID:PPU61320"  
/issue\_type="protonemata: 7 day old tissue  
ammonium-grown"

/lab\_host="DH10B"  
/clone\_11b="Mose EST library PPU"  
/note="Vector: Bluescript SK-; Site 1: EcoRI, Site 2:  
XhoI; Construction of the cDNA library was carried out  
using Stratagene's 'Unizap - cDNA synthesis kit'. cDNA  
was constructed using an oligo dt primer/liner that  
contains a XhoI site within it. Following ds cDNA  
synthesis, EcoRI adapters were ligated to the blunt ends  
and sample was digested with XhoI. The result is cDNA  
with an EcoRI sticky end on one side and a XhoI sticky  
end on the other. This cDNA was ligated directionally in  
the Unizap arms. The vector is designed containing the  
Bluescript sequence as well as lambda DNA and cDNA is  
cloned within this Bluescript sequence. The vector was  
then packaged using Gold gigaPackaging extracts. Library  
was grown in XL1Blue MRF' cells and amplified. The library  
was excised by mass excision using Stratagene's 'Mass  
excision kit' that uses exsacit as a helper phage that  
releases the Bluescript sequence and circularises it as  
single stranded plasmids that are then packaged (by helper  
phage) and secreted out of the host cell as phagemids.  
SOR cells were transformed with phagemids and the library  
was plated out on LB-amp plates to select for  
transformants. Approximately 1,000,000 colonies were grown  
and recovered. The double stranded plasmid library was  
recovered by using QiaGen Midl prep kit. 2 micro grams of  
each library were used to transform DH10B cells by  
electroporation."

## ORIGIN

Query Match 82.0%; Score 16.4; DB 1; Length 373;  
Best Local Similarity 83.3%; Pred. No. 3.3e+03;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
2 GGUACAGCCAGACGACGAC 19  
|||:|||||:|||||:|||||:  
330 GGTACAGCCAGACGACGAC 347

RESULT 41  
CV320420/c 385 bp mRNA linear EST 24-SEP-2004  
LOCUS CM3-CN0094-230101-645-b02 CN0094 Homo sapiens cDNA, mRNA sequence.  
DEFINITION CV320420  
ACCESSION CV320420.1 GI:52643634  
VERSION  
KEYWORDS  
EST.

REFERENCE  
AUTHORS

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

1 (bases 1 to 385)  
Dias Neto, E., Garcia, R., Verjovski-Almeida, S., Briones, M.,  
Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,  
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.V.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

TITLE  
JOURNAL  
PUBMED  
COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922

Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPBSF/LICR Human Cancer Genome  
 Project. <http://www.ludwig.org.br>.  
 Location/Qualifiers

## FEATURES

source

1..385

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_1lb="CN0094"

/note="Organ: colon normal; Vector: puc18; Site 1: Sma1;  
 Site 2: Sma1; A mini-library was made by cloning products  
 derived from ORSITES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the pUC 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."

## ORIGIN

Query Match 82.0%; Score 16.4; DB 7; Length 385;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 AGUACAGCCAGACUAC 18  
 |||:|||||:|||||:  
 Db 172 AGTACAGCCAGACTTC 155

RESULT 42 390 bp mRNA linear EST 13-JUN-2005  
 B0949932  
 LOCUS B0949932 pphf full-length cDNA library Physcomitrella patens subsp.  
 DEFINITION  
 ACCESSION B0949932  
 VERSION B0949932.1 GI:6757765  
 KEYWORDS EST.

ORGANISM Physcomitrella patens subsp. patens  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;  
 Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.

REFERENCE Fujita, T., Nishiyama, T., Shin-i, T., Kohara, Y. and Hasebe, M.  
 1 (bases 1 to 390)  
 TITLE Physcomitrella patens EST at a stage of the first asymmetric cell  
 division of protoplasts  
 JOURNAL Unpublished (2005)  
 COMMENT Contact: Tadao Shin-i  
 Center For Genetic Resource Information  
 National Institute of Genetics  
 111 Yata, Mishima, Shizuoka 411-8540, Japan  
 Tel: 81-559-81-6856  
 Fax: 81-559-81-6855  
 Email: tshin@genes.nig.ac.jp

PROTOPLASTS were isolated from the protonemata, further incubated  
 at 25C under continuous light for 2-3 days. The regenerated cells,  
 which were rich in cells at a stage during the first asymmetric  
 cell division, were collected. Total RNA was extracted for  
 constructing a full-length cDNA library. The database of the EST  
 clones is available at the PHYSCOBASE (<http://moss.nibb.ac.jp>).  
 Location/Qualifiers

## FEATURES

source

1..390

/organism="Physcomitrella patens subsp. patens"  
 /mol\_type="mRNA"  
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 /clone="pphf5022"  
 /tissue\_type="regenerated protoplasts (chloronemata)"  
 /dev\_stage="at the first asymmetric cell division of  
 protoplasts"  
 /clone\_1lb="pphf full-length cDNA library"  
 /note="Protonemata were inoculated on BCDATG medium for  
 every ca. 5 days. Protoplasts were isolated from the

## FEATURES

source

1..390

/organism="Physcomitrella patens subsp. patens"  
 /mol\_type="mRNA"  
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 /dev\_stage="at the first asymmetric cell division of  
 protoplasts"  
 /clone\_1lb="pphf full-length cDNA library"  
 /note="Protonemata were inoculated on BCDATG medium for  
 every ca. 5 days. Protoplasts were isolated from the

protonemata, further incubated at 25C under continuous  
 light for 2-3 days. The regenerated cells, which were rich  
 in cells at a stage during the first asymmetric cell  
 division, were collected. Total RNA was extracted for  
 constructing a full-length cDNA library."

## ORIGIN

Query Match 82.0%; Score 16.4; DB 3; Length 390;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 2 GGUACAGCCAGACUACG 19  
 |||:|||||:|||||:  
 Db 368 GGTACAGCCAGACTTACG 385

RESULT 43 395 bp mRNA linear EST 13-JUN-2005  
 B0949577  
 LOCUS B0949577 pphf full-length cDNA library Physcomitrella patens subsp.  
 DEFINITION  
 ACCESSION B0949577  
 VERSION B0949577.1 GI:67576753  
 KEYWORDS EST.

ORGANISM Physcomitrella patens subsp. patens  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;  
 Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.

REFERENCE Fujita, T., Nishiyama, T., Shin-i, T., Kohara, Y. and Hasebe, M.  
 1 (bases 1 to 395)  
 TITLE Physcomitrella patens EST at a stage of the first asymmetric cell  
 division of protoplasts  
 JOURNAL Unpublished (2005)  
 COMMENT Contact: Tadao Shin-i  
 Center For Genetic Resource Information  
 National Institute of Genetics  
 111 Yata, Mishima, Shizuoka 411-8540, Japan  
 Tel: 81-559-81-6856  
 Fax: 81-559-81-6855  
 Email: tshin@genes.nig.ac.jp

PROTOPLASTS were isolated from the protonemata, further incubated  
 at 25C under continuous light for 2-3 days. The regenerated cells,  
 which were rich in cells at a stage during the first asymmetric  
 cell division, were collected. Total RNA was extracted for  
 constructing a full-length cDNA library. The database of the EST  
 clones is available at the PHYSCOBASE (<http://moss.nibb.ac.jp>).  
 Location/Qualifiers

## FEATURES

source

1..395

/organism="Physcomitrella patens subsp. patens"  
 /mol\_type="mRNA"  
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 /clone="pphf4c21"  
 /tissue\_type="regenerated protoplasts (chloronemata)"  
 /dev\_stage="at the first asymmetric cell division of  
 protoplasts"  
 /clone\_1lb="pphf full-length cDNA library"  
 /note="Protonemata were inoculated on BCDATG medium for  
 every ca. 5 days. Protoplasts were isolated from the  
 protonemata, further incubated at 25C under continuous  
 light for 2-3 days. The regenerated cells, which were rich  
 in cells at a stage during the first asymmetric cell  
 division, were collected. Total RNA was extracted for  
 constructing a full-length cDNA library."

## ORIGIN

Query Match 82.0%; Score 16.4; DB 3; Length 395;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 2 GGUACAGCCAGACUACG 19  
 |||:|||||:|||||:

DB 308 GGTAACGACGACTACG 325

RESULT 44  
BI436739 400 bp mRNA linear EST 21-AUG-2001  
gcs1e03.y1 Moss EST library PPN Physcomitrella patens cDNA clone  
PSP SOURCE ID:PPN180905 5' similar to SW:RS8\_MALIZR 008069 40S  
RIBOSOMAL PROTEIN S8. [1] ; mRNA sequence.

ACCESSION  
BI436739 GI:15261436

VERSION  
EST.

KEYWORDS  
Physcomitrella patens

SOURCE  
Physcomitrella patens

ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.

REFERENCE  
Quatrano, R., Bashlades, S., Cove, D., Cumling, A., Knight, C., Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Steptoe, M., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.  
Leeds/Wash U Moss EST Project  
Unpublished (1999)  
Contact: Ralph Quatrano  
Leeds/Wash U Moss EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watsn.wustl.edu  
Libraries were constructed by Dr. Stavros Bashlades as part of the Physcomitrella EST program (PSP) at the Univ. of Leeds (UK) and Washington Univ. in St. Louis (USA) DNA sequencing by: Washington University Genome Sequencing Center for information on obtaining a clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)  
Trace considered overall poor quality  
High quality sequence stop: 1.  
Location/Qualifiers  
1..400  
/organism="Physcomitrella patens"  
/mol\_type="mRNA"  
/db\_xref="taxon:3218"  
/clone="PSP SOURCE ID:PPN180905"  
/tissue\_type="protonemata: 7 day old tissue auxin treated"  
/lab\_host="DH10B"  
/clone\_lib="Moss EST library PPN"  
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Construction of the cDNA library was carried out using Stratagene's 'Unizap' - cDNA synthesis kit'. cDNA was constructed using an oligo dt primer/linker that contains a XhoI site within it. Following de cDNA synthesis, EcoRI adapters were ligated to the blunt ends and sample was digested with XhoI. The result is cDNA with an EcoRI sticky end on one side and a XhoI sticky end on the other. This cDNA was ligated directionally in Unizap arms. The vector is designed containing the pBluescript sequence as well as lambda DNA and cDNA is cloned within this pBluescript sequence. The vector was then packaged using Gold gigapackaging extracts. Library was grown in XL1Blue MR<sup>+</sup> cells and amplified. The library was excised by mass excision using Stratagene's 'Mass excision kit' that uses exsist as a helper phage that releases the pBluescript sequence and circularises it as single stranded plasmids that are then packaged (by helper phage) and secreted out of the host cell as phagemids. SOLR cells were transformed with phagemids and the library was plated out on LB-amp plates to select for transformants. Approximately 1,000,000 colonies were grown and recovered. The double stranded plasmid library was recovered by using Qiaagen MidI prep kit. 2 micro grams of each library were used to transform DH10B cells by electroporation."

FEATURES  
source

Query Match 82.0%; Score 16.4; DB 3; Length 400;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DB 93 GGTAACGACGACTACG 110

OR 2 GGTAACGACGACTACG 19

RESULT 45  
BB819360 401 bp mRNA linear EST 19-NOV-2001  
BB819360 RIKEN full-length enriched, lung RCB-0558 LLC cDNA Mus musculus cDNA clone G730049G01 3', mRNA sequence.

ACCESSION  
BB819360 GI:16991989

VERSION  
EST.

KEYWORDS  
Mus musculus (house mouse)

SOURCE  
Mus musculus

ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE  
Akimura, T., Aikawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Komno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaki-Akahira, S., Tanaka, T., Tomaru, A., Toy, T., Watanabe, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
RIKEN Encyclopedia of Mouse Full-length cDNAs (AKimura, T., et al. 2001)  
Unpublished (2001)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Saitoh-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cdp-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagl, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
Komno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.  
e mouse tissues.  
Location/Qualifiers  
1..401  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="G730049G01"  
/tissue\_type="lung"  
/cell\_line="RCB-0558 LLC"  
/clone\_lib="RIKEN full-length enriched, lung RCB-0558 LLC

FEATURES  
source

ORIGIN CDNA"

Query Match 82.0%; Score 16.4; DB 2; Length 401;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGACGACGACGACTAC 18  
DB 131 AGGACGACGACGACTAC 148

RESULT 46  
LOCUS B959669/c 404 bp mRNA linear EST 14-JUN-2005  
DEFINITION B959669 pphf full-length cDNA library Physcomitrella patens subsp.  
ACCESSION B959669  
VERSION B959669  
KEYWORDS B959669.1 GI:67699436  
SOURCE EST  
ORGANISM Physcomitrella patens subsp. patens  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;  
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.

REFERENCE  
AUTHORS Fujita, T., Nishiyama, T., Shin-i, T., Kohara, Y. and Hasebe, M.  
TITLE Physcomitrella patens EST at a stage of the first asymmetric cell  
division of protoplasts  
JOURNAL Unpublished (2005)  
COMMENT Contact: Tadao Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6855  
Fax: 81-559-81-6855  
Email: tshin@genes.nig.ac.jp

Protonemata were inoculated on BCDATG medium for every ca. 5 days.  
Protoplasts were isolated from the protonemata, further incubated  
at 25C under continuous light for 2-3 days. The regenerated cells,  
which were rich in cells at a stage during the first asymmetric  
cell division, were collected. Total RNA was extracted for  
constructing a full-length cDNA library. The database of the EST  
clones is available at the PHSCDBase (<http://moss.nibb.ac.jp>).

FEATURES  
SOURCE location/Qualifiers

1..404  
/organism="Physcomitrella patens subsp. patens"  
/mol\_type="mRNA"  
/sub\_species="patens"  
/db\_xref="taxon:145481"  
/clone="pphf320"  
/tissue\_type="regenerated protoplasts (chloronemata)"  
/dev\_stage="at the first asymmetric cell division of  
protoplasts"  
/clone\_id="pphf full-length cDNA library"  
/note="Protonemata were inoculated on BCDATG medium for  
every ca. 5 days. Protoplasts were isolated from the  
protonemata, further incubated at 25C under continuous  
light for 2-3 days. The regenerated cells, which were rich  
in cells at a stage during the first asymmetric cell  
division, were collected. Total RNA was extracted for  
constructing a full-length cDNA library."

ORIGIN

Query Match 82.0%; Score 16.4; DB 3; Length 404;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGUACAGCGACGACGACG 19  
DB 371 GGUACAGCGACGACGACG 354

RESULT 47

CK499977/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

Cheng, T., Chai, C., Pan, G., Xu, J., Liu, C., Lin, Y., Qian, J., Hou, Y.,  
Wu, Z., Li, G., Pan, M., Li, C., Shen, Y., Lan, X., Yuan, L., Li, T.,  
Xu, H., Yang, G., Wan, Y., Zhu, Y., Yu, M., Shen, W., Wu, D., Xiang, Z.,  
Yu, J., Wang, J., Li, R. Q., Shi, J. P., Li, H., Li, G. Y., Su, J. N.,  
Wang, X. L., Li, G. Q., Zhang, Z. J., Wu, Q. F., Li, J., Zhang, Q. P., Wei, N.,  
Xu, J. Z., Sun, H. B., Dong, L., Liu, D. Y., Zhao, S. L., Zhao, X. L.,  
Meng, Q. S., Lan, F. D., Huang, X. G., Li, Y. Z., Fang, F., Li, C. F.,  
Li, D. W., Sun, Y. Q., Zhang, Z. P., Yang, Z., Huang, Y. Q., Xi, Y., Qi, Q. H.,  
He, D. D., Huang, H. Y., Zhang, X. W., Wang, Z. Q., Li, W. J., Cao, Y. Z.,  
Ye, J., Yu, H., Ji, H., Ye, J., Chen, H., Zhou, Y., Liu, B., Wang, J.,  
Ye, J., Ji, H., Li, S., Ni, P., Zhang, J., Zhang, Y., Zheng, H., Mao, B.,  
Mao, B., Ye, C., Li, S., Wang, J., Wong, G. K. and Yang, H.

A draft sequence for the genome of the domesticated silkworm  
(*Bombyx mori*)

Science 306 (5703), 1937-1940 (2004)

JOURNAL

PUBMED

COMMENT

Contact: Zhonghui Xiang  
Southwest Agricultural University  
Chongqing Beibei  
Tel: 86-23-68251123  
Fax: 86-23-68251128  
Email: xzh@swu.cn

FEATURES

SOURCE

1..405  
/organism="Bombyx mori"  
/mol\_type="mRNA"  
/strain="Dazhao (P50)"  
/db\_xref="taxon:7091"  
/sex="mixed"  
/tissue\_type="midgut"  
/dev\_stage="5th-instar day-3 larva"  
/clone\_id="swb"  
/note="Vector: Bluescript II SK(+)"

ORIGIN

Query Match 82.0%; Score 16.4; DB 7; Length 405;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGUACAGCGACGACGACG 19  
DB 131 GGUACAGCGACGACGACG 114

RESULT 48  
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DEFINITION B960521 pphf full-length cDNA library Physcomitrella patens subsp.  
ACCESSION B960521  
VERSION B960521.1 GI:67700288  
KEYWORDS EST  
SOURCE Physcomitrella patens subsp. patens  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;  
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.

REFERENCE  
AUTHORS Fujita, T., Nishiyama, T., Shin-i, T., Kohara, Y. and Hasebe, M.  
TITLE Physcomitrella patens EST at a stage of the first asymmetric cell  
division of protoplasts



JOURNAL  
COMMENT

Unpublished (2005)  
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Center For Genetic Resource Information  
National Institute of Genetics  
111 Yata, Mishima, Shizuoka 411-8540, Japan  
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Fax: 81-559-81-6855  
Email: tsuhigene@nig.ac.jp

Protonemata were inoculated on BCDATG medium for every ca. 5 days. Protonemata were isolated from the protonemata, further incubated at 25C under continuous light for 2-3 days. The regenerated cells, which were rich in cells at a stage during the first asymmetric cell division, were collected. Total RNA was extracted for constructing a full-length cDNA library. The database of the EST clones is available at the PHYSCOBASE (<http://mos.nbhb.ac.jp>).  
Location/Qualifiers

FEATURES  
source

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## ORIGIN

Query Match 82.0%; Score 16.4; DB 3; Length 406;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION RPCI-23-114A5, genomic survey sequence.  
ACCESSION BH405922  
VERSION BH405922.1 GI:17460837  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

## REFERENCE

Young,J.M., Friedman,C., Williams,E.M., Ross,J.A., Tonnes-Priddy,L. and Trask,B.J.  
Different evolutionary processes shaped the mouse and human olfactory receptor gene families  
Hum. Mol. Genet. 11 (5), 535-546 (2002)

## TITLE

11875048  
Contact: Young JM  
Barbara Trask, Division of Human Biology  
Fred Hutchinson Cancer Research Center  
1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA  
98109-1024, USA.  
Tel: 206 667 1471  
Fax: 206 667 6524  
Email: jayoung@hcr.org

JOURNAL  
PUBMED  
COMMENT

Young,J.M., Swartzell,S., Friedman,C., Tonnes-Priddy,L., Lane,R.P.,

FEATURES  
source

Wallace,J.C., Mahairas,G.G., Hood,L., and Trask,B.J. End sequences of mouse BACs containing olfactory receptor genes. Unpublished plates 114 row: A column: 5  
Seq primer: SP6S  
Class: BAC ends.  
Location/Qualifiers

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## ORIGIN

Query Match 82.0%; Score 16.4; DB 9; Length 413;  
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Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION genomic survey sequence.  
ACCESSION AZ222766  
VERSION AZ222766.1 GI:8530815  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.  
Zhao,S., Nierman,W., Feldblum,T., Malek,J., Shatman,S., Aktirec,B., Levins,M., McGinn,S., Teegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.  
Mouse BAC End Sequences from Library RPCI-23  
Unpublished (1999)  
Other\_GSSs: RPCI-23-46J7.TV  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhaoc@igf.org

Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@jlong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (<http://resgcn.com>). BAC end page: [http://www.tigr.org/cdb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/cdb/bac_ends/mouse/bac_end_intro.html)  
Plate: 46 row: J column: 7  
Seq primer: SP6  
Class: BAC ends.

## TITLE

11875048  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhaoc@igf.org

## FEATURES

Location/Qualifiers  
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brain genomic DNA was isolated and partially digested  
with a combination of EcoRI and EcoRI Methylase. Size  
selected DNA was cloned into the pBACe3.6 vector at the  
EcoRI sites. The ligation products were transformed into  
DH10B electrocompetent cells (BRL Life Technologies). "

## ORIGIN

Query Match 82.0%; Score 16.4; DB 9; Length 426;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 AGGACAGCCAGAGCTAC 18  
| | : | | | | | | | | : | |  
Db 26 AAGTACAGCCAGAGCTAC 43

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Job time : 1948.08 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 18:35:23 ; Search time 76.5385 Seconds  
(without alignments)  
464.468 Million cell updates/sec

Title: US-10-800-926-3

Perfect score: 20

Sequence: 1 agnucagccagcagcagcagc 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

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- 2: /cgm2\_6/ptodata/1/ina/5 COMB.seq:\*
- 3: /cgm2\_6/ptodata/1/ina/6A COMB.seq:\*
- 4: /cgm2\_6/ptodata/1/ina/6B COMB.seq:\*
- 5: /cgm2\_6/ptodata/1/ina/H COMB.seq:\*
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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126	14.4	72.0	78720	3	US-09-949-016-12710	Sequence 12710, A	199	14.2	71.0	1515	3	US-09-205-258-18	Sequence 18, Appl1
127	14.4	72.0	78720	3	US-09-949-016-12710	Sequence 12710, A	200	14.2	71.0	1515	3	US-09-205-258-18	Sequence 18, Appl1
128	14.2	71.0	25	3	US-09-396-196G-1066	Sequence 1066, Ap	201	14.2	71.0	1515	3	US-10-004-860-40	Sequence 40, Appl1
129	14.2	71.0	99	2	US-08-247-475-13	Sequence 13, Appl1	202	14.2	71.0	1570	2	US-08-239-276-5	Sequence 5, Appl1
130	14.2	71.0	99	2	US-08-479-650-13	Sequence 13, Appl1	203	14.2	71.0	1570	2	US-08-468-579B-5	Sequence 5, Appl1
131	14.2	71.0	99	2	US-08-191-866D-15	Sequence 15, Appl1	204	14.2	71.0	1570	2	US-08-468-579B-5	Sequence 5, Appl1
132	14.2	71.0	99	2	US-08-674-169-13	Sequence 13, Appl1	205	14.2	71.0	1570	2	US-08-468-579B-5	Sequence 5, Appl1
133	14.2	71.0	435	3	US-08-185-949B-15	Sequence 15, Appl1	206	14.2	71.0	1633	2	US-08-468-579B-5	Sequence 5, Appl1
134	14.2	71.0	435	3	US-09-937-787-170	Sequence 170, App	207	14.2	71.0	1633	2	US-08-468-579B-5	Sequence 5, Appl1
135	14.2	71.0	465	3	US-09-621-976-3563	Sequence 3563, Ap	208	14.2	71.0	1633	2	US-08-468-579B-5	Sequence 5, Appl1
136	14.2	71.0	522	3	US-09-824-893A-17	Sequence 17, Appl1	209	14.2	71.0	1707	3	US-08-459-214-42	Sequence 42, Appl1
137	14.2	71.0	527	3	US-09-270-767-1983	Sequence 1983, Ap	210	14.2	71.0	1826	3	US-09-252-991A-5890	Sequence 5890, Ap
138	14.2	71.0	527	3	US-09-270-767-17265	Sequence 17265, A	211	14.2	71.0	1833	3	US-09-949-016-6654	Sequence 6654, Ap
139	14.2	71.0	580	3	US-09-919-039-169	Sequence 169, App	212	14.2	71.0	1833	3	US-09-120-365-6	Sequence 6, Appl1
140	14.2	71.0	601	3	US-09-949-016-26746	Sequence 26746, A	213	14.2	71.0	1840	3	US-09-515-039-6	Sequence 6, Appl1
141	14.2	71.0	601	3	US-09-949-016-33118	Sequence 33118, A	214	14.2	71.0	1920	3	US-09-016-434-1200	Sequence 1200, Ap
142	14.2	71.0	601	3	US-09-949-016-66046	Sequence 66046, A	215	14.2	71.0	1920	3	US-09-160-436-4	Sequence 4, Appl1
143	14.2	71.0	601	3	US-09-949-016-66047	Sequence 66047, A	216	14.2	71.0	1950	3	US-09-902-540-6894	Sequence 6894, Ap
144	14.2	71.0	601	3	US-09-949-016-66759	Sequence 66759, A	217	14.2	71.0	2070	3	US-09-949-016-5405	Sequence 5405, Ap
145	14.2	71.0	601	3	US-09-949-016-66760	Sequence 66760, A	218	14.2	71.0	2084	3	US-09-311-021-35	Sequence 35, Appl1
146	14.2	71.0	601	3	US-09-949-016-66761	Sequence 66761, A	219	14.2	71.0	2085	3	US-09-252-991A-5910	Sequence 5910, Ap
147	14.2	71.0	601	3	US-09-949-016-108848	Sequence 108848, A	220	14.2	71.0	2469	3	US-09-270-767-14504	Sequence 14504, A
148	14.2	71.0	601	3	US-09-949-016-108849	Sequence 108849, A	221	14.2	71.0	2469	3	US-09-270-767-14504	Sequence 14504, A
149	14.2	71.0	601	3	US-09-949-016-108850	Sequence 108850, A	222	14.2	71.0	2469	3	US-09-270-767-14504	Sequence 14504, A
150	14.2	71.0	601	3	US-09-949-016-131807	Sequence 131807, A	223	14.2	71.0	3074	3	US-09-949-016-5542	Sequence 5542, Ap
151	14.2	71.0	601	3	US-09-949-016-170319	Sequence 170319, A	224	14.2	71.0	3074	3	US-09-949-016-5542	Sequence 5542, Ap
152	14.2	71.0	601	3	US-09-949-016-170320	Sequence 170320, A	225	14.2	71.0	3243	2	US-08-239-276-6	Sequence 6, Appl1
153	14.2	71.0	601	3	US-09-949-016-183345	Sequence 183345, A	226	14.2	71.0	3243	2	US-08-239-276-6	Sequence 6, Appl1
154	14.2	71.0	601	3	US-09-949-016-195274	Sequence 195274, A	227	14.2	71.0	3243	2	US-08-468-579B-6	Sequence 6, Appl1
155	14.2	71.0	601	3	US-09-949-016-206547	Sequence 206547, A	228	14.2	71.0	3243	2	US-08-468-579B-6	Sequence 6, Appl1
156	14.2	71.0	606	3	US-09-252-991A-10578	Sequence 10578, A	229	14.2	71.0	3384	3	US-09-252-991A-10278	Sequence 10278, A
157	14.2	71.0	621	3	US-09-252-991A-5963	Sequence 5963, Ap	230	14.2	71.0	3384	3	US-09-252-991A-10278	Sequence 10278, A
158	14.2	71.0	627	3	US-09-902-540-3041	Sequence 3041, Ap	231	14.2	71.0	3482	3	US-09-949-016-87878	Sequence 87878, Ap
159	14.2	71.0	642	3	US-10-131-827-8495	Sequence 8495, Ap	232	14.2	71.0	3482	3	US-09-902-540-87878	Sequence 87878, Ap
160	14.2	71.0	680	3	US-09-533-559-1166	Sequence 7166, Ap	233	14.2	71.0	3482	3	US-09-902-540-87878	Sequence 87878, Ap
161	14.2	71.0	686	3	US-09-221-017B-15	Sequence 15, Appl1	234	14.2	71.0	3955	2	US-09-949-016-780	Sequence 14, Appl1
162	14.2	71.0	718	3	US-09-902-540-5917	Sequence 5917, Ap	235	14.2	71.0	4351	3	US-08-445-865-14	Sequence 14, Appl1
163	14.2	71.0	752	3	US-10-144-929-46	Sequence 46, Appl1	236	14.2	71.0	4351	3	US-08-445-865-14	Sequence 14, Appl1
164	14.2	71.0	774	3	US-09-252-991A-5924	Sequence 5924, Ap	237	14.2	71.0	4351	3	US-08-445-865-14	Sequence 14, Appl1
165	14.2	71.0	775	3	US-09-786-025A-3	Sequence 3, Appl1	238	14.2	71.0	4351	3	US-08-445-865-14	Sequence 14, Appl1
166	14.2	71.0	806	3	US-09-257-583-13	Sequence 13, Appl1	239	14.2	71.0	5105	3	US-09-902-540-791	Sequence 791, Ap
167	14.2	71.0	909	3	US-09-257-991A-12690	Sequence 12690, A	240	14.2	71.0	5105	3	US-09-902-540-791	Sequence 791, Ap
168	14.2	71.0	963	3	US-09-758-759-110	Sequence 110, App	241	14.2	71.0	6192	3	US-09-573-425E-11	Sequence 11, Appl1
169	14.2	71.0	1056	3	US-09-252-991A-13107	Sequence 13107, A	242	14.2	71.0	6192	3	US-09-573-425E-11	Sequence 11, Appl1
170	14.2	71.0	1059	3	US-09-252-991A-2019	Sequence 2019, Ap	243	14.2	71.0	6192	3	US-09-573-425E-11	Sequence 11, Appl1

244	14.2	71.0	6192	3	US-09-949-016-3142	Sequence 3142, Ap	317	13.8	69.0	387	3	US-09-270-767-22438	Sequence 22438, A
245	14.2	71.0	6192	3	US-09-949-016-3143	Sequence 3143, Ap	318	13.8	69.0	429	3	US-09-080-855-27	Sequence 27, Appl
246	14.2	71.0	6192	3	US-09-949-016-3144	Sequence 3144, Ap	319	13.8	69.0	429	3	US-09-566-076-27	Sequence 27, Appl
247	14.2	71.0	6192	3	US-09-949-016-3145	Sequence 3145, Ap	320	13.8	69.0	522	3	US-09-252-991A-5285	Sequence 5285, Ap
248	14.2	71.0	6192	3	US-09-949-016-3146	Sequence 3146, Ap	321	13.8	69.0	540	3	US-10-029-180-37	Sequence 37, Appl
249	14.2	71.0	6678	3	US-08-816-617A-1	Sequence 1, Appl1	322	13.8	69.0	543	3	US-09-252-991A-5243	Sequence 5243, Ap
250	14.2	71.0	7734	3	US-09-949-016-1095	Sequence 1095, Ap	323	13.8	69.0	545	3	US-09-080-855-23	Sequence 23, Appl
251	14.2	71.0	8145	3	US-09-949-016-1093	Sequence 1093, Ap	324	13.8	69.0	545	3	US-09-566-076-23	Sequence 23, Appl
252	14.2	71.0	8207	3	US-09-902-540-925	Sequence 925, App	325	13.8	69.0	587	3	US-09-535-559-1002	Sequence 1002, Ap
253	14.2	71.0	8220	3	US-09-949-016-1094	Sequence 1094, Ap	326	13.8	69.0	594	3	US-09-385-982-481	Sequence 481, App
254	14.2	71.0	8280	3	US-09-949-016-5	Sequence 5, Appl1	327	13.8	69.0	601	3	US-09-949-016-55442	Sequence 55442, A
255	14.2	71.0	9274	3	US-09-811-115-4	Sequence 4, Appl1	328	13.8	69.0	601	3	US-09-949-016-67436	Sequence 67436, A
256	14.2	71.0	12214	3	US-09-949-016-17284	Sequence 17284, A	329	13.8	69.0	601	3	US-09-949-016-67506	Sequence 67506, A
257	14.2	71.0	12309	3	US-09-949-016-13709	Sequence 13709, A	330	13.8	69.0	601	3	US-09-949-016-67575	Sequence 67506, A
258	14.2	71.0	15271	3	US-09-949-016-17396	Sequence 17396, A	331	13.8	69.0	601	3	US-09-949-016-67575	Sequence 67506, A
259	14.2	71.0	15559	3	US-09-902-540-1128	Sequence 1128, Ap	332	13.8	69.0	601	3	US-09-949-016-67575	Sequence 67506, A
260	14.2	71.0	15389	3	US-09-741-154-3	Sequence 3, Appl1	333	13.8	69.0	601	3	US-09-949-016-67575	Sequence 67506, A
261	14.2	71.0	16388	3	US-10-187-900-3	Sequence 3, Appl1	334	13.8	69.0	601	3	US-09-949-016-67575	Sequence 67506, A
262	14.2	71.0	19009	3	US-09-949-016-12522	Sequence 12522, A	335	13.8	69.0	601	3	US-09-949-016-82212	Sequence 82212, A
263	14.2	71.0	19012	3	US-09-949-016-16999	Sequence 16999, A	336	13.8	69.0	601	3	US-09-949-016-82212	Sequence 82212, A
264	14.2	71.0	19182	2	US-08-850-880-11	Sequence 11, Appl	337	13.8	69.0	601	3	US-09-949-016-82212	Sequence 82212, A
265	14.2	71.0	19182	2	US-08-944-916-11	Sequence 11, Appl	338	13.8	69.0	601	3	US-09-949-016-143561	Sequence 143561, A
266	14.2	71.0	19182	2	US-09-272-432A-11	Sequence 11, Appl	339	13.8	69.0	601	3	US-09-949-016-177627	Sequence 177627, A
267	14.2	71.0	21856	3	US-09-949-016-12205	Sequence 12205, A	340	13.8	69.0	601	3	US-09-949-016-177628	Sequence 177628, A
268	14.2	71.0	24299	3	US-09-949-016-15452	Sequence 15452, A	341	13.8	69.0	601	3	US-09-949-016-189805	Sequence 189804, A
269	14.2	71.0	31422	3	US-09-914-286-2	Sequence 2, Appl1	342	13.8	69.0	601	3	US-09-949-016-192739	Sequence 192739, A
270	14.2	71.0	36302	3	US-09-949-016-11998	Sequence 11998, A	343	13.8	69.0	601	3	US-09-949-016-192740	Sequence 192740, A
271	14.2	71.0	36302	3	US-09-949-016-13891	Sequence 13891, A	344	13.8	69.0	601	3	US-09-949-016-192741	Sequence 192741, A
272	14.2	71.0	36412	3	US-08-311-731A-132	Sequence 132, App	345	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
273	14.2	71.0	41768	3	US-09-902-540-1266	Sequence 1266, App	346	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
274	14.2	71.0	44952	3	US-09-949-016-12197	Sequence 12197, A	347	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
275	14.2	71.0	44960	3	US-09-949-016-17583	Sequence 17583, A	348	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
276	14.2	71.0	51552	3	US-09-733-294A-30	Sequence 30, Appl	349	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
277	14.2	71.0	75929	3	US-09-949-016-15543	Sequence 15543, A	350	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
278	14.2	71.0	75929	3	US-09-949-016-15544	Sequence 15544, A	351	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
279	14.2	71.0	84916	3	US-09-949-016-14736	Sequence 14736, A	352	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
280	14.2	71.0	87562	3	US-09-949-016-13685	Sequence 13685, A	353	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
281	14.2	71.0	87617	3	US-09-949-016-16551	Sequence 16551, A	354	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
282	14.2	71.0	109519	3	US-09-758-759-1	Sequence 1, Appl1	355	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
283	14.2	71.0	109519	3	US-09-758-759-1	Sequence 1, Appl1	356	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
284	14.2	71.0	118136	3	US-09-949-016-12439	Sequence 12439, A	357	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
285	14.2	71.0	128470	3	US-09-949-016-13765	Sequence 13765, A	358	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
286	14.2	71.0	131631	3	US-09-949-016-11757	Sequence 11757, A	359	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
287	14.2	71.0	145928	3	US-09-949-016-15444	Sequence 15444, A	360	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
288	14.2	71.0	146307	3	US-09-949-016-14881	Sequence 14881, A	361	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
289	14.2	71.0	146307	3	US-09-949-016-14882	Sequence 14882, A	362	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
290	14.2	71.0	146307	3	US-09-949-016-14883	Sequence 14883, A	363	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
291	14.2	71.0	146307	3	US-09-949-016-14884	Sequence 14884, A	364	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
292	14.2	71.0	146307	3	US-09-949-016-14885	Sequence 14885, A	365	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
293	14.2	71.0	146307	3	US-09-949-016-14886	Sequence 14886, A	366	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
294	14.2	71.0	146307	3	US-09-949-016-14887	Sequence 14887, A	367	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
295	14.2	71.0	146307	3	US-09-949-016-14888	Sequence 14888, A	368	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
296	14.2	71.0	148405	3	US-09-949-016-11747	Sequence 11747, A	369	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
297	14.2	71.0	148405	3	US-09-949-016-11747	Sequence 11747, A	370	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
298	14.2	71.0	148405	3	US-09-949-016-12836	Sequence 12836, A	371	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
299	14.2	71.0	148405	3	US-09-949-016-12837	Sequence 12837, A	372	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
300	14.2	71.0	175236	3	US-09-949-016-14353	Sequence 14353, A	373	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
301	14.2	71.0	175236	3	US-09-949-016-13113	Sequence 13113, A	374	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
302	14.2	71.0	360470	3	US-08-952-793-225	Sequence 225, App	375	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
303	14.2	71.0	35	6	PCT-US96-09455A-225	Sequence 225, App	376	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
304	14.2	71.0	35	6	PCT-US96-09455A-225	Sequence 225, App	377	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
305	14.2	71.0	601	3	US-09-949-016-44263	Sequence 44263, A	378	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
306	14.2	71.0	601	3	US-09-949-016-44263	Sequence 44263, A	379	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
307	14.2	71.0	1023	3	US-09-940-244-483	Sequence 343, App	380	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
308	14.2	71.0	1053	3	US-09-940-244-394	Sequence 394, App	381	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
309	14.2	71.0	1053	3	US-09-940-244-393	Sequence 393, App	382	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
310	14.2	71.0	2037	3	US-09-252-991A-3631	Sequence 1631, App	383	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
311	14.2	71.0	136264	3	US-09-949-016-12756	Sequence 12756, A	384	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
312	14.2	71.0	136265	3	US-09-949-016-13001	Sequence 13001, A	385	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
313	13.8	69.0	47	3	US-09-396-196G-83371	Sequence 83271, A	386	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
314	13.8	69.0	25	3	US-09-422-978-3435	Sequence 3435, Ap	387	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
315	13.8	69.0	191	3	US-09-513-999C-25265	Sequence 25265, A	388	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A
316	13.8	69.0	387	3	US-09-270-767-7156	Sequence 7156, Ap	389	13.8	69.0	601	3	US-09-949-016-192743	Sequence 192743, A

390	13.8	69.0	2162	3	US-09-991-181-339	Sequence 339, App	463	13.8	69.0	11740	3	US-09-507-362-103	Sequence 103, App
391	13.8	69.0	2162	3	US-09-990-444-339	Sequence 339, App	464	13.8	69.0	11927	3	US-09-193-707-5	Sequence 5, Appl1
392	13.8	69.0	2162	3	US-09-997-333-339	Sequence 339, App	465	13.8	69.0	12905	3	US-09-949-016-12188	Sequence 12188, A
393	13.8	69.0	2162	3	US-09-992-598-339	Sequence 339, App	466	13.8	69.0	13505	3	US-08-972-218-1	Sequence 1, Appl1
394	13.8	69.0	2163	3	US-09-252-991A-15344	Sequence 15344, A	467	13.8	69.0	13505	3	US-09-193-707-1	Sequence 1, Appl1
395	13.8	69.0	2190	3	US-09-107-433-2104	Sequence 2104, Ap	468	13.8	69.0	13930	3	US-09-976-594-1011	Sequence 20, Appl
396	13.8	69.0	2193	2	US-08-731-716-1	Sequence 1, Appl1	469	13.8	69.0	14070	3	US-09-120-132-20	Sequence 2, Appl1
397	13.8	69.0	2193	2	US-08-731-716-3	Sequence 3, Appl1	470	13.8	69.0	15482	3	US-09-108-006C-2	Sequence 1067, Ap
398	13.8	69.0	2193	5	US-09-014-897-1	Sequence 3, Appl1	471	13.8	69.0	15482	3	US-09-902-540-1067	Sequence 1653, A
399	13.8	69.0	2193	5	US-09-014-897-3	Sequence 2059, Ap	472	13.8	69.0	15621	3	US-09-949-016-16564	Sequence 16564, A
400	13.8	69.0	2196	3	US-09-583-110-2059	Sequence 246, App	473	13.8	69.0	15621	3	US-08-741-881-1	Sequence 1, Appl1
401	13.8	69.0	2235	3	US-09-453-702B-246	Sequence 146, App	474	13.8	69.0	16656	2	US-08-739-158-1	Sequence 1, Appl1
402	13.8	69.0	2235	3	US-10-114-170-246	Sequence 15, Appl	475	13.8	69.0	16656	2	US-08-739-167-1	Sequence 1, Appl1
403	13.8	69.0	2242	3	US-09-620-312D-15	Sequence 1853, A	476	13.8	69.0	16656	3	US-08-404-796-1	Sequence 1, Appl1
404	13.8	69.0	2256	3	US-09-252-991A-10853	Sequence 18, Appl	477	13.8	69.0	16656	3	US-08-321-869-1	Sequence 1, Appl1
405	13.8	69.0	2284	3	US-09-578-063-18	Sequence 1417, A	478	13.8	69.0	16656	3	US-09-350-399-1	Sequence 1, Appl1
406	13.8	69.0	2543	3	US-09-252-991A-13417	Sequence 5, Appl1	480	13.8	69.0	16742	3	US-09-949-016-12782	Sequence 12782, A
407	13.8	69.0	2626	3	US-09-590-740-5	Sequence 595, App	481	13.8	69.0	18034	3	US-09-266-965-75	Sequence 75, Appl
408	13.8	69.0	2990	3	US-10-104-047-595	Sequence 17, Appl	482	13.8	69.0	19167	3	US-09-949-016-17174	Sequence 17174, A
409	13.8	69.0	3104	3	US-09-578-063-17	Sequence 225, App	483	13.8	69.0	20850	3	US-09-949-016-15789	Sequence 15789, A
410	13.8	69.0	3114	3	US-09-252-991A-225	Sequence 276, App	484	13.8	69.0	22306	3	US-09-453-702B-251	Sequence 251, App
411	13.8	69.0	3143	3	US-10-012-221A-276	Sequence 276, App	485	13.8	69.0	22306	3	US-09-453-702B-251	Sequence 251, App
412	13.8	69.0	3143	3	US-10-015-389A-276	Sequence 276, App	486	13.8	69.0	22306	3	US-10-114-170-251	Sequence 17483, A
413	13.8	69.0	3143	3	US-10-006-768A-276	Sequence 276, App	487	13.8	69.0	22306	3	US-09-949-016-17483	Sequence 11931, A
414	13.8	69.0	3143	3	US-10-015-393A-276	Sequence 276, App	488	13.8	69.0	229037	3	US-09-949-016-11953	Sequence 11953, A
415	13.8	69.0	3143	3	US-10-011-393A-276	Sequence 276, App	489	13.8	69.0	29966	3	US-09-949-016-16778	Sequence 16728, A
416	13.8	69.0	3143	3	US-10-006-041A-276	Sequence 276, App	490	13.8	69.0	30245	3	US-09-949-016-13550	Sequence 13550, A
417	13.8	69.0	3143	3	US-10-012-064A-276	Sequence 78, Appl	491	13.8	69.0	32417	3	US-09-453-702B-206	Sequence 1765, A
418	13.8	69.0	3230	9	US-09-280-799-78	Patent No. 5324640	492	13.8	69.0	43360	3	US-09-453-702B-261	Sequence 261, App
419	13.8	69.0	3230	9	5324640-1	Sequence 6, Appl1	493	13.8	69.0	43360	3	US-10-114-170-206	Sequence 206, App
420	13.8	69.0	3242	2	US-07-951-715A-6	Sequence 6, Appl1	494	13.8	69.0	43360	3	US-09-453-702B-261	Sequence 261, App
421	13.8	69.0	3242	2	US-08-459-448A-6	Sequence 6, Appl1	495	13.8	69.0	43325	3	US-10-114-170-261	Sequence 13727, A
422	13.8	69.0	3242	2	US-08-459-595A-6	Sequence 6, Appl1	496	13.8	69.0	43325	3	US-09-949-016-13727	Sequence 13728, A
423	13.8	69.0	3242	3	US-08-459-504B-6	Sequence 6, Appl1	497	13.8	69.0	44931	3	US-09-949-016-13728	Sequence 13729, A
424	13.8	69.0	3242	3	US-08-459-444-6	Sequence 7, Appl1	498	13.8	69.0	44931	3	US-09-949-016-13729	Sequence 3, Appl1
425	13.8	69.0	3242	3	US-09-053-549-7	Sequence 6, Appl1	499	13.8	69.0	70900	3	US-09-851-896-3	Sequence 16819, A
426	13.8	69.0	3242	3	US-09-547-422-6	Sequence 8379, Ap	500	13.8	69.0	76399	3	US-09-949-016-16819	Sequence 15116, A
427	13.8	69.0	3242	3	US-09-988-462-6	Sequence 15251, A	501	13.8	69.0	83462	3	US-09-949-016-15116	Sequence 14018, A
428	13.8	69.0	3242	3	US-09-902-540-8379	Sequence 1, Appl1	502	13.8	69.0	92505	3	US-09-949-016-15095	Sequence 15095, A
429	13.8	69.0	3810	3	US-09-552-991A-15251	Sequence 1, Appl1	503	13.8	69.0	92505	3	US-09-949-016-14018	Sequence 14169, A
430	13.8	69.0	4260	3	US-08-961-527-2	Sequence 101, App	504	13.8	69.0	109159	3	US-09-949-016-11770	Sequence 14170, A
431	13.8	69.0	7571	3	US-09-368-590-1	Sequence 101, App	505	13.8	69.0	109159	3	US-09-949-016-13180	Sequence 14205, A
432	13.8	69.0	7812	3	US-09-415-784-101	Sequence 101, App	506	13.8	69.0	109159	3	US-09-949-016-11724	Sequence 14266, A
433	13.8	69.0	8000	3	US-09-415-784-101	Sequence 101, App	507	13.8	69.0	109159	3	US-09-949-016-12724	Sequence 12724, A
434	13.8	69.0	8000	3	US-09-415-784-101	Sequence 101, App	508	13.8	69.0	112871	3	US-09-949-016-12725	Sequence 12725, A
435	13.8	69.0	8000	3	US-09-415-784-101	Sequence 101, App	509	13.8	69.0	112871	3	US-09-949-016-12725	Sequence 13352, A
436	13.8	69.0	8000	3	US-09-415-784-101	Sequence 101, App	510	13.8	69.0	135010	3	US-09-949-016-13362	Sequence 17434, A
437	13.8	69.0	8000	3	US-08-944-465-101	Sequence 101, App	511	13.8	69.0	135010	3	US-09-949-016-14734	Sequence 56526, A
438	13.8	69.0	8000	3	US-08-944-465-101	Sequence 101, App	512	13.8	69.0	161652	3	US-09-396-196G-56526	Sequence 98308, A
439	13.8	69.0	8000	3	US-09-415-868-102	Sequence 101, App	513	13.8	69.0	161652	3	US-09-396-196G-95308	Sequence 15, Appl
440	13.8	69.0	8000	3	US-09-415-868-102	Sequence 101, App	514	13.8	69.0	223471	3	US-08-072-063-15	Sequence 15, Appl
441	13.8	69.0	8000	3	US-09-415-868-102	Sequence 101, App	515	13.8	69.0	223471	3	US-08-064-693-15	Sequence 15, Appl
442	13.8	69.0	8000	3	US-09-415-868-102	Sequence 101, App	516	13.8	69.0	223471	3	US-08-885-366-15	Sequence 15, Appl
443	13.8	69.0	8000	3	US-09-507-362-101	Sequence 101, App	517	13.8	69.0	223471	3	US-08-885-366-15	Sequence 15, Appl
444	13.8	69.0	8000	3	US-09-507-362-102	Sequence 101, App	518	13.8	69.0	223471	3	US-08-885-366-14	Sequence 14, Appl
445	13.8	69.0	8367	2	US-08-583-562B-7	Sequence 7, Appl1	519	13.6	68.0	226	2	US-08-885-366-14	Sequence 14, Appl
446	13.8	69.0	8367	2	US-08-779-113-7	Sequence 211, App	520	13.6	68.0	226	2	US-08-885-366-14	Sequence 14, Appl
447	13.8	69.0	8368	3	US-09-949-016-211	Sequence 486, Ap	521	13.6	68.0	226	2	US-08-885-366-14	Sequence 14, Appl
448	13.8	69.0	8368	3	US-09-949-016-1986	Sequence 138, Ap	522	13.6	68.0	226	2	US-08-885-366-14	Sequence 14, Appl
449	13.8	69.0	8756	3	US-09-949-016-1438	Sequence 1, Appl1	523	13.6	68.0	226	2	US-08-885-366-14	Sequence 14, Appl
450	13.8	69.0	8854	3	US-09-053-549-1	Sequence 983, App	524	13.6	68.0	226	2	US-08-885-366-14	Sequence 14, Appl
451	13.8	69.0	9039	3	US-09-902-540-983	Sequence 3, Appl1	525	13.6	68.0	226	2	US-08-885-366-14	Sequence 14, Appl
452	13.8	69.0	9951	3	US-09-193-707-3	Sequence 4, Appl1	526	13.6	68.0	226	2	US-08-885-366-14	Sequence 14, Appl
453	13.8	69.0	10524	3	US-09-193-707-4	Sequence 1, Appl1	527	13.6	68.0	226	2	US-08-885-366-14	Sequence 14, Appl
454	13.8	69.0	11282	3	US-09-733-042-1	Sequence 1, Appl1	528	13.6	68.0	226	2	US-08-885-366-14	Sequence 14, Appl
455	13.8	69.0	11703	2	US-08-801-263A-8	Sequence 8, Appl1	529	13.6	68.0	226	2	US-08-885-366-14	Sequence 14, Appl
456	13.8	69.0	11703	2	US-09-102-248-8	Sequence 8, Appl1	530	13.6	68.0	226	2	US-08-885-366-14	Sequence 14, Appl
457	13.8	69.0	11703	3	US-09-367-764-8	Sequence 8, Appl1	531	13.6	68.0	226	2	US-08-885-366-14	Sequence 14, Appl
458	13.8	69.0	11740	3	US-09-415-784-103	Sequence 103, App	532	13.6	68.0	226	2	US-08-885-366-14	Sequence 14, Appl
459	13.8	69.0	11740	3	US-09-415-785A-103	Sequence 103, App	533	13.6	68.0	226	2	US-08-885-366-14	Sequence 14, Appl
460	13.8	69.0	11740	3	US-08-944-465-103	Sequence 103, App	534	13.6	68.0	226	2	US-08-885-366-14	Sequence 14, Appl
461	13.8	69.0	11740	3	US-09-415-868-103	Sequence 103, App	535	13.6	68.0	226	2	US-08-885-366-14	Sequence 14, Appl
462	13.8	69.0	11740	3	US-09-415-900-103	Sequence 103, App	535	13.6	68.0	226	2	US-08-885-366-14	Sequence 14, Appl

536	13.6	68.0	348	3	US-09-252-991A-15819	Sequence 15819, A	609	13.6	68.0	900	2	US-08-653-632-1	Sequence 1, Appl1
C 537	13.6	68.0	368	3	US-10-131-827-8202	Sequence 8202, Ap	C 610	13.6	68.0	900	3	US-09-270-767-10438	Sequence 10438, A
C 538	13.6	68.0	410	3	US-09-702-705-847	Sequence 847, App	611	13.6	68.0	924	3	US-09-919-172-94	Sequence 94, Appl1
C 539	13.6	68.0	410	3	US-09-736-457-847	Sequence 847, App	612	13.6	68.0	924	3	US-09-919-172-94	Sequence 94, Appl1
C 540	13.6	68.0	410	3	US-09-614-124B-847	Sequence 847, App	613	13.6	68.0	933	3	US-09-248-796A-13100	Sequence 13100, A
C 541	13.6	68.0	410	3	US-09-671-325-847	Sequence 847, App	614	13.6	68.0	960	3	US-09-107-532A-736	Sequence 736, App
C 542	13.6	68.0	410	3	US-09-658-824-847	Sequence 847, App	615	13.6	68.0	963	3	US-09-248-796A-6339	Sequence 6339, App
C 543	13.6	68.0	410	3	US-10-017-754-847	Sequence 847, App	616	13.6	68.0	984	3	US-09-252-991A-9330	Sequence 9330, App
C 544	13.6	68.0	410	3	US-09-651-565-847	Sequence 847, App	617	13.6	68.0	1029	3	US-09-252-991A-5867	Sequence 5867, App
C 545	13.6	68.0	426	3	US-09-134-001C-467	Sequence 467, App	C 618	13.6	68.0	1143	3	US-09-252-991A-15899	Sequence 15899, A
546	13.6	68.0	432	2	US-07-915-720D-26	Sequence 26, Appl	C 619	13.6	68.0	1152	3	US-09-252-991A-13050	Sequence 13050, A
547	13.6	68.0	432	3	US-09-025-545-26	Sequence 26, Appl	C 620	13.6	68.0	1154	3	US-09-949-016-1145	Sequence 4144, Ap
C 548	13.6	68.0	432	3	US-09-252-991A-5818	Sequence 5818, Ap	C 621	13.6	68.0	1154	3	US-09-949-016-1145	Sequence 4145, Ap
C 549	13.6	68.0	444	3	US-09-902-540-6312	Sequence 6312, Ap	C 622	13.6	68.0	1194	3	US-09-949-016-1791	Sequence 3791, Ap
C 550	13.6	68.0	515	3	US-09-621-976-2823	Sequence 2823, Ap	C 623	13.6	68.0	1194	3	US-09-023-655-1506	Sequence 1506, Ap
C 551	13.6	68.0	538	3	US-09-270-767-927	Sequence 927, App	C 624	13.6	68.0	1194	3	US-09-023-655-1506	Sequence 1506, Ap
C 552	13.6	68.0	538	3	US-09-270-767-927	Sequence 927, App	C 625	13.6	68.0	1210	3	PCT-US95-06406A-10	Sequence 10, Appl1
C 553	13.6	68.0	547	3	US-08-998-416-227	Sequence 16209, A	C 626	13.6	68.0	1224	6	US-09-252-991A-4649	Sequence 4649, Ap
C 554	13.6	68.0	554	3	US-09-270-767-12653	Sequence 12653, A	C 627	13.6	68.0	1224	3	US-09-270-767-11278	Sequence 11278, A
C 555	13.6	68.0	557	3	US-09-270-767-26828	Sequence 26828, A	C 628	13.6	68.0	1355	3	US-09-023-655-1481	Sequence 1481, Ap
C 556	13.6	68.0	601	3	US-09-949-016-25352	Sequence 25352, A	C 629	13.6	68.0	1360	3	US-09-426-557-5	Sequence 5, Appl1
C 557	13.6	68.0	601	3	US-09-949-016-27407	Sequence 27407, A	C 630	13.6	68.0	1381	3	US-09-712-363-16	Sequence 36, Appl1
C 558	13.6	68.0	601	3	US-09-949-016-27408	Sequence 27408, A	C 631	13.6	68.0	1395	3	US-09-489-039A-2766	Sequence 2766, Ap
C 559	13.6	68.0	601	3	US-09-949-016-27409	Sequence 27409, A	C 632	13.6	68.0	1434	3	US-09-252-991A-7598	Sequence 7598, Ap
C 560	13.6	68.0	601	3	US-09-949-016-27410	Sequence 27410, A	C 633	13.6	68.0	1437	3	US-09-252-991A-7598	Sequence 7598, Ap
C 561	13.6	68.0	601	3	US-09-949-016-69273	Sequence 69273, A	C 634	13.6	68.0	1458	3	US-09-426-557-7	Sequence 7, Appl1
C 562	13.6	68.0	601	3	US-09-949-016-69274	Sequence 69274, A	C 635	13.6	68.0	1478	3	US-09-426-557-7	Sequence 7, Appl1
C 563	13.6	68.0	601	3	US-09-949-016-69275	Sequence 69275, A	C 636	13.6	68.0	1541	3	US-09-426-557-3	Sequence 3, Appl1
C 564	13.6	68.0	601	3	US-09-949-016-69276	Sequence 69276, A	C 637	13.6	68.0	1541	3	US-09-426-557-3	Sequence 3, Appl1
C 565	13.6	68.0	601	3	US-09-949-016-69682	Sequence 69682, A	C 638	13.6	68.0	1618	2	US-07-885-970A-24	Sequence 24, Appl1
C 566	13.6	68.0	601	3	US-09-949-016-69683	Sequence 69683, A	C 639	13.6	68.0	1618	2	US-08-298-687A-24	Sequence 24, Appl1
C 567	13.6	68.0	601	3	US-09-949-016-69684	Sequence 69684, A	C 640	13.6	68.0	1618	2	US-08-530-797-14	Sequence 14, Appl1
C 568	13.6	68.0	601	3	US-09-949-016-69735	Sequence 69735, A	C 641	13.6	68.0	1618	2	US-08-298-687A-24	Sequence 24, Appl1
C 569	13.6	68.0	601	3	US-09-949-016-80879	Sequence 80879, A	C 642	13.6	68.0	1618	2	US-08-298-687A-24	Sequence 24, Appl1
C 570	13.6	68.0	601	3	US-09-949-016-81306	Sequence 81306, A	C 643	13.6	68.0	1621	3	US-09-991-181-170	Sequence 170, App
C 571	13.6	68.0	601	3	US-09-949-016-112369	Sequence 112369, A	C 644	13.6	68.0	1621	3	US-09-991-181-170	Sequence 170, App
C 572	13.6	68.0	601	3	US-09-949-016-112424	Sequence 112424, A	C 645	13.6	68.0	1621	3	US-09-991-181-170	Sequence 170, App
C 573	13.6	68.0	601	3	US-09-949-016-112425	Sequence 112425, A	C 646	13.6	68.0	1621	3	US-09-991-181-170	Sequence 170, App
C 574	13.6	68.0	601	3	US-09-949-016-112427	Sequence 112427, A	C 647	13.6	68.0	1633	2	US-08-218-026-3	Sequence 2, Appl1
C 575	13.6	68.0	601	3	US-09-949-016-121254	Sequence 121254, A	C 648	13.6	68.0	1633	2	US-08-653-632-3	Sequence 3, Appl1
C 576	13.6	68.0	601	3	US-09-949-016-125332	Sequence 125332, A	C 649	13.6	68.0	1665	3	US-09-805-127-7	Sequence 7, Appl1
C 577	13.6	68.0	601	3	US-09-949-016-125333	Sequence 125333, A	C 650	13.6	68.0	1761	3	US-09-252-991A-13349	Sequence 13349, A
C 578	13.6	68.0	601	3	US-09-949-016-137575	Sequence 137575, A	C 651	13.6	68.0	1771	3	US-08-818-112-13	Sequence 13, Appl1
C 579	13.6	68.0	601	3	US-09-949-016-146580	Sequence 146580, A	C 652	13.6	68.0	1771	3	US-08-818-112-13	Sequence 13, Appl1
C 580	13.6	68.0	601	3	US-09-949-016-146581	Sequence 146581, A	C 653	13.6	68.0	1771	3	US-09-056-556-13	Sequence 13, Appl1
C 581	13.6	68.0	601	3	US-09-949-016-156850	Sequence 156850, A	C 654	13.6	68.0	1771	3	US-09-072-596-13	Sequence 13, Appl1
C 582	13.6	68.0	601	3	US-09-949-016-156851	Sequence 156851, A	C 655	13.6	68.0	1771	3	US-09-072-596-13	Sequence 13, Appl1
C 583	13.6	68.0	601	3	US-09-949-016-164717	Sequence 164717, A	C 656	13.6	68.0	1771	3	US-10-193-002-13	Sequence 13, Appl1
C 584	13.6	68.0	601	3	US-09-949-016-171537	Sequence 171537, A	C 657	13.6	68.0	1771	3	US-10-193-002-13	Sequence 13, Appl1
C 585	13.6	68.0	601	3	US-09-949-016-179855	Sequence 179855, A	C 658	13.6	68.0	1813	2	US-08-030-644-13	Sequence 13, Appl1
C 586	13.6	68.0	601	3	US-09-949-016-179855	Sequence 179855, A	C 659	13.6	68.0	1813	2	US-08-013-801-1	Sequence 1, Appl1
C 587	13.6	68.0	601	3	US-09-949-016-194994	Sequence 194994, A	C 660	13.6	68.0	1813	2	US-08-072-063-1	Sequence 1, Appl1
C 588	13.6	68.0	601	3	US-09-949-016-194995	Sequence 194995, A	C 661	13.6	68.0	1813	2	US-08-212-132-1	Sequence 1, Appl1
C 589	13.6	68.0	601	3	US-09-949-016-194996	Sequence 194996, A	C 662	13.6	68.0	1813	2	US-08-414-324-1	Sequence 1, Appl1
C 590	13.6	68.0	601	3	US-09-949-002-3887	Sequence 3887, Ap	C 663	13.6	68.0	1813	2	US-08-311-611A-145	Sequence 145, App
C 591	13.6	68.0	601	3	US-09-949-002-3888	Sequence 3888, Ap	C 664	13.6	68.0	1813	2	US-08-332-527-1	Sequence 145, App
C 592	13.6	68.0	601	3	US-09-949-002-3889	Sequence 3889, Ap	C 665	13.6	68.0	1813	2	US-08-372-783-145	Sequence 145, App
C 593	13.6	68.0	601	3	US-09-949-002-3890	Sequence 3890, Ap	C 666	13.6	68.0	1813	2	US-08-372-783-145	Sequence 145, App
C 594	13.6	68.0	601	3	US-09-949-002-5834	Sequence 5834, Ap	C 667	13.6	68.0	1813	2	US-08-415-158-1	Sequence 1, Appl1
C 595	13.6	68.0	601	3	US-09-949-002-5835	Sequence 5835, Ap	C 668	13.6	68.0	1813	2	US-08-415-158-1	Sequence 1, Appl1
C 596	13.6	68.0	601	3	US-09-949-002-5836	Sequence 5836, Ap	C 669	13.6	68.0	1813	2	US-08-415-158-1	Sequence 1, Appl1
C 597	13.6	68.0	601	3	US-09-949-002-5837	Sequence 5837, Ap	C 670	13.6	68.0	1813	2	US-08-291-112-1	Sequence 1, Appl1
C 598	13.6	68.0	601	3	US-09-949-002-5837	Sequence 5837, Ap	C 671	13.6	68.0	1813	2	US-08-306-473A-145	Sequence 145, App
C 599	13.6	68.0	601	3	US-09-949-002-5837	Sequence 5837, Ap	C 672	13.6	68.0	1813	2	US-08-306-473A-145	Sequence 145, App
C 600	13.6	68.0	601	3	US-07-801-814D-3	Sequence 3, Appl1	C 673	13.6	68.0	1813	2	US-08-306-473A-145	Sequence 145, App
C 601	13.6	68.0	700	3	US-09-673-395A-38	Sequence 38, Appl1	C 674	13.6	68.0	1813	2	US-08-306-473A-145	Sequence 145, App
C 602	13.6	68.0	700	3	US-09-735-271-316	Sequence 316, App	C 675	13.6	68.0	1813	2	US-08-306-473A-145	Sequence 145, App
C 603	13.6	68.0	700	3	US-09-735-271-317	Sequence 317, App	C 676	13.6	68.0	1813	2	US-08-306-473A-145	Sequence 145, App
C 604	13.6	68.0	729	3	US-09-252-991A-9385	Sequence 9385, App	C 677	13.6	68.0	1813	2	US-08-306-473A-145	Sequence 145, App
C 605	13.6	68.0	729	3	US-09-252-991A-9385	Sequence 9385, App	C 678	13.6	68.0	1813	2	US-08-306-473A-145	Sequence 145, App
C 606	13.6	68.0	864	3	US-09-902-540-5749	Sequence 5749, Ap	C 679	13.6	68.0	1813	2	US-08-306-473A-145	Sequence 145, App
C 607	13.6	68.0	867	2	US-08-181-471-3	Sequence 3, Appl1	C 680	13.6	68.0	1813	2	US-08-306-473A-145	Sequence 145, App
C 608	13.6	68.0	900	2	US-08-218-026-1	Sequence 1, Appl1	C 681	13.6	68.0	1813	2	US-08-306-473A-145	Sequence 145, App



682	13.6	68.0	1813	2	US-08-466-624-1	Sequence 1, Appl1	755	13.6	68.0	2004	3	US-09-902-540-8007	Sequence 8007, Ap
683	13.6	68.0	1813	2	US-08-621-803-264	Sequence 264, App	756	13.6	68.0	2064	3	US-09-248-796A-8923	Sequence 8923, Ap
684	13.6	68.0	1813	2	US-08-466-826-1	Sequence 1, Appl1	757	13.6	68.0	2106	3	US-08-613-009A-4	Sequence 4, Appl1
685	13.6	68.0	1813	2	US-08-704-504-1	Sequence 1, Appl1	758	13.6	68.0	2106	3	US-08-778-570B-4	Sequence 4, Appl1
686	13.6	68.0	1813	2	US-08-485-445A-145	Sequence 145, App	759	13.6	68.0	2106	3	US-09-059-584-4	Sequence 4, Appl1
687	13.6	68.0	1813	2	US-08-621-259A-251	Sequence 251, App	760	13.6	68.0	2115	3	US-09-252-991A-5782	Sequence 5782, Ap
688	13.6	68.0	1813	2	US-08-586-133-1	Sequence 1, Appl1	761	13.6	68.0	2133	3	US-09-252-991A-4162	Sequence 4162, Ap
689	13.6	68.0	1813	2	US-09-063-465-1	Sequence 1, Appl1	762	13.6	68.0	2247	3	US-08-613-009A-3	Sequence 3, Appl1
690	13.6	68.0	1813	2	US-08-862-785A-1	Sequence 1, Appl1	763	13.6	68.0	2247	3	US-08-778-570B-3	Sequence 3, Appl1
691	13.6	68.0	1813	2	US-09-081-166-1	Sequence 1, Appl1	764	13.6	68.0	2272	3	US-09-059-584-3	Sequence 3, Appl1
692	13.6	68.0	1813	2	US-09-203-159-1	Sequence 1, Appl1	765	13.6	68.0	2272	3	US-10-114-170-126	Sequence 126, App
693	13.6	68.0	1813	2	US-09-039-725-1	Sequence 1, Appl1	766	13.6	68.0	2306	3	US-09-620-3120-166	Sequence 126, App
694	13.6	68.0	1813	3	US-08-756-124-1	Sequence 1, Appl1	767	13.6	68.0	2397	3	US-09-954-556-30	Sequence 166, App
695	13.6	68.0	1813	3	US-09-119-263-145	Sequence 1, Appl1	768	13.6	68.0	2498	2	US-07-943-843-3	Sequence 30, Appl1
696	13.6	68.0	1813	3	US-08-336-402-1	Sequence 1, Appl1	769	13.6	68.0	2577	2	US-08-439-118A-4	Sequence 3, Appl1
697	13.6	68.0	1813	3	US-08-879-565-1	Sequence 14, Appl1	770	13.6	68.0	2577	2	US-08-751-965-4	Sequence 4, Appl1
698	13.6	68.0	1813	3	US-09-025-543-14	Sequence 1, Appl1	771	13.6	68.0	2577	2	US-08-738-975-4	Sequence 4, Appl1
699	13.6	68.0	1813	3	US-09-299-319-1	Sequence 1, Appl1	772	13.6	68.0	2577	2	US-08-728-626-4	Sequence 4, Appl1
700	13.6	68.0	1813	3	US-08-657-162-145	Sequence 1, Appl1	773	13.6	68.0	2577	2	US-08-808-599A-4	Sequence 4, Appl1
701	13.6	68.0	1813	3	US-09-285-124-1	Sequence 1, Appl1	774	13.6	68.0	2577	2	US-08-317-522A-4	Sequence 4, Appl1
702	13.6	68.0	1813	3	US-09-224-480-145	Sequence 1, Appl1	775	13.6	68.0	2577	2	US-10-197-220-149	Sequence 4, Appl1
703	13.6	68.0	1813	3	US-09-281-985-1	Sequence 1, Appl1	776	13.6	68.0	2624	3	US-09-949-016-5604	Sequence 149, App
704	13.6	68.0	1813	3	US-08-626-646-1	Sequence 1, Appl1	777	13.6	68.0	2682	3	US-09-949-016-298	Sequence 149, App
705	13.6	68.0	1813	3	US-09-271-970-15	Sequence 1, Appl1	778	13.6	68.0	2690	3	US-09-949-016-694	Sequence 149, App
706	13.6	68.0	1813	3	US-09-365-858-1	Sequence 1, Appl1	779	13.6	68.0	2690	3	US-09-949-016-298	Sequence 149, App
707	13.6	68.0	1813	3	US-08-431-517F-3	Sequence 3, Appl1	780	13.6	68.0	2847	3	US-09-556-877-186	Sequence 186, App
708	13.6	68.0	1813	3	US-09-217-352-264	Sequence 264, App	781	13.6	68.0	2847	3	US-09-620-412C-186	Sequence 186, App
709	13.6	68.0	1813	3	US-08-885-366-1	Sequence 1, Appl1	782	13.6	68.0	2885	3	US-09-598-419-186	Sequence 510, App
710	13.6	68.0	1813	3	US-09-223-342-1	Sequence 1, Appl1	783	13.6	68.0	2920	3	US-10-104-047-810	Sequence 10, Appl1
711	13.6	68.0	1813	3	US-09-344-541A-53	Sequence 53, Appl1	784	13.6	68.0	2920	3	US-08-976-259-10	Sequence 10, Appl1
712	13.6	68.0	1813	3	US-09-545-112-1	Sequence 1, Appl1	785	13.6	68.0	2998	3	US-09-956-004-10	Sequence 37, App
713	13.6	68.0	1813	3	US-09-280-909A-11	Sequence 11, Appl1	786	13.6	68.0	3209	3	US-09-902-540-87	Sequence 1385, A
714	13.6	68.0	1813	3	US-09-541-821-1	Sequence 1, Appl1	787	13.6	68.0	3299	3	US-09-270-767-14385	Sequence 14385, Ap
715	13.6	68.0	1813	3	US-09-344-827A-16	Sequence 16, Appl1	788	13.6	68.0	3597	3	US-09-252-991A-4445	Sequence 19, Appl1
716	13.6	68.0	1813	3	US-09-425-034A-1	Sequence 1, Appl1	789	13.6	68.0	3812	2	US-08-188-582-19	Sequence 19, Appl1
717	13.6	68.0	1813	3	US-09-543-955-1	Sequence 1, Appl1	790	13.6	68.0	3812	2	US-08-646-715-179	Sequence 679, App
718	13.6	68.0	1813	3	US-09-543-955-1	Sequence 1, Appl1	791	13.6	68.0	3830	3	US-09-949-016-3359	Sequence 2359, App
719	13.6	68.0	1813	3	US-09-255-245-1	Sequence 1, Appl1	792	13.6	68.0	3831	3	US-09-949-016-2854	Sequence 4864, App
720	13.6	68.0	1813	3	US-09-760-397-15	Sequence 15, Appl1	793	13.6	68.0	4119	3	US-09-949-016-4864	Sequence 457, App
721	13.6	68.0	1813	3	US-09-488-979-1	Sequence 1, Appl1	794	13.6	68.0	4119	3	US-09-949-016-457	Sequence 164, App
722	13.6	68.0	1813	3	US-09-344-219-12	Sequence 12, Appl1	795	13.6	68.0	4257	3	US-10-197-220-164	Sequence 149, App
723	13.6	68.0	1813	3	US-09-699-625-1	Sequence 1, Appl1	796	13.6	68.0	4285	3	US-07-620-312D-149	Sequence 2, Appl1
724	13.6	68.0	1813	3	US-09-733-613-1	Sequence 1, Appl1	797	13.6	68.0	5124	3	US-09-534-638-2	Sequence 173, App
725	13.6	68.0	1813	3	US-09-728-938-1	Sequence 1, Appl1	798	13.6	68.0	5331	3	US-09-556-877-173	Sequence 173, App
726	13.6	68.0	1813	3	US-09-579-403-1	Sequence 1, Appl1	799	13.6	68.0	5331	3	US-09-620-412C-173	Sequence 173, App
727	13.6	68.0	1813	3	US-09-610-785-1	Sequence 1, Appl1	800	13.6	68.0	5331	3	US-09-598-419-173	Sequence 173, App
728	13.6	68.0	1813	3	US-09-023-655-1017	Sequence 1017, Ap	801	13.6	68.0	5308	2	US-08-471-058-20	Sequence 20, Appl1
729	13.6	68.0	1813	3	US-09-782-642-1	Sequence 1, Appl1	802	13.6	68.0	5408	3	US-08-471-058-20	Sequence 20, Appl1
730	13.6	68.0	1813	3	US-09-866-514-1	Sequence 1, Appl1	803	13.6	68.0	5408	3	US-08-471-058-20	Sequence 20, Appl1
731	13.6	68.0	1813	3	US-09-677-664B-251	Sequence 251, App	804	13.6	68.0	5408	3	US-08-471-058-20	Sequence 20, Appl1
732	13.6	68.0	1813	3	US-09-586-850-1	Sequence 1, Appl1	805	13.6	68.0	8266	3	US-09-059-584-54	Sequence 54, Appl1
733	13.6	68.0	1813	3	US-09-689-097-1	Sequence 1, Appl1	806	13.6	68.0	8674	3	US-09-949-016-11381	Sequence 1281, A
734	13.6	68.0	1813	3	US-09-416-828-1	Sequence 1, Appl1	807	13.6	68.0	8674	3	US-09-949-016-15381	Sequence 15381, A
735	13.6	68.0	1813	3	US-09-949-016-249	Sequence 249, App	808	13.6	68.0	9125	3	US-09-949-016-15381	Sequence 959, App
736	13.6	68.0	1813	3	US-10-196-460-1	Sequence 1, Appl1	809	13.6	68.0	9455	3	US-09-949-016-15478	Sequence 15478, A
737	13.6	68.0	1813	3	US-09-696-709-1	Sequence 1, Appl1	810	13.6	68.0	10684	3	US-08-618-100B-3	Sequence 3, Appl1
738	13.6	68.0	1813	3	US-10-359-013-12	Sequence 12, Appl1	811	13.6	68.0	11766	3	US-09-949-016-12531	Sequence 12531, A
739	13.6	68.0	1813	6	PCT-US93-04754-1	Sequence 1, Appl1	812	13.6	68.0	11770	3	US-09-949-016-12720	Sequence 12720, A
740	13.6	68.0	1813	6	PCT-US94-01235-1	Sequence 1, Appl1	813	13.6	68.0	11770	3	US-09-949-016-13487	Sequence 13487, A
741	13.6	68.0	1813	6	PCT-US94-02461-1	Sequence 1, Appl1	814	13.6	68.0	11922	3	US-09-949-016-1388	Sequence 13488, A
742	13.6	68.0	1813	6	PCT-US94-06931-11	Sequence 11, Appl1	815	13.6	68.0	11922	3	US-09-949-016-1388	Sequence 13488, A
743	13.6	68.0	1813	6	PCT-US94-07834-1	Sequence 1, Appl1	816	13.6	68.0	12608	3	US-09-949-016-15533	Sequence 15533, A
744	13.6	68.0	1813	6	PCT-US94-00498-145	Sequence 145, App	817	13.6	68.0	13203	3	US-09-949-016-16063	Sequence 16066, A
745	13.6	68.0	1813	6	PCT-US95-00656-145	Sequence 145, App	818	13.6	68.0	13535	3	US-09-949-016-16259	Sequence 16259, A
746	13.6	68.0	1813	6	PCT-US95-00656-145	Sequence 1, Appl1	819	13.6	68.0	13970	3	US-09-949-016-16590	Sequence 16590, A
747	13.6	68.0	1813	6	PCT-US95-03262-205	Sequence 205, App	820	13.6	68.0	14272	3	US-09-516-914-23	Sequence 23, Appl1
748	13.6	68.0	1813	6	PCT-US95-03262-205	Sequence 1, Appl1	821	13.6	68.0	18196	3	US-09-949-016-15126	Sequence 15126, A
749	13.6	68.0	1814	2	US-07-801-814D-1	Sequence 1, Appl1	822	13.6	68.0	22357	3	US-09-949-002-779	Sequence 779, App
750	13.6	68.0	1815	2	US-08-173-968-1	Sequence 1, Appl1	823	13.6	68.0	22357	3	US-09-949-002-780	Sequence 780, App
751	13.6	68.0	1839	3	US-09-516-914-6	Sequence 6, Appl1	824	13.6	68.0	24951	3	US-09-949-016-16255	Sequence 16255, A
752	13.6	68.0	1903	3	US-10-104-047-1266	Sequence 1266, Ap	825	13.6	68.0	25512	3	US-09-949-016-15886	Sequence 15886, A
753	13.6	68.0	1934	3	US-08-653-648A-9	Sequence 9, Appl1	826	13.6	68.0	25512	3	US-09-949-016-15887	Sequence 15887, A
754	13.6	68.0	1983	3	US-09-252-991A-5825	Sequence 5825, Ap	827	13.6	68.0	27752	3	US-09-949-016-16444	Sequence 16444, A

C 828	13.6	68.0	28864	3	US-09-949-016-12250	Sequence 12250, A
C 829	13.6	68.0	28865	3	US-09-949-016-13647	Sequence 13647, A
C 830	13.6	68.0	30146	3	US-09-949-002-559	Sequence 559, App
C 831	13.6	68.0	30146	3	US-09-949-002-858	Sequence 858, App
C 832	13.6	68.0	31960	3	US-09-453-702B-11	Sequence 11, App1
C 833	13.6	68.0	31960	3	US-10-114-170-11	Sequence 11, App1
C 834	13.6	68.0	32488	3	US-09-949-016-15490	Sequence 15490, A
C 835	13.6	68.0	34422	3	US-09-949-016-12701	Sequence 12701, A
C 836	13.6	68.0	34422	3	US-09-949-016-16075	Sequence 16075, A
C 837	13.6	68.0	36579	3	US-09-949-016-12732	Sequence 12732, A
C 838	13.6	68.0	37004	3	US-09-949-016-15317	Sequence 15317, A
C 839	13.6	68.0	38207	3	US-09-949-016-17274	Sequence 17274, A
C 840	13.6	68.0	39376	3	US-09-949-016-17536	Sequence 17536, A
C 841	13.6	68.0	40505	3	US-09-949-016-14339	Sequence 14339, A
C 842	13.6	68.0	40505	3	US-09-292-542A-1	Sequence 1, App1
C 843	13.6	68.0	44971	3	US-09-949-016-17049	Sequence 17049, A
C 844	13.6	68.0	45365	3	US-09-949-016-11893	Sequence 11893, A
C 845	13.6	68.0	45365	3	US-09-949-016-17007	Sequence 17007, A
C 846	13.6	68.0	46340	3	US-09-719-554-66	Sequence 66, App1
C 847	13.6	68.0	54484	3	US-09-902-540-1372	Sequence 1272, App
C 848	13.6	68.0	60593	3	US-09-949-016-13779	Sequence 13779, A
C 849	13.6	68.0	60990	3	US-09-949-016-11080	Sequence 14080, A
C 850	13.6	68.0	65300	3	US-09-949-016-16813	Sequence 16813, A
C 851	13.6	68.0	65518	3	US-09-949-016-1421	Sequence 1421, A
C 852	13.6	68.0	65518	3	US-09-949-016-14101	Sequence 14101, A
C 853	13.6	68.0	70262	3	US-09-949-016-13375	Sequence 13375, A
C 854	13.6	68.0	70262	3	US-09-949-016-12748	Sequence 12748, A
C 855	13.6	68.0	70213	3	US-09-949-002-714	Sequence 714, App
C 856	13.6	68.0	70563	3	US-09-949-016-16743	Sequence 16743, A
C 857	13.6	68.0	72048	3	US-09-949-002-600	Sequence 600, App
C 858	13.6	68.0	72048	3	US-09-949-002-684	Sequence 684, App
C 859	13.6	68.0	72278	3	US-09-949-016-16113	Sequence 16113, A
C 860	13.6	68.0	72347	3	US-09-949-002-633	Sequence 633, App
C 861	13.6	68.0	72455	3	US-09-949-016-11793	Sequence 13793, A
C 862	13.6	68.0	72455	3	US-09-949-016-11793	Sequence 13793, A
C 863	13.6	68.0	72843	3	US-09-949-016-12574	Sequence 12574, A
C 864	13.6	68.0	80490	3	US-09-949-002-733	Sequence 733, App
C 865	13.6	68.0	82048	3	US-09-949-002-696	Sequence 696, App
C 866	13.6	68.0	82619	3	US-09-949-002-579	Sequence 579, App
C 867	13.6	68.0	86880	3	US-09-949-016-1837	Sequence 14837, A
C 868	13.6	68.0	87648	3	US-09-949-016-13655	Sequence 13655, A
C 869	13.6	68.0	96739	3	US-09-949-016-15606	Sequence 15606, A
C 870	13.6	68.0	98864	3	US-09-949-016-15403	Sequence 15403, A
C 871	13.6	68.0	104475	3	US-09-949-016-12115	Sequence 12115, A
C 872	13.6	68.0	104475	3	US-09-949-016-12115	Sequence 12115, A
C 873	13.6	68.0	107800	3	US-09-949-016-12115	Sequence 12115, A
C 874	13.6	68.0	109038	3	US-09-949-016-13119	Sequence 13119, A
C 875	13.6	68.0	111282	3	US-09-754-250-3	Sequence 3, App1
C 876	13.6	68.0	111282	3	US-09-754-250-3	Sequence 3, App1
C 877	13.6	68.0	111282	3	US-10-094-989-3	Sequence 3, App1
C 878	13.6	68.0	111282	3	US-10-094-989-3	Sequence 3, App1
C 879	13.6	68.0	116425	3	US-09-949-016-11809	Sequence 11809, A
C 880	13.6	68.0	119594	3	US-09-949-016-12080	Sequence 12080, A
C 881	13.6	68.0	119594	3	US-09-949-016-15952	Sequence 15952, A
C 882	13.6	68.0	123513	3	US-09-949-016-15794	Sequence 15794, A
C 883	13.6	68.0	123513	3	US-09-949-016-15794	Sequence 15794, A
C 884	13.6	68.0	139552	3	US-09-949-016-15300	Sequence 15300, A
C 885	13.6	68.0	145320	3	US-09-949-016-15858	Sequence 15858, A
C 886	13.6	68.0	185504	3	US-09-949-002-711	Sequence 711, App
C 887	13.6	68.0	194889	3	US-09-949-016-15654	Sequence 15654, A
C 888	13.6	68.0	200918	3	US-09-949-002-647	Sequence 647, App
C 889	13.6	68.0	2003475	3	US-09-949-016-14517	Sequence 14517, A
C 890	13.6	68.0	2003475	3	US-09-949-016-14517	Sequence 14517, A
C 891	13.6	68.0	203475	3	US-09-949-016-14518	Sequence 14518, A
C 892	13.6	68.0	203475	3	US-09-949-016-14518	Sequence 14518, A
C 893	13.6	68.0	203475	3	US-09-949-016-17226	Sequence 17226, A
C 894	13.6	68.0	203475	3	US-09-949-016-17226	Sequence 17226, A
C 895	13.6	68.0	203475	3	US-09-949-016-17228	Sequence 17228, A
C 896	13.6	68.0	203475	3	US-09-949-016-17228	Sequence 17228, A
C 897	13.6	68.0	223471	3	US-09-949-016-12387	Sequence 12387, A
C 898	13.6	68.0	223471	3	US-09-949-016-12725	Sequence 12725, A
C 899	13.6	68.0	223471	3	US-09-949-016-12725	Sequence 12725, A
C 900	13.6	68.0	246444	3	US-09-949-016-13113	Sequence 13113, A
C 901	13.6	68.0	296336	3	US-09-949-016-16600	Sequence 16600, A
C 902	13.6	68.0	301828	3	US-09-949-016-13969	Sequence 13969, A
C 903	13.6	68.0	314792	3	US-09-949-016-13539	Sequence 13539, A
C 904	13.6	68.0	387908	3	US-09-949-016-14543	Sequence 14543, A
C 905	13.6	68.0	394000	3	US-09-949-016-16923	Sequence 16923, A
C 906	13.6	68.0	394000	3	US-10-027-983-11	Sequence 11, App1
C 907	13.6	68.0	421883	3	US-09-949-016-12557	Sequence 12557, A
C 908	13.6	68.0	455726	3	US-09-949-016-14157	Sequence 14157, A
C 909	13.6	68.0	455726	3	US-09-949-016-14157	Sequence 14157, A
C 910	13.6	68.0	481115	3	US-09-949-016-11940	Sequence 11940, A
C 911	13.6	68.0	481115	3	US-09-949-016-11940	Sequence 11940, A
C 912	13.6	68.0	524032	3	US-09-949-016-16928	Sequence 16928, A
C 913	13.6	68.0	524032	3	US-09-949-016-16928	Sequence 16928, A
C 914	13.6	68.0	524032	3	US-09-949-016-16930	Sequence 16930, A
C 915	13.6	68.0	524032	3	US-09-949-016-16931	Sequence 16931, A
C 916	13.6	68.0	528885	3	US-09-949-016-14340	Sequence 14340, A
C 917	13.6	68.0	528885	3	US-09-949-016-14341	Sequence 14341, A
C 918	13.6	68.0	528885	3	US-09-949-016-14342	Sequence 14342, A
C 919	13.6	68.0	528885	3	US-09-949-016-14343	Sequence 14343, A
C 920	13.6	68.0	528885	3	US-09-949-016-14344	Sequence 14344, A
C 921	13.6	68.0	528885	3	US-09-949-016-14345	Sequence 14345, A
C 922	13.6	68.0	528885	3	US-09-949-016-14346	Sequence 14346, A
C 923	13.6	68.0	528885	3	US-09-949-016-14347	Sequence 14347, A
C 924	13.6	68.0	4403765	3	US-09-103-840A-2	Sequence 2, App1
C 925	13.6	68.0	4411529	3	US-09-103-840A-1	Sequence 1, App1
C 926	13.6	67.0	192	3	US-09-134-000C-619	Sequence 619, App
C 927	13.6	67.0	194	3	US-08-946-914-25	Sequence 25, App1
C 928	13.6	67.0	194	3	US-09-656-450-25	Sequence 25, App1
C 929	13.6	67.0	207	3	US-09-513-999C-13056	Sequence 13056, A
C 930	13.6	67.0	242	3	US-09-817-318-4	Sequence 4, App1
C 931	13.6	67.0	246	3	US-09-489-039A-2507	Sequence 2507, App
C 932	13.6	67.0	354	3	US-08-946-914-22	Sequence 22, App1
C 933	13.6	67.0	354	3	US-09-656-450-22	Sequence 22, App1
C 934	13.6	67.0	374	3	US-10-101-463A-216	Sequence 216, App
C 935	13.6	67.0	396	3	US-09-640-173-13	Sequence 13, App1
C 936	13.6	67.0	396	3	US-09-713-550-13	Sequence 13, App1
C 937	13.6	67.0	396	3	US-09-825-254-13	Sequence 13, App1
C 938	13.6	67.0	396	3	US-09-970-966-13	Sequence 13, App1
C 939	13.6	67.0	399	3	US-09-861-893-39	Sequence 29, App1
C 940	13.6	67.0	507	3	US-09-401-064-171	Sequence 171, App
C 941	13.6	67.0	516	3	US-09-252-991A-16162	Sequence 16162, A
C 942	13.6	67.0	567	3	US-09-902-540A-145	Sequence 145, App
C 943	13.6	67.0	601	3	US-09-949-016-17220	Sequence 47230, A
C 944	13.6	67.0	601	3	US-09-949-016-17221	Sequence 47231, A
C 945	13.6	67.0	601	3	US-09-949-016-17222	Sequence 47232, A
C 946	13.6	67.0	601	3	US-09-949-016-17223	Sequence 47233, A
C 947	13.6	67.0	601	3	US-09-949-016-17224	Sequence 47234, A
C 948	13.6	67.0	601	3	US-09-949-016-17225	Sequence 47235, A
C 949	13.6	67.0	601	3	US-09-949-016-17226	Sequence 47236, A
C 950	13.6	67.0	601	3	US-09-949-016-17227	Sequence 47237, A
C 951	13.6	67.0	601	3	US-09-949-016-17228	Sequence 47238, A
C 952	13.6	67.0	601	3	US-09-949-016-17229	Sequence 47239, A
C 953	13.6	67.0	606	3	US-09-949-016-17230	Sequence 47240, A
C 954	13.6	67.0	621	3	US-09-252-991A-12650	Sequence 12650, A
C 955	13.6	67.0	621	3	US-09-270-767-1736	Sequence 1736, App
C 956	13.6	67.0	621	3	US-09-270-767-17018	Sequence 17018, App
C 957	13.6	67.0	639	3	US-09-134-000C-618	Sequence 618, App
C 958	13.6	67.0	645	3	US-09-533-559-2050	Sequence 2050, App
C 959	13.6	67.0	753	2	US-07-612-674-4	Sequence 4, App1
C 960	13.6	67.0	849	3	US-09-252-991A-16471	Sequence 16471, A
C 961	13.6	67.0	885	3	US-09-252-991A-16130	Sequence 16130, A
C 962	13.6	67.0	933	3	US-09-252-991A-12792	Sequence 12792, A
C 963	13.6	67.0	985	3	US-09-940-244-397	Sequence 397, App
C 964	13.6	67.0	1023	3	US-09-940-244-364	Sequence 364, App
C 965	13.6	67.0	1041	2	US-07-612-674-6	Sequence 6, App1
C 966	13.6	67.0	1053	3	US-09-252-991A-13541	Sequence 13541, A
C 967	13.6	67.0	1059	3	US-09-791-165-5	Sequence 5, App1
C 968	13.6	67.0	1059	3	US-09-791-165-5	Sequence 5, App1
C 969	13.6	67.0	1080	3	US-09-489-039A-5941	Sequence 5941, App
C 970	13.6	67.0	1117	3	US-09-949-016-1380	Sequence 1380, App
C 971	13.6	67.0	1117	2	US-08-469-667-15	Sequence 15, App1
C 972	13.6	67.0	1121	3	US-09-224-110-15	Sequence 15, App1
C 973	13.6	67.0	1121	3	US-09-988-292A-15	Sequence 15, App1

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c 974 13.4 67.0 1121 6 PCT-US95-07289-15 Sequence 15, Appl
c 975 13.4 67.0 1138 3 US-08-946-914-1 Sequence 1, Appl
c 976 13.4 67.0 1138 3 US-09-656-450-1 Sequence 1, Appl
c 977 13.4 67.0 1299 3 US-09-252-991A-12484 Sequence 12484, A
c 978 13.4 67.0 1299 2 US-08-453-472-3 Sequence 3, Appl
c 979 13.4 67.0 1299 2 US-08-453-952-3 Sequence 3, Appl
c 980 13.4 67.0 1299 2 US-08-453-952-3 Sequence 3, Appl
c 981 13.4 67.0 1299 2 US-08-862-903-3 Sequence 3, Appl
c 982 13.4 67.0 1299 2 US-08-862-903-3 Sequence 3, Appl
c 983 13.4 67.0 1299 2 US-08-862-903-3 Sequence 3, Appl
c 984 13.4 67.0 1299 2 US-08-862-903-3 Sequence 3, Appl
c 985 13.4 67.0 1299 2 US-08-862-903-3 Sequence 3, Appl
c 986 13.4 67.0 1299 2 US-08-862-903-3 Sequence 3, Appl
c 987 13.4 67.0 1299 2 US-08-862-903-3 Sequence 3, Appl
c 988 13.4 67.0 1299 2 US-08-862-903-3 Sequence 3, Appl
c 989 13.4 67.0 1299 2 US-08-862-903-3 Sequence 3, Appl
c 990 13.4 67.0 1299 2 US-08-862-903-3 Sequence 3, Appl
c 991 13.4 67.0 1299 2 US-08-862-903-3 Sequence 3, Appl
c 992 13.4 67.0 1299 2 US-08-862-903-3 Sequence 3, Appl
c 993 13.4 67.0 1299 2 US-08-862-903-3 Sequence 3, Appl
c 994 13.4 67.0 1299 2 US-08-862-903-3 Sequence 3, Appl
c 995 13.4 67.0 1299 2 US-08-862-903-3 Sequence 3, Appl
c 996 13.4 67.0 1299 2 US-08-862-903-3 Sequence 3, Appl
c 997 13.4 67.0 1299 2 US-08-862-903-3 Sequence 3, Appl
c 998 13.4 67.0 1299 2 US-08-862-903-3 Sequence 3, Appl
c 999 13.4 67.0 1299 2 US-08-862-903-3 Sequence 3, Appl
c1000 13.4 67.0 1299 2 US-08-862-903-3 Sequence 3, Appl

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## ALIGNMENTS

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RESULT 1
US-09-252-991A-7959
; Sequence 7959, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7959
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7959

Query Match      84.0%; Score 16.8; DB 3; Length 735;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 AGGACGCCAGCAGCTACGA 20
Db      139 AAGACAGCCAGCAGCTACGA 158

RESULT 2
US-09-533-559-3156
; Sequence 3156, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen

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; APPLICANT: Peter Bjørke Olsen
; TITLE OF INVENTION: Methods for Monitoring Multiple Gene
; FILE REFERENCE: 5849,200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3156
; LENGTH: 246
; TYPE: DNA
; ORGANISM: Fusarium venenatum
US-09-533-559-3156

Query Match      82.0%; Score 16.4; DB 3; Length 246;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY      3 GUACAGCCAGCAGCTACGA 20
Db      154 GTACAGCCAGCAGCTACGA 171

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RESULT 3
US-09-270-767-12904
; Sequence 12904, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 12904
; LENGTH: 1564
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-12904

Query Match      80.0%; Score 16; DB 3; Length 1564;
Best Local Similarity 87.5%; Pred. No. 3.3e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY      3 GUACAGCCAGCAGCTAC 18
Db      537 GTACAGCCAGCAGCTAC 552

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RESULT 4
US-09-252-991A-14549/c
; Sequence 14549, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14549
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14549

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Query Match 79.0%; Score 15.8; DB 3; Length 411;  
Best Local Similarity 78.9%; Pred. No. 3.9e+02;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACAGCCGAGGACG 19  
DB 346 AGCTACAGCTGACTACG 328

RESULT 5  
US-09-252-991A-14815  
Sequence 14815, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 14815  
LENGTH: 537  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-14815

Query Match 79.0%; Score 15.8; DB 3; Length 537;  
Best Local Similarity 78.9%; Pred. No. 3.9e+02;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACAGCCGAGGACG 19  
DB 162 AGCTACAGCTGACTACG 180

RESULT 6  
US-09-270-767-11626/C  
Sequence 11626, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 11626  
LENGTH: 576  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
US-09-270-767-11626

Query Match 79.0%; Score 15.8; DB 3; Length 576;  
Best Local Similarity 78.9%; Pred. No. 3.9e+02;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACAGCCGAGGACG 19  
DB 236 AGGATACGCTGACTACG 218

RESULT 7  
US-09-949-016-64679  
Sequence 64679, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
PRIOR FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 64679  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-64679

Query Match 79.0%; Score 15.8; DB 3; Length 601;  
Best Local Similarity 84.2%; Pred. No. 3.9e+02;  
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGACAGCCGAGGACG 20  
DB 442 GGACAGCCGAGGACTAGA 460

RESULT 8  
US-09-949-016-64680  
Sequence 64680, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
PRIOR FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 64680  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-64680

Query Match 79.0%; Score 15.8; DB 3; Length 601;  
Best Local Similarity 84.2%; Pred. No. 3.9e+02;  
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGACAGCCGAGGACG 20  
DB 309 GGACAGCCGAGGACTAGA 327

RESULT 9  
US-09-949-016-64681  
Sequence 64681, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016

;; CURRENT FILING DATE: 2000-04-14  
;; PRIOR APPLICATION NUMBER: 60/241,755  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/237,768  
;; PRIOR FILING DATE: 2000-10-03  
;; PRIOR APPLICATION NUMBER: 60/231,498  
;; PRIOR FILING DATE: 2000-09-08  
;; NUMBER OF SEQ ID NOS: 207012  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 64681  
;; LENGTH: 601  
;; TYPE: DNA  
;; ORGANISM: Human  
US-09-949-016-64681

Query Match 79.0%; Score 15.8; DB 3; Length 601;  
Best Local Similarity 84.2%; Pred. No. 3.9e+02;  
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGACUACGA 20  
DB 118 GGCACAGCCAGACTACGA 136

RESULT 10  
US-09-252-991A-15076  
; Sequence 15076, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 15076  
; LENGTH: 1044  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-15076

Query Match 79.0%; Score 15.8; DB 3; Length 1044;  
Best Local Similarity 78.9%; Pred. No. 4e+02;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUACG 19  
DB 184 AGCTACAGCTTGACACTACG 202

RESULT 11  
US-09-188-930-18  
; Sequence 18, Application US/09188930A  
; Patent No. 6150502  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.  
; APPLICANT: Strachan, Lorna  
; APPLICANT: Sleeman, Matthew  
; APPLICANT: Onrust, Rene  
; APPLICANT: Murison, James Greg  
; TITLE OF INVENTION: Compositions Isolated From Skin Cells  
; FILE REFERENCE: 11000.1011c1  
; CURRENT APPLICATION NUMBER: US/09/188,930A  
; CURRENT FILING DATE: 1998-11-09  
; NUMBER OF SEQ ID NOS: 348  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 18

;; LENGTH: 1057  
;; TYPE: DNA  
;; ORGANISM: Rat  
;; FEATURE:  
;; NAME/KEY: unsure  
;; LOCATION: (45)...(45)  
;; NAME/KEY: unsure  
;; LOCATION: (53)...(53)  
;; NAME/KEY: unsure  
;; LOCATION: (116)...(116)  
;; NAME/KEY: unsure  
;; LOCATION: (118)...(118)  
US-09-188-930-18

Query Match 79.0%; Score 15.8; DB 3; Length 1057;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGACUACGA 20  
DB 1022 GCTACAGCCAGACACGA 1040

RESULT 12  
US-09-312-283C-18  
; Sequence 18, Application US/09312283C  
; Patent No. 6573095  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.  
; APPLICANT: Strachan, Lorna  
; APPLICANT: Sleeman, Matthew  
; APPLICANT: Onrust, Rene  
; APPLICANT: Murison, James G.  
; APPLICANT: Kumble, Krishanand D.  
; TITLE OF INVENTION: Compositions Isolated from Skin Cells  
; FILE REFERENCE: 11000.1011c2  
; CURRENT APPLICATION NUMBER: US/09/312,283C  
; CURRENT FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 425  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 1057  
; TYPE: DNA  
; ORGANISM: Mouse  
US-09-312-283C-18

Query Match 79.0%; Score 15.8; DB 3; Length 1057;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGACUACGA 20  
DB 1022 GCTACAGCCAGACACGA 1040

RESULT 13  
US-09-252-991A-14679/C  
; Sequence 14679, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 14679

LENGTH: 1452  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-14679

Query Match 79.0%; Score 15.8; DB 3; Length 1452;  
Best Local Similarity 78.9%; Pred. No. 4e+02;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACAGCCAGGACTUACG 19  
DB 693 AGCTACAGCCTGACTACG 675

RESULT 14  
US-09-188-930-230  
Sequence 230, Application US/09188930A  
Patent No. 6150502  
GENERAL INFORMATION:  
APPLICANT: Watson, James D.  
APPLICANT: Strachan, Lorna  
APPLICANT: Sleeman, Matthew  
APPLICANT: Onrust, Rene  
APPLICANT: Murison, James Greg  
TITLE OF INVENTION: Compositions Isolated From Skin Cells  
TITLE OF INVENTION: and Methods For Their Use  
FILE REFERENCE: 11000.1011c1  
CURRENT APPLICATION NUMBER: US/09/188,930A  
CURRENT FILING DATE: 1998-11-09  
NUMBER OF SEQ ID NOS: 348  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 230  
LENGTH: 2004  
TYPE: DNA  
ORGANISM: Rat  
US-09-188-930-230

Query Match 79.0%; Score 15.8; DB 3; Length 2004;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGGACTUACG 20  
DB 995 GCTACAGCCAGGACTUACG 1013

RESULT 15  
US-09-312-283C-230  
Sequence 230, Application US/09312283C  
Patent No. 6573095  
GENERAL INFORMATION:  
APPLICANT: Watson, James D.  
APPLICANT: Strachan, Lorna  
APPLICANT: Sleeman, Matthew  
APPLICANT: Onrust, Rene  
APPLICANT: Murison, James G.  
APPLICANT: Kumble, Krishnand D.  
TITLE OF INVENTION: Compositions Isolated from Skin Cells  
TITLE OF INVENTION: and Methods for Their Use  
FILE REFERENCE: 11000.1011c2  
CURRENT APPLICATION NUMBER: US/09/312,283C  
CURRENT FILING DATE: 1999-05-14  
NUMBER OF SEQ ID NOS: 425  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 230  
LENGTH: 2004  
TYPE: DNA  
ORGANISM: Mouse  
US-09-312-283C-230

Query Match 79.0%; Score 15.8; DB 3; Length 2004;  
Best Local Similarity 84.2%; Pred. No. 4e+02;  
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGGACTUACG 20  
DB 995 GCTACAGCCAGGACTUACG 1013

RESULT 16  
US-09-252-991A-14954  
Sequence 14954, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107136.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 14954  
LENGTH: 2550  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-14954

Query Match 79.0%; Score 15.8; DB 3; Length 2550;  
Best Local Similarity 78.9%; Pred. No. 4.1e+02;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACAGCCAGGACTUACG 19  
DB 680 AGCTACAGCCTGACTACG 698

RESULT 17  
US-09-949-016-13629  
Sequence 13629, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13629  
LENGTH: 93894  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(93894)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-13629

Query Match 79.0%; Score 15.8; DB 3; Length 93894;  
Best Local Similarity 84.2%; Pred. No. 4.4e+02;  
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGGACTUACG 20  
DB 80915 GGCACAGCCAGGACTUACG 80933





SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/925,695  
FILING DATE: 19920807  
CLASSIFICATION: 435  
PRIOR APPLICATION: JP 287402/91  
APPLICATION NUMBER: JP 287402/91  
FILING DATE: 09-AUG-1991  
PRIOR APPLICATION DATA: JP 360441/91  
APPLICATION NUMBER: JP 360441/91  
FILING DATE: 05-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Weillacher, Robert G.  
REGISTRATION NUMBER: 20,531  
REFERENCE/DOCKET NUMBER: 06/87-48009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 659-2811  
TELEFAX: (202) 659-1462  
TELEX: WUI 64470  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9511 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-925-695-7

Query Match 77.0%; Score 15.4; DB 3; Length 9511;  
Best Local Similarity 73.7%; Pred. No. 6.4e+02;  
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGGACTUACA 20  
DB 2764 GGTAAAGCCAGGACTUACA 2746

RESULT 22  
US-09-949-016-17037  
Sequence 17037, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 17037  
LENGTH: 260286  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-17037

Query Match 77.0%; Score 15.4; DB 3; Length 260286;  
Best Local Similarity 82.4%; Pred. No. 6.6e+02;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGGACTU 17  
DB 105679 AGGTAGCCAGGACTU 105695

RESULT 23  
US-09-949-016-12106  
Sequence 12106, Application US/09949016

Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12106  
LENGTH: 260293  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-12106

Query Match 77.0%; Score 15.4; DB 3; Length 260293;  
Best Local Similarity 82.4%; Pred. No. 6.6e+02;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGGACTU 17  
DB 105687 AGGTAGCCAGGACTU 105703

RESULT 24  
US-09-252-991A-15084  
Sequence 15084, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 15084  
LENGTH: 546  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-15084

Query Match 76.0%; Score 15.2; DB 3; Length 546;  
Best Local Similarity 80.0%; Pred. No. 7.4e+02;  
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGGACTU 20  
DB 353 AGCTACCGCCAGGACTU 372

RESULT 25  
US-09-105-390-33  
Sequence 33, Application US/09105390  
Patent No. 6288303  
GENERAL INFORMATION:  
APPLICANT: Rodriguez, Raymond  
TITLE OF INVENTION: Rice Beta-Glucanase Enzymes  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESS: Dehlinger & Associates

STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/105,390  
FILING DATE: Filed herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/050,675  
FILING DATE: 25-JUN-97  
ATTORNEY/AGENT INFORMATION:  
NAME: Pelichory, Joanne R.  
REGISTRATION NUMBER: P42,995  
REFERENCE/DOCKET NUMBER: 2000-0455.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 924 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...924  
OTHER INFORMATION:  
US-09-105-390-33

Query Match 76.0%; Score 15.2; DB 3; Length 924;  
Best Local Similarity 85.0%; Pred. No. 7.5e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUACGA 20  
DB 514 AGGACAGCCAGACATCGA 533

RESULT 26  
US-09-270-767-10699/c  
Sequence 10699, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10699  
LENGTH: 987  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
US-09-270-767-10699

Query Match 76.0%; Score 15.2; DB 3; Length 987;  
Best Local Similarity 80.0%; Pred. No. 7.5e+02;  
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUACGA 20  
DB 650 AGGACAGCCAGACATCGA 631

RESULT 27  
US-09-270-767-4796  
Sequence 4796, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4796  
LENGTH: 1029  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
US-09-270-767-4796

Query Match 76.0%; Score 15.2; DB 3; Length 1029;  
Best Local Similarity 80.0%; Pred. No. 7.5e+02;  
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUACGA 20  
DB 114 ATGTACAGCTTGACACGA 133

RESULT 28  
US-09-270-767-20078  
Sequence 20078, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 20078  
LENGTH: 1029  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
US-09-270-767-20078

Query Match 76.0%; Score 15.2; DB 3; Length 1029;  
Best Local Similarity 80.0%; Pred. No. 7.5e+02;  
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUACGA 20  
DB 114 ATGTACAGCTTGACACGA 133

RESULT 29  
US-09-105-390-49  
Sequence 49, Application US/09105390  
Patent No. 6288303  
GENERAL INFORMATION:  
APPLICANT: Rodriguez, Raymond  
TITLE OF INVENTION: Rice Beta-Glucanase Enzymes  
TITLE OF INVENTION: and Genes  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Dehlinger & Associates  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible

```

1  OPERATING SYSTEM: DOS
2  SOFTWARE: PASESEO for Windows Version 2.0
3  CURRENT APPLICATION DATA:
4  APPLICATION NUMBER: US/09/105,390
5  FILING DATE: Filed herewith
6  CLASSIFICATION:
7  PRIORITY APPLICATION DATA:
8  APPLICATION NUMBER: 60/050,675
9  FILING DATE: 25-JUN-97
10 ATTORNEY/AGENT INFORMATION:
11 NAME: Petichory, Joanne R.
12 REGISTRATION NUMBER: P42,995
13 REFERENCE/DOCKET NUMBER: 2000-0455.30
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: 650-324-0880
16 TELEFAX: 650-324-0960
17
18 TELEX:
19
20 INFORMATION FOR SEQ ID NO: 49:
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 1035 base pairs
23 TYPE: nucleic acid
24 STRANDEDNESS: single
25 TOPOLOGY: linear
26
27 FEATURE:
28 NAME/KEY: Coding Sequence
29 LOCATION: 1..1035
30 OTHER INFORMATION:
31
32 US-09-105-390-49

```

Query Match Similarity	76.0%	Score 15.2	DB 3	Length 1035
Best Local Similarity	85.0%	Pred. No. 7.5e+02		
Matches 17, Conservative	0	Mismatches 3	Indels 0	Gaps 0

QY 1 AGGUA CAGCCAGACUACGA 20  
||| ||| ||| ||| ||| |||  
Db 625 AGGACA GCGCAGGACATCGA 644

```

RESULT 30
US-09-252-991A-14826
; Sequence 14826, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ. ID NOS: 31142
; SEQ ID NO 14826
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-14826

```

Query Match	76.0%	Score 15.2;	DB 3;	Length 1521;
Best Local Similarly	80.0%;	Pred. No. 7.6e+02;		
Matches 16;	Conservative 3;	Mismatches 0;	Gaps 0;	

QY 1 AGGUACAGCCAGACUACGA 20  
||:|||||||  
Db 985 AGCTACCGCCAGAGCAGCGA 1004

RESULT 31  
US-09-252-991A-14538/c  
; Sequence 14538, Application US/09252991A  
; Patent No. 6551795

```

: GENERAL INFORMATION:
: APPLICANT: Marc J. Rubenfield et al.
: TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO PSEUDOMONAS
: TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 107196.136
: CURRENT APPLICATION NUMBER: US/09/252,991A
: CURRENT FILING DATE: 1999-02-18
: PRIOR APPLICATION NUMBER: US 60/074,788
: PRIOR FILING DATE: 1998-02-18
: PRIOR APPLICATION NUMBER: US 60/094,190
: PRIOR FILING DATE: 1998-07-27
: NUMBER OF SEQ ID NOS: 33142
: SEQ ID NO 14538
: LENGTH: 1596
: TYPE: DNA
: ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14538

```

Query Match	76.0%	Score 15.2;	DB 3;	Length 1596;
Best Local Similarity	80.0%	Pred. No. 7.6e+02;		
Matches 16; Conservative	1;	Mismatches 3;	Indels 0;	Gaps 0

QY 1 AGGACAGCCAGACUACGA 20  
||:|||||||  
Db 606 AGCTACCGCCAGAGACGA 587

RESULT 32  
US-09-105-390-1

Sequence 4, Application US/03103350  
; Patent No. 6288303  
; GENERAL INFORMATION:

```

;
;  APPLICANT: Rodriguez, Raymond
;  TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
;  TITLE OF INVENTION: and Genes
;  NUMBER OF SEQUENCES: 66
;  CORRESPONDENCE ADDRESS:
;

```

ADDRESS: Delinger & Associates  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA

```

1 COMPUTER READABLE FORM:
2
3 MEDIUM TYPE: Diskette
4
5 COMPUTER: IBM Compatible
6
7 OPERATING SYSTEM: DOS
8
9 SOFTWARE: PARSECQ for Windows Version 2.0
10
11 CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/09/105,350  
FILING DATE: Filed herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/050,675  
FILING DATE: 25-JUN-97  
ATTORNEY/AGENT INFORMATION:

NAME: Peltchory, Joanne R.  
REGISTRATION NUMBER: P42,995  
REFERENCE/DOCKET NUMBER: 2000-0455.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
TELEX:

```

; INFORMATION FOR SEQ ID NO: 1:
;
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 2230 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear

```

Query Match	76.0%;	Score 15.2;	DB 3;	Length 2230;
Best Local Similarity	85.0%;	Pred. No. 7.7e+02;		

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 AGGACAGCCAGGACGACGA 20  
1817 AGGACAGCCAGGACGACGA 1836  
DB

RESULT 33  
US-09-949-016-13044  
; Sequence 13044, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13044  
; LENGTH: 9319  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(9319)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-13044

Query Match 76.0%; Score 15.2; DB 3; Length 9319;  
Best Local Similarity 75.0%; Pred. No. 7.9e+02;  
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGACAGCCAGGACGACGA 20  
DB 8946 AGGACAGCCAGGACGACGA 8965

RESULT 34  
US-09-949-016-14958/C  
; Sequence 14958, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14958  
; LENGTH: 23406  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-14958

Query Match 76.0%; Score 15.2; DB 3; Length 23406;  
Best Local Similarity 80.0%; Pred. No. 8.1e+02;  
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGACAGCCAGGACGACGA 20  
DB 12749 AGGACAGCCAGGACGACGA 12730

RESULT 35  
US-09-949-016-15248  
; Sequence 15248, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15248  
; LENGTH: 28283  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(28283)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-15248

Query Match 76.0%; Score 15.2; DB 3; Length 28283;  
Best Local Similarity 80.0%; Pred. No. 8.1e+02;  
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGACAGCCAGGACGACGA 20  
DB 22011 AGGACAGCCAGGACGACGA 22030

RESULT 36  
US-09-949-016-14213/C  
; Sequence 14213, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14213  
; LENGTH: 30456  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(30456)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14213

Query Match 76.0%; Score 15.2; DB 3; Length 30456;  
Best Local Similarity 75.0%; Pred. No. 8.1e+02;  
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGUACAGCCAGGACTUACA 20  
Db 6160 AGCTCTGCTCCAGGCTTACGA 6141

RESULT 37  
US-09-949-016-15420  
; Sequence 15420, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15420  
; LENGTH: 47375  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURES:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(47375)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-15420

Query Match 76.0%; Score 15.2; DB 3; Length 47375;  
Best Local Similarity 75.0%; Pred. No. 8.2e+02;  
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGUACAGCCAGGACTUACA 20  
Db 2718 AGCTACAGCCAGGCTTACGA 2737

RESULT 38  
US-09-949-016-11995/c  
; Sequence 11995, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11995  
; LENGTH: 60304  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-11995

Query Match 76.0%; Score 15.2; DB 3; Length 60304;

Best Local Similarity 80.0%; Pred. No. 8.2e+02;  
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGUACAGCCAGGACTUACA 20  
Db 12691 AGCTACAGCCAGGACTUACA 12672

RESULT 39  
US-09-949-016-17264/c  
; Sequence 17264, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17264  
; LENGTH: 60304  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-17264

Query Match 76.0%; Score 15.2; DB 3; Length 60304;  
Best Local Similarity 80.0%; Pred. No. 8.2e+02;  
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGGUACAGCCAGGACTUACA 20  
Db 12691 AGCTACAGCCAGGACTUACA 12672

RESULT 40  
US-09-949-016-12361/c  
; Sequence 12361, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12361  
; LENGTH: 69874  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURES:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(69874)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-12361

Query Match 76.0%; Score 15.2; DB 3; Length 69874;  
Best Local Similarity 80.0%; Pred. No. 8.2e+02;

Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 Oy 1 AGGACAGCAGAGCAGCAGCA 20  
 |||||  
 Db 1721 AGGACAGCAGCAGCAGCAGCA 1702

RESULT 41  
 US-09-949-016-13049/c  
 ; Sequence 13049, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CLO01307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 13049  
 ; LENGTH: 69874  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)...(69874)  
 ; OTHER INFORMATION: n = A,T,C or G  
 ; US-09-949-016-13049

Query Match 76.0%; Score 15.2; DB 3; Length 69874;  
 Best Local Similarity 80.0%; Pred. No. 8.2e+02;  
 Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 AGGACAGCAGCAGCAGCAGCA 20  
 |||||  
 Db 1721 AGGACAGCAGCAGCAGCAGCA 1702

RESULT 42  
 US-09-750-580-1/c  
 ; Sequence 1, Application US/09750580  
 ; Patent No. 6453280  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yen, Frances  
 ; APPLICANT: Denison, Blake  
 ; APPLICANT: Bour, Barbara  
 ; APPLICANT: Bihain, Bernard  
 ; APPLICANT: Dumas, Milne Edwards, Jean-Baptiste  
 ; APPLICANT: Duclert, Aymeric  
 ; APPLICANT: Bouguetieret, Lydie  
 ; APPLICANT: Ebbets-Reed, Dana  
 ; APPLICANT: Salter-Cid, Luisa  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITTING NEOPLASTIC CELL GROWTH  
 ; FILE REFERENCE: 89.US2.CIP  
 ; CURRENT APPLICATION NUMBER: US/09/750,580  
 ; CURRENT FILING DATE: 2000-12-28  
 ; PRIOR APPLICATION NUMBER: US 09/599,362  
 ; PRIOR FILING DATE: 2000-06-21  
 ; PRIOR APPLICATION NUMBER: PCT/IB00/0101  
 ; PRIOR FILING DATE: 2000-06-21  
 ; PRIOR APPLICATION NUMBER: PCT/IB99/02058  
 ; PRIOR FILING DATE: 1999-12-20  
 ; PRIOR APPLICATION NUMBER: US 49/469/099  
 ; PRIOR FILING DATE: 1999-12-21  
 ; PRIOR APPLICATION NUMBER: US 60/113,686  
 ; PRIOR FILING DATE: 1998-12-22

PRIOR APPLICATION NUMBER: US 60/141,032  
 PRIOR FILING DATE: 1999-06-25  
 NUMBER OF SEQ ID NOS: 6  
 SOFTWARE: Patent.pm  
 SEQ ID NO 1  
 LENGTH: 81001  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 10946..12946  
 OTHER INFORMATION: 5'regulatory region  
 NAME/KEY: exon  
 LOCATION: 12947..12958  
 OTHER INFORMATION: exon 1  
 NAME/KEY: exon  
 LOCATION: 13470..13526  
 OTHER INFORMATION: exon 2  
 NAME/KEY: exon  
 LOCATION: 13641..13752  
 OTHER INFORMATION: exon 3  
 NAME/KEY: exon  
 LOCATION: 14271..15968  
 OTHER INFORMATION: exon 4  
 NAME/KEY: misc\_feature  
 LOCATION: 15969..17969  
 OTHER INFORMATION: 3'regulatory region  
 NAME/KEY: allele  
 LOCATION: 1239  
 OTHER INFORMATION: 20-828-311 : polymorphic base C or T  
 NAME/KEY: allele  
 LOCATION: 12347  
 OTHER INFORMATION: 17-42-319 : polymorphic base C or T  
 NAME/KEY: allele  
 LOCATION: 15241  
 OTHER INFORMATION: 17-41-250 : polymorphic base C or T  
 NAME/KEY: allele  
 LOCATION: 42218  
 OTHER INFORMATION: 20-841-149 : polymorphic base A or G  
 NAME/KEY: allele  
 LOCATION: 45442  
 OTHER INFORMATION: 20-842-115 : polymorphic base A or G  
 NAME/KEY: allele  
 LOCATION: 77058  
 OTHER INFORMATION: 20-853-415 : polymorphic base C or T  
 NAME/KEY: primer\_bind  
 LOCATION: 929..949  
 OTHER INFORMATION: 20-828.pu  
 NAME/KEY: primer\_bind  
 LOCATION: 1357..1377  
 OTHER INFORMATION: 20-828.rp complement  
 NAME/KEY: primer\_bind  
 LOCATION: 12029..12050  
 OTHER INFORMATION: 17-42.pu  
 NAME/KEY: primer\_bind  
 LOCATION: 12581..12603  
 OTHER INFORMATION: 17-42.rp complement  
 NAME/KEY: primer\_bind  
 LOCATION: 14992..15012  
 OTHER INFORMATION: 17-41.pu  
 NAME/KEY: primer\_bind  
 LOCATION: 15460..15482  
 OTHER INFORMATION: 17-41.rp complement  
 NAME/KEY: primer\_bind  
 LOCATION: 42070..42090  
 OTHER INFORMATION: 20-841.pu  
 NAME/KEY: primer\_bind  
 LOCATION: 42572..42591  
 OTHER INFORMATION: 20-841.rp complement  
 NAME/KEY: primer\_bind  
 LOCATION: 45328..45347  
 OTHER INFORMATION: 20-842.pu  
 NAME/KEY: primer\_bind

```
LOCATION: 45863..45883
OTHER INFORMATION: 20-842..rp complement
NAME/KEY: primer bind
LOCATION: 76644..76664
OTHER INFORMATION: 20-853..pu
NAME/KEY: primer bind
LOCATION: 77166..77185
OTHER INFORMATION: 20-853..rp complement
NAME/KEY: primer bind
LOCATION: 1220..1238
OTHER INFORMATION: 20-828-311.mis
NAME/KEY: primer bind
LOCATION: 1240..1258
OTHER INFORMATION: 20-828-311.mis complement
NAME/KEY: primer bind
LOCATION: 12328..12346
OTHER INFORMATION: 17-42-319.mis
NAME/KEY: primer bind
LOCATION: 12348..12366
OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: primer bind
LOCATION: 15222..15240
OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer bind
LOCATION: 15242..15260
OTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: primer bind
LOCATION: 42199..42217
OTHER INFORMATION: 20-841-149.mis
NAME/KEY: primer bind
LOCATION: 42219..42237
OTHER INFORMATION: 20-841-149.mis complement
NAME/KEY: primer bind
LOCATION: 45423..45441
OTHER INFORMATION: 20-842-115.mis
NAME/KEY: primer bind
LOCATION: 45443..45461
OTHER INFORMATION: 20-842-115.mis complement
NAME/KEY: primer bind
LOCATION: 77039..77057
OTHER INFORMATION: 20-853-415.mis
NAME/KEY: primer bind
LOCATION: 77059..77077
OTHER INFORMATION: 20-853-415.mis complement
NAME/KEY: misc binding
LOCATION: 1227..1251
OTHER INFORMATION: 20-828-311.probe
NAME/KEY: misc binding
LOCATION: 12335..12359
OTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc binding
LOCATION: 15229..15253
OTHER INFORMATION: 17-41-250.probe
NAME/KEY: misc binding
LOCATION: 42206..42230
OTHER INFORMATION: 20-841-149.probe
NAME/KEY: misc binding
LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc binding
LOCATION: 77046..77070
OTHER INFORMATION: 20-853-415.probe
US-09-750-580-1
```

```
Query Match 76.0%; Score 15.2; DB 3; Length 81001;
Best Local Similarity 75.0%; Pred. No. 8.2e+02;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 AGGACAGCCAGGAGCTCAGA 20
DB 65250 AGGTAAGCCAGGAGTAAGA 65231
```

```
RESULT 43
US-09-949-016-14881/c
Sequence 14881, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14881
LENGTH: 146307
TYPE: DNA
ORGANISM: Human
US-09-949-016-14881
```

```
Query Match 76.0%; Score 15.2; DB 3; Length 146307;
Best Local Similarity 80.0%; Pred. No. 8.2e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 AGGACAGCCAGGAGCTCAGA 20
DB 39701 AGGACAGCCAGGAGCTCAGA 39682
```

```
RESULT 44
US-09-949-016-14882/c
Sequence 14882, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14882
LENGTH: 146307
TYPE: DNA
ORGANISM: Human
US-09-949-016-14882
```

```
Query Match 76.0%; Score 15.2; DB 3; Length 146307;
Best Local Similarity 80.0%; Pred. No. 8.2e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 AGGACAGCCAGGAGCTCAGA 20
DB 39701 AGGACAGCCAGGAGCTCAGA 39682
```

```
RESULT 45
US-09-949-016-14883/c
Sequence 14883, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
```



```

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14883
; LENGTH: 146307
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14883

Query Match          76.0%; Score 15.2; DB 3; Length 146307;
Best Local Similarity 80.0%; Pred. No. 8.2e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGACAGCCAGGACTCAGA 20
DB 39701 AGGACAGCCAGGACTCAGA 39682

RESULT 46
US-09-949-016-14884/c
; Sequence 14884, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14884
; LENGTH: 146307
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14884

Query Match          76.0%; Score 15.2; DB 3; Length 146307;
Best Local Similarity 80.0%; Pred. No. 8.2e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGACAGCCAGGACTCAGA 20
DB 39701 AGGACAGCCAGGACTCAGA 39682

RESULT 47
US-09-949-016-14885/c
; Sequence 14885, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
```

```

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14885
; LENGTH: 146307
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14885

Query Match          76.0%; Score 15.2; DB 3; Length 146307;
Best Local Similarity 80.0%; Pred. No. 8.2e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGACAGCCAGGACTCAGA 20
DB 39701 AGGACAGCCAGGACTCAGA 39682

RESULT 48
US-09-949-016-14886/c
; Sequence 14886, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14886
; LENGTH: 146307
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14886

Query Match          76.0%; Score 15.2; DB 3; Length 146307;
Best Local Similarity 80.0%; Pred. No. 8.2e+02;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGACAGCCAGGACTCAGA 20
DB 39701 AGGACAGCCAGGACTCAGA 39682

RESULT 49
US-09-949-016-14887/c
; Sequence 14887, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
```

; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 14887  
; LENGTH: 146307  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-14887

Query Match 76.0%; Score 15.2; DB 3; Length 146307;  
Best Local Similarity 80.0%; Pred. No. 8.2e+02;  
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 AGGACAGCCAGGACTCAGA 20  
Db 39701 AGGACAGCCAGGACTCAGA 39682

RESULT 50  
US-09-949-016-14888/c  
; Sequence 14888, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 14888  
; LENGTH: 146307  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-14888

Query Match 76.0%; Score 15.2; DB 3; Length 146307;  
Best Local Similarity 80.0%; Pred. No. 8.2e+02;  
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 AGGACAGCCAGGACTCAGA 20  
Db 39701 AGGACAGCCAGGACTCAGA 39682

Search completed: March 18, 2006, 18:40:11  
Job time : 103.538 secs

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OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 18:35:47 ; Search time 2395.38 seconds  
(without alignments)  
55.214 Million cell updates/sec

Title: US-10-800-926-3

Perfect score: 20

Sequence: 1 agnagacgcagacacgca 20

Scoring table: IDENTITY NUC

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications NA Main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	US-09-888-326-68	Sequence 68, Appl
2	20	100.0	20	US-09-776-479-391	Sequence 391, Appl
3	20	100.0	20	US-09-776-479-391	Sequence 391, Appl
4	20	100.0	20	US-10-112-653-379	Sequence 379, Appl
5	20	100.0	20	US-10-017-995-391	Sequence 391, Appl
6	20	100.0	20	US-10-314-578-391	Sequence 391, Appl
7	20	100.0	20	US-10-831-778-391	Sequence 391, Appl
8	20	100.0	20	US-10-800-926-3	Sequence 391, Appl
9	18	90.0	20	US-10-152-319A-532	Sequence 532, Appl
10	16.8	84.0	281	US-10-425-115-14343	Sequence 14343, A
11	16.8	84.0	605	US-09-925-065A-693333	Sequence 69333, A
12	16.8	84.0	740	US-09-925-065A-78830	Sequence 78830, A
13	16.8	84.0	145068	US-10-322-281-33	Sequence 33, Appl
14	16.4	82.0	246	US-10-653-047-3156	Sequence 3156, Ap
15	16.4	82.0	586	US-09-925-065A-369463	Sequence 369463, A
16	16.4	82.0	1308	US-10-425-114-8343	Sequence 8343, Ap
17	16.4	82.0	31632	US-10-034-650-1	Sequence 1, Appl
18	16.4	82.0	96599	US-09-997-722-199	Sequence 199, Appl
19	16.4	82.0	168749	US-10-085-117-250	Sequence 250, Appl
20	16	80.0	2550	US-11-097-143-27752	Sequence 27752, A
21	16	80.0	2668	US-11-097-143-21095	Sequence 12095, A
22	16	80.0	4972	US-11-097-143-27751	Sequence 27751, A
23	16	80.0	4989	US-11-097-143-12094	Sequence 12094, A

24	16	80.0	96600	3	US-09-997-722-85	Sequence 85, Appl
25	16	80.0	145597	7	US-10-624-149A-2	Sequence 2, Appl
26	15.8	79.0	364	4	US-09-925-065A-132060	Sequence 132060, A
27	15.8	79.0	533	4	US-09-925-065A-290634	Sequence 290634, A
28	15.8	79.0	533	4	US-09-925-065A-290636	Sequence 290636, A
29	15.8	79.0	542	8	US-10-357-930-15913	Sequence 15913, A
30	15.8	79.0	572	4	US-09-925-065A-813093	Sequence 813093, A
31	15.8	79.0	592	8	US-10-357-930-45741	Sequence 45741, A
32	15.8	79.0	610	7	US-10-767-701-25552	Sequence 25552, A
33	15.8	79.0	678	8	US-10-425-115-59643	Sequence 59643, A
34	15.8	79.0	693	5	US-10-450-753-25544	Sequence 25544, A
35	15.8	79.0	752	5	US-10-027-632-113386	Sequence 113386, A
36	15.8	79.0	752	5	US-10-027-632-113387	Sequence 113387, A
37	15.8	79.0	752	6	US-10-027-632-113386	Sequence 113386, A
38	15.8	79.0	752	6	US-10-027-632-113387	Sequence 113387, A
39	15.8	79.0	978	10	US-11-097-143-33487	Sequence 33487, A
40	15.8	79.0	1023	7	US-10-389-647-172	Sequence 172, Appl
41	15.8	79.0	1057	3	US-09-866-050A-18	Sequence 18, Appl
42	15.8	79.0	1057	5	US-10-152-661-18	Sequence 18, Appl
43	15.8	79.0	1890	3	US-09-866-050A-447	Sequence 447, Appl
44	15.8	79.0	1890	5	US-10-152-661-230	Sequence 230, Appl
45	15.8	79.0	2004	3	US-09-866-050A-230	Sequence 230, Appl
46	15.8	79.0	2407	5	US-10-152-661-230	Sequence 230, Appl
47	15.8	79.0	2407	5	US-10-027-632-101774	Sequence 101774, A
48	15.8	79.0	2412	7	US-10-282-122A-35246	Sequence 35246, A
49	15.8	79.0	2412	7	US-10-282-122A-35246	Sequence 35246, A
50	15.8	79.0	3265	10	US-11-097-143-3448	Sequence 3448, Ap
51	15.8	79.0	15051	10	US-11-097-143-2839	Sequence 2839, Ap
52	15.8	79.0	19183	3	US-09-764-877-2799	Sequence 2799, Ap
53	15.8	79.0	19183	3	US-10-242-515-2799	Sequence 2799, Ap
54	15.4	77.0	301	7	US-10-424-599-66714	Sequence 66714, A
55	15.4	77.0	363	4	US-09-925-065A-173502	Sequence 173502, A
56	15.4	77.0	538	4	US-09-925-065A-90145	Sequence 90145, A
57	15.4	77.0	538	4	US-09-925-065A-90146	Sequence 90146, A
58	15.4	77.0	593	4	US-09-925-065A-135672	Sequence 135672, A
59	15.4	77.0	610	7	US-09-925-065A-768047	Sequence 768047, A
60	15.4	77.0	1265	7	US-10-424-599-26098	Sequence 26098, A
61	15.4	77.0	1286	7	US-10-425-114-10780	Sequence 10780, A
62	15.4	77.0	1353	5	US-10-369-493-10600	Sequence 10600, A
63	15.4	77.0	1367	5	US-10-105-637-2	Sequence 2, Appl
64	15.4	77.0	1367	6	US-10-034-650-44	Sequence 44, Appl
65	15.4	77.0	1515	5	US-10-105-637-6	Sequence 6, Appl
66	15.4	77.0	1515	6	US-10-034-650-48	Sequence 48, Appl
67	15.4	77.0	1837	9	US-10-705-432-2	Sequence 2, Appl
68	15.4	77.0	2111	8	US-10-357-930-22054	Sequence 22054, A
69	15.4	77.0	2111	8	US-10-357-930-27912	Sequence 27912, A
70	15.4	77.0	2129	6	US-10-238-075-420	Sequence 420, Appl
71	15.4	77.0	2208	5	US-10-105-637-5	Sequence 5, Appl
72	15.4	77.0	2208	6	US-10-034-650-47	Sequence 47, Appl
73	15.4	77.0	2208	7	US-10-200-012-5	Sequence 5, Appl
74	15.4	77.0	2755	7	US-10-424-599-60887	Sequence 60887, A
75	15.4	77.0	3504	5	US-10-105-637-3	Sequence 3, Appl
76	15.4	77.0	3504	6	US-10-034-650-45	Sequence 45, Appl
77	15.4	77.0	770	6	US-10-156-761-284	Sequence 284, Appl
78	15.4	77.0	7092	5	US-10-012-608-125	Sequence 125, Appl
79	15.4	77.0	26565	5	US-10-085-959-91	Sequence 91, Appl
80	15.4	77.0	27920	5	US-10-087-192-1339	Sequence 1393, Ap
81	15.4	77.0	28614	5	US-10-087-192-1027	Sequence 1027, Ap
82	15.4	77.0	29956	3	US-09-997-722-229	Sequence 229, Appl
83	15.4	77.0	47322	5	US-10-322-281-507	Sequence 507, Appl
84	15.4	77.0	63720	5	US-10-105-637-4	Sequence 4, Appl
85	15.4	77.0	63720	6	US-10-034-650-46	Sequence 46, Appl
86	15.4	77.0	69515	5	US-10-087-192-1219	Sequence 1219, Ap
87	15.4	77.0	90442	5	US-10-105-637-1	Sequence 1, Appl
88	15.4	77.0	90442	6	US-10-034-650-43	Sequence 43, Appl
89	15.4	77.0	165221	5	US-10-087-192-1015	Sequence 1015, Ap
90	15.4	77.0	173808	5	US-10-003-806-10	Sequence 10, Appl
91	15.4	77.0	433631	5	US-10-087-192-205	Sequence 205, Appl
92	15.4	77.0	3186778	5	US-10-027-632-114961	Sequence 114961, A
93	15.4	77.0	3186778	6	US-10-027-632-114961	Sequence 114961, A
94	15.4	77.0	9025608	6	US-10-156-761-1	Sequence 1, Appl
95	15.2	76.0	393	3	US-09-974-300-2989	Sequence 2989, Ap
96	15.2	76.0	419	8	US-10-357-930-20801	Sequence 20801, A

C 97	15.2	76.0	419	8	US-10-357-930-26646	Sequence 26646, A	C 170	15.2	76.0	5004	10	US-11-097-143-25279	Sequence 25279, A
C 98	15.2	76.0	433	8	US-10-357-930-10437	Sequence 10437, A	C 171	15.2	76.0	6240	10	US-11-097-143-6905	Sequence 6905, A
C 99	15.2	76.0	458	8	US-09-925-065A-591902	Sequence 591902, A	C 172	15.2	76.0	6251	10	US-11-097-143-19175	Sequence 19175, A
C 100	15.2	76.0	468	8	US-10-357-930-31634	Sequence 31634, A	C 173	15.2	76.0	8414	10	US-11-097-143-40570	Sequence 40570, A
C 101	15.2	76.0	468	8	US-10-357-930-40603	Sequence 40603, A	C 174	15.2	76.0	9933	10	US-11-097-143-6804	Sequence 6804, A
C 102	15.2	76.0	476	3	US-09-918-995-30467	Sequence 30467, A	C 175	15.2	76.0	10200	10	US-11-097-143-15174	Sequence 15174, A
C 103	15.2	76.0	487	4	US-09-925-065A-22627	Sequence 22627, A	C 176	15.2	76.0	10397	10	US-11-097-143-18784	Sequence 18784, A
C 104	15.2	76.0	525	4	US-09-925-065A-20701	Sequence 20701, A	C 177	15.2	76.0	14820	9	US-10-893-671-32	Sequence 32, App1
C 105	15.2	76.0	525	4	US-09-925-065A-50283	Sequence 50283, A	C 178	15.2	76.0	14820	9	US-10-893-671-32	Sequence 32, App1
C 106	15.2	76.0	582	4	US-09-925-065A-191670	Sequence 191670, A	C 179	15.2	76.0	21437	7	US-10-322-281-633	Sequence 633, App
C 107	15.2	76.0	598	4	US-09-925-065A-544123	Sequence 544123, A	C 180	15.2	76.0	21996	10	US-10-322-281-8113	Sequence 8113, App
C 108	15.2	76.0	598	4	US-10-779-532-21076	Sequence 21076, A	C 181	15.2	76.0	41061	7	US-10-322-281-302	Sequence 3, App1
C 109	15.2	76.0	600	9	US-10-972-079-61938	Sequence 61938, A	C 182	15.2	76.0	46649	3	US-09-805-456-3	Sequence 3, App1
C 110	15.2	76.0	633	8	US-10-425-115-42292	Sequence 42292, A	C 183	15.2	76.0	46649	3	US-10-679-192-70	Sequence 70, App1
C 111	15.2	76.0	669	7	US-10-437-963-17154	Sequence 17154, A	C 184	15.2	76.0	76410	5	US-10-087-192-70	Sequence 11, App1
C 112	15.2	76.0	692	8	US-10-425-115-24560	Sequence 24560, A	C 185	15.2	76.0	77992	6	US-10-225-810-11	Sequence 647, App
C 113	15.2	76.0	708	5	US-10-027-632-15934	Sequence 15934, A	C 186	15.2	76.0	80557	6	US-10-080-170-647	Sequence 647, App
C 114	15.2	76.0	708	5	US-10-027-632-15934	Sequence 15934, A	C 187	15.2	76.0	80557	6	US-10-080-170-647	Sequence 647, App
C 115	15.2	76.0	733	6	US-10-027-632-249031	Sequence 249031, A	C 188	15.2	76.0	80557	8	US-10-468-356-647	Sequence 1, App1
C 116	15.2	76.0	733	6	US-10-027-632-249031	Sequence 249031, A	C 189	15.2	76.0	81001	3	US-09-751-877-1	Sequence 1, App1
C 117	15.2	76.0	818	8	US-10-425-115-144373	Sequence 144373, A	C 190	15.2	76.0	81001	3	US-09-842-364-1	Sequence 1, App1
C 118	15.2	76.0	839	7	US-10-424-599-95087	Sequence 95087, A	C 191	15.2	76.0	81001	3	US-09-751-877-1	Sequence 1, App1
C 119	15.2	76.0	861	5	US-10-027-632-163526	Sequence 163526, A	C 192	15.2	76.0	81001	3	US-10-121-034-1	Sequence 1, App1
C 120	15.2	76.0	861	6	US-10-027-632-163526	Sequence 163526, A	C 193	15.2	76.0	85435	6	US-10-121-034-1	Sequence 1, App1
C 121	15.2	76.0	908	5	US-10-027-632-163940	Sequence 163940, A	C 194	15.2	76.0	85435	6	US-10-085-117-127	Sequence 1, App1
C 122	15.2	76.0	908	5	US-10-027-632-163941	Sequence 163941, A	C 195	15.2	76.0	87331	5	US-10-087-192-286	Sequence 286, App
C 123	15.2	76.0	908	5	US-10-027-632-163940	Sequence 163940, A	C 196	15.2	76.0	101046	8	US-10-741-601-6689	Sequence 6689, App
C 124	15.2	76.0	908	5	US-10-027-632-163940	Sequence 163940, A	C 197	15.2	76.0	101046	8	US-10-741-601-6689	Sequence 6689, App
C 125	15.2	76.0	908	6	US-10-027-632-163941	Sequence 163941, A	C 198	15.2	76.0	149497	8	US-10-723-860-1744	Sequence 1744, App
C 126	15.2	76.0	908	6	US-10-027-632-163942	Sequence 163942, A	C 199	15.2	76.0	149497	9	US-10-756-149-615	Sequence 615, App
C 127	15.2	76.0	908	6	US-10-027-632-163943	Sequence 163943, A	C 200	15.2	76.0	188977	7	US-10-235-192A-27	Sequence 27, App1
C 128	15.2	76.0	908	6	US-08-886-055-420	Sequence 420, App	C 201	15.2	76.0	250000	6	US-10-067-514-1	Sequence 26, App1
C 129	15.2	76.0	936	3	US-09-804-251-420	Sequence 420, App	C 202	15.2	76.0	1691139	5	US-10-067-514-1	Sequence 1, App1
C 130	15.2	76.0	936	3	US-10-343-650A-517	Sequence 517, App	C 203	15.2	76.0	1691139	7	US-10-419-123-1	Sequence 1, App1
C 131	15.2	76.0	936	7	US-10-819-316-420	Sequence 420, App	C 204	15.2	76.0	1691139	7	US-10-255-120-1	Sequence 1, App1
C 132	15.2	76.0	936	7	US-10-819-316-420	Sequence 420, App	C 205	15.2	76.0	1691139	9	US-10-868-397-1	Sequence 1, App1
C 133	15.2	76.0	942	3	US-09-907-218-9	Sequence 9, App1	C 206	15.2	76.0	1691139	9	US-10-868-397-1	Sequence 1, App1
C 134	15.2	76.0	984	7	US-10-437-963-17153	Sequence 17153, A	C 207	15.2	76.0	902608	6	US-10-156-761-1	Sequence 1, App1
C 135	15.2	76.0	987	6	US-10-156-761-1945	Sequence 1945, App	C 208	15.2	76.0	4775	4	US-09-925-065A-139000	Sequence 439000, A
C 136	15.2	76.0	1125	7	US-10-425-114-14054	Sequence 14054, A	C 209	15.2	76.0	502	8	US-10-425-115-92548	Sequence 92548, A
C 137	15.2	76.0	1149	8	US-10-425-115-109968	Sequence 109968, A	C 210	15.2	76.0	506	4	US-09-925-065A-193457	Sequence 193457, A
C 138	15.2	76.0	1156	8	US-10-425-115-141524	Sequence 141524, A	C 211	15.2	76.0	532	4	US-09-925-065A-161014	Sequence 161014, A
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C 140	15.2	76.0	1307	8	US-10-425-115-55748	Sequence 55748, A	C 213	15.2	76.0	540	6	US-10-029-386-11520	Sequence 361019, A
C 141	15.2	76.0	1336	7	US-10-767-701-11179	Sequence 11179, A	C 214	15.2	76.0	577	4	US-09-925-065A-178453	Sequence 178453, A
C 142	15.2	76.0	1342	7	US-10-427-632-249030	Sequence 249030, A	C 215	15.2	76.0	577	4	US-09-925-065A-361017	Sequence 361017, A
C 143	15.2	76.0	1351	5	US-10-027-632-249030	Sequence 249030, A	C 216	15.2	76.0	638	4	US-09-925-065A-636833	Sequence 636833, A
C 144	15.2	76.0	1371	6	US-11-097-143-29795	Sequence 29795, A	C 217	15.2	76.0	638	4	US-09-925-065A-286697	Sequence 286697, A
C 145	15.2	76.0	1380	10	US-10-369-493-46575	Sequence 46575, A	C 218	15.2	76.0	1025	4	US-09-925-065A-41299	Sequence 41299, A
C 146	15.2	76.0	1401	6	US-11-097-143-10667	Sequence 10667, A	C 219	15.2	76.0	1044	7	US-10-322-281-633	Sequence 633, App
C 147	15.2	76.0	1447	10	US-11-097-143-10667	Sequence 10667, A	C 220	15.2	76.0	1185	4	US-09-925-065A-41299	Sequence 41299, A
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C 149	15.2	76.0	1485	7	US-10-260-238-593	Sequence 593, App	C 222	15.2	76.0	1930	5	US-10-027-632-265379	Sequence 265379, A
C 150	15.2	76.0	1485	7	US-10-260-238-593	Sequence 593, App	C 223	15.2	76.0	1930	5	US-10-027-632-265380	Sequence 265380, A
C 151	15.2	76.0	1612	8	US-10-425-115-14325	Sequence 14325, A	C 224	15.2	76.0	1930	5	US-10-027-632-265381	Sequence 265381, A
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C 155	15.2	76.0	2049	6	US-09-925-065A-15531	Sequence 15531, A	C 228	15.2	76.0	4924	8	US-10-723-860-5043	Sequence 5043, App
C 156	15.2	76.0	2067	6	US-10-017-161-573	Sequence 161, App	C 229	15.2	76.0	4924	8	US-10-723-860-5043	Sequence 5043, App
C 157	15.2	76.0	2153	9	US-10-510-408-60	Sequence 60, App1	C 230	15.2	76.0	5440	3	US-09-764-891-7928	Sequence 7928, App
C 158	15.2	76.0	2218	10	US-11-097-143-25280	Sequence 25280, A	C 231	15.2	76.0	5440	3	US-09-764-891-7928	Sequence 7928, App
C 159	15.2	76.0	2673	3	US-09-815-242-6217	Sequence 6217, App	C 232	15.2	76.0	81684	5	US-10-087-192-145	Sequence 145, App
C 160	15.2	76.0	2673	3	US-09-815-242-6217	Sequence 6217, App	C 233	15.2	76.0	81684	5	US-10-087-192-145	Sequence 145, App
C 161	15.2	76.0	2673	3	US-09-815-242-6217	Sequence 6217, App	C 234	15.2	76.0	81684	5	US-10-087-192-145	Sequence 145, App
C 162	15.2	76.0	2832	10	US-11-097-143-8114	Sequence 8114, App	C 235	15.2	76.0	130427	5	US-10-175-523-87	Sequence 87, App1
C 163	15.2	76.0	3013	10	US-11-097-143-8239	Sequence 8239, App	C 236	15.2	76.0	130427	5	US-10-175-523-87	Sequence 87, App1
C 164	15.2	76.0	3636	10	US-11-097-143-10666	Sequence 10666, App	C 237	15.2	76.0	174424	3	US-09-967-768A-314	Sequence 314, App1
C 165	15.2	76.0	3637	10	US-11-097-143-10666	Sequence 10666, App	C 238	15.2	76.0	174424	3	US-09-967-768A-314	Sequence 314, App1
C 166	15.2	76.0	4181	8	US-10-425-115-109139	Sequence 109139, A	C 239	15.2	76.0	174424	3	US-09-967-768A-314	Sequence 314, App1
C 167	15.2	76.0	4530	10	US-10-425-115-109139	Sequence 109139, A	C 240	15.2	76.0	181343	9	US-10-756-149-2215	Sequence 2215, App
C 168	15.2	76.0	4949	7	US-10-437-963-50966	Sequence 50966, A	C 241	15.2	76.0	181343	9	US-10-756-149-2215	Sequence 2215, App
C 169	15.2	76.0	4949	7	US-10-437-963-50966	Sequence 50966, A	C 242	15.2	76.0	203070	5	US-10-087-192-247	Sequence 247, App

243	14.8	74.0	25	9	US-10-956-157-184260	Sequence 184260,	316	14.8	74.0	637	4	US-09-925-065A-861299	Sequence 861299,
244	14.8	74.0	25	9	US-10-956-157-252781	Sequence 252781,	317	14.8	74.0	650	5	US-10-027-632-142586	Sequence 142586,
245	14.8	74.0	25	9	US-10-956-157-280655	Sequence 280655,	318	14.8	74.0	650	5	US-10-027-632-142587	Sequence 142587,
246	14.8	74.0	25	10	US-11-036-317-170060	Sequence 170060,	319	14.8	74.0	650	6	US-10-027-632-142586	Sequence 142586,
247	14.8	74.0	25	10	US-11-036-317-172245	Sequence 172245,	320	14.8	74.0	650	6	US-10-027-632-142587	Sequence 142587,
248	14.8	74.0	25	10	US-11-036-317-211728	Sequence 211728,	321	14.8	74.0	665	4	US-09-925-065A-486114	Sequence 486114,
249	14.8	74.0	25	10	US-11-036-317-220557	Sequence 220557,	322	14.8	74.0	672	7	US-10-437-963-87539	Sequence 87539,
250	14.8	74.0	25	10	US-11-036-317-691276	Sequence 691276,	323	14.8	74.0	707	3	US-10-487-901-2776	Sequence 2776,
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254	14.8	74.0	225	8	US-10-357-930-35273	Sequence 35273,	327	14.8	74.0	810	9	US-10-952-045-19	Sequence 19,
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256	14.8	74.0	319	8	US-10-357-930-61982	Sequence 61982,	329	14.8	74.0	857	4	US-09-925-065A-93303	Sequence 93303,
257	14.8	74.0	319	8	US-10-357-930-62180	Sequence 62180,	330	14.8	74.0	857	4	US-09-925-065A-93305	Sequence 93304,
258	14.8	74.0	319	8	US-10-357-930-62180	Sequence 62180,	331	14.8	74.0	857	4	US-09-925-065A-93305	Sequence 93304,
259	14.8	74.0	329	7	US-10-242-535A-18318	Sequence 18318,	332	14.8	74.0	957	9	US-10-450-763-12628	Sequence 12628,
260	14.8	74.0	372	6	US-10-085-783A-18318	Sequence 18318,	333	14.8	74.0	978	10	US-11-060-756-3321	Sequence 3321,
261	14.8	74.0	372	6	US-10-002-631C-251	Sequence 251,	334	14.8	74.0	978	10	US-11-060-756-7593	Sequence 7593,
262	14.8	74.0	373	3	US-09-803-719-2350	Sequence 2350,	335	14.8	74.0	1122	8	US-10-877-683-7	Sequence 7,
263	14.8	74.0	373	3	US-10-424-599-93445	Sequence 93445,	336	14.8	74.0	1189	4	US-09-925-065A-727134	Sequence 727134,
264	14.8	74.0	373	3	US-10-779-543-1620	Sequence 15620,	337	14.8	74.0	1291	8	US-10-425-115-73218	Sequence 73218,
265	14.8	74.0	383	6	US-10-007-926A-263	Sequence 263,	338	14.8	74.0	1327	3	US-09-978-295A-170	Sequence 170,
266	14.8	74.0	411	4	US-09-925-065A-440135	Sequence 440135,	339	14.8	74.0	1327	3	US-09-978-697-170	Sequence 170,
267	14.8	74.0	414	7	US-10-767-701-18687	Sequence 18687,	340	14.8	74.0	1327	3	US-09-978-192A-170	Sequence 170,
268	14.8	74.0	432	8	US-10-425-115-2262	Sequence 2262,	341	14.8	74.0	1327	3	US-09-999-832A-170	Sequence 170,
269	14.8	74.0	447	7	US-10-085-783A-27992	Sequence 27992,	342	14.8	74.0	1327	3	US-09-978-189-170	Sequence 170,
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272	14.8	74.0	453	9	US-09-960-352-9344	Sequence 9344,	345	14.8	74.0	1327	3	US-09-978-191A-170	Sequence 170,
273	14.8	74.0	470	9	US-10-450-763-21554	Sequence 21554,	346	14.8	74.0	1327	3	US-09-978-403A-170	Sequence 170,
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275	14.8	74.0	498	3	US-09-918-995-32318	Sequence 32318,	348	14.8	74.0	1327	3	US-09-999-833A-170	Sequence 170,
276	14.8	74.0	500	5	US-10-027-632-287423	Sequence 287423,	349	14.8	74.0	1327	3	US-09-981-915A-170	Sequence 170,
277	14.8	74.0	500	5	US-10-027-632-287424	Sequence 287424,	350	14.8	74.0	1327	3	US-09-981-915A-170	Sequence 170,
278	14.8	74.0	500	5	US-10-027-632-287425	Sequence 287425,	351	14.8	74.0	1327	3	US-09-978-824-170	Sequence 170,
279	14.8	74.0	500	5	US-10-027-632-287426	Sequence 287426,	352	14.8	74.0	1327	3	US-09-998-585A-170	Sequence 170,
280	14.8	74.0	500	6	US-10-027-632-287423	Sequence 287423,	353	14.8	74.0	1327	3	US-09-998-834A-170	Sequence 170,
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283	14.8	74.0	500	6	US-10-027-632-287426	Sequence 287426,	356	14.8	74.0	1327	3	US-09-999-830A-170	Sequence 170,
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285	14.8	74.0	503	4	US-09-925-065A-454207	Sequence 454207,	358	14.8	74.0	1327	3	US-09-978-187A-170	Sequence 170,
286	14.8	74.0	513	4	US-09-925-065A-440046	Sequence 440046,	359	14.8	74.0	1327	3	US-09-978-643A-170	Sequence 170,
287	14.8	74.0	527	5	US-10-198-846-9543	Sequence 9543,	360	14.8	74.0	1327	3	US-09-978-355A-170	Sequence 170,
288	14.8	74.0	527	7	US-10-767-701-23977	Sequence 23977,	361	14.8	74.0	1327	3	US-09-978-298A-170	Sequence 170,
289	14.8	74.0	537	4	US-09-925-065A-197434	Sequence 197434,	362	14.8	74.0	1327	3	US-09-978-188A-170	Sequence 170,
290	14.8	74.0	553	4	US-09-925-065A-611690	Sequence 611690,	363	14.8	74.0	1327	3	US-09-978-681A-170	Sequence 170,
291	14.8	74.0	554	4	US-09-925-065A-955304	Sequence 955304,	364	14.8	74.0	1327	3	US-09-999-829A-170	Sequence 170,
292	14.8	74.0	562	4	US-09-925-065A-954327	Sequence 954327,	365	14.8	74.0	1327	3	US-09-978-299A-170	Sequence 170,
293	14.8	74.0	565	6	US-10-027-632-322186	Sequence 322186,	366	14.8	74.0	1327	3	US-09-978-544A-170	Sequence 170,
294	14.8	74.0	565	6	US-10-027-632-322186	Sequence 322186,	367	14.8	74.0	1327	3	US-09-978-665A-170	Sequence 170,
295	14.8	74.0	567	7	US-10-767-701-24257	Sequence 24257,	368	14.8	74.0	1327	3	US-09-978-802A-170	Sequence 170,
296	14.8	74.0	581	4	US-09-925-065A-339158	Sequence 339158,	369	14.8	74.0	1327	3	US-09-999-831A-170	Sequence 170,
297	14.8	74.0	583	4	US-09-925-065A-307355	Sequence 307355,	370	14.8	74.0	1327	5	US-09-978-824-170	Sequence 170,
298	14.8	74.0	583	4	US-09-925-065A-307356	Sequence 307356,	371	14.8	74.0	1327	5	US-10-017-081A-170	Sequence 170,
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300	14.8	74.0	583	4	US-09-925-065A-307358	Sequence 307358,	373	14.8	74.0	1327	5	US-10-013-921A-170	Sequence 170,
301	14.8	74.0	584	3	US-09-777-566A-1627	Sequence 1627,	374	14.8	74.0	1327	5	US-10-013-929A-170	Sequence 170,
302	14.8	74.0	584	5	US-10-015-219-1627	Sequence 1627,	375	14.8	74.0	1327	5	US-10-016-177A-170	Sequence 170,
303	14.8	74.0	589	5	US-10-027-632-41685	Sequence 41685,	376	14.8	74.0	1327	5	US-10-166-709A-170	Sequence 170,
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305	14.8	74.0	600	9	US-10-956-157-7858	Sequence 7858,	378	14.8	74.0	1327	6	US-10-143-031A-170	Sequence 170,
306	14.8	74.0	607	4	US-09-925-065A-802169	Sequence 802169,	379	14.8	74.0	1327	6	US-10-143-030A-170	Sequence 170,
307	14.8	74.0	612	5	US-10-027-632-72616	Sequence 72616,	380	14.8	74.0	1327	6	US-10-017-088A-170	Sequence 170,
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312	14.8	74.0	612	6	US-10-027-632-312759	Sequence 312759,	385	14.8	74.0	1327	6	US-10-143-029A-170	Sequence 170,
313	14.8	74.0	615	6	US-09-925-065A-748996	Sequence 748996,	386	14.8	74.0	1327	6	US-10-145-089A-170	Sequence 170,
314	14.8	74.0	616	4	US-09-925-065A-751234	Sequence 751234,	387	14.8	74.0	1327	6	US-10-165-067A-170	Sequence 170,
315	14.8	74.0	622	4	US-09-925-065A-602820	Sequence 602820,	388	14.8	74.0	1327	6	US-10-145-017A-170	Sequence 170,

389	14.8	74.0	1327	6	US-10-013-926A-170	Sequence 170, App	C 462	14.8	74.0	2238	8	US-10-489-372-50	Sequence 50, Appl
390	14.8	74.0	1327	6	US-10-165-247A-170	Sequence 170, App	463	14.8	74.0	2283	7	US-10-437-963-47732	Sequence 47732, A
391	14.8	74.0	1327	6	US-10-145-124A-170	Sequence 170, App	464	14.8	74.0	2356	7	US-10-302-172-54	Sequence 54, Appl
392	14.8	74.0	1327	6	US-10-160-502A-170	Sequence 170, App	465	14.8	74.0	2409	3	US-09-888-615-54	Sequence 54, Appl
393	14.8	74.0	1327	6	US-10-145-087A-170	Sequence 170, App	466	14.8	74.0	2587	10	US-11-097-191-9	Sequence 16721, A
394	14.8	74.0	1327	6	US-10-017-086A-170	Sequence 170, App	467	14.8	74.0	2672	1	US-09-776-191-9	Sequence 9, Appl
395	14.8	74.0	1327	6	US-10-164-829A-170	Sequence 170, App	468	14.8	74.0	2672	6	US-10-156-214A-9	Sequence 9, Appl
396	14.8	74.0	1327	6	US-10-164-929A-170	Sequence 170, App	469	14.8	74.0	2706	6	US-10-369-493-42251	Sequence 42251, A
397	14.8	74.0	1327	6	US-10-013-922A-170	Sequence 170, App	470	14.8	74.0	2913	6	US-10-437-963-77151	Sequence 77151, A
398	14.8	74.0	1327	6	US-10-020-445A-170	Sequence 170, App	471	14.8	74.0	2981	6	US-10-104-047-319	Sequence 319, Appl
399	14.8	74.0	1327	6	US-10-013-924A-170	Sequence 170, App	C 472	14.8	74.0	3042	3	US-09-774-434-5	Sequence 5, Appl
400	14.8	74.0	1327	6	US-10-017-086A-170	Sequence 170, App	473	14.8	74.0	3104	3	US-09-776-191-7	Sequence 7, Appl
401	14.8	74.0	1327	6	US-10-145-016A-170	Sequence 170, App	474	14.8	74.0	3104	6	US-10-156-214A-7	Sequence 7, Appl
402	14.8	74.0	1327	6	US-10-145-088A-170	Sequence 170, App	475	14.8	74.0	3143	3	US-09-978-295A-168	Sequence 168, App
403	14.8	74.0	1327	6	US-10-145-092A-170	Sequence 170, App	476	14.8	74.0	3143	3	US-09-978-697-168	Sequence 168, App
404	14.8	74.0	1327	6	US-10-145-129A-170	Sequence 170, App	477	14.8	74.0	3143	3	US-09-978-192A-168	Sequence 168, App
405	14.8	74.0	1327	6	US-10-165-038A-170	Sequence 170, App	478	14.8	74.0	3143	3	US-09-999-832A-168	Sequence 168, App
406	14.8	74.0	1327	6	US-10-165-353A-170	Sequence 170, App	479	14.8	74.0	3143	3	US-09-978-189-168	Sequence 168, App
407	14.8	74.0	1327	6	US-10-167-600-170	Sequence 170, App	480	14.8	74.0	3143	3	US-09-978-608A-168	Sequence 168, App
408	14.8	74.0	1327	6	US-10-170-481A-170	Sequence 170, App	481	14.8	74.0	3143	3	US-09-978-585A-168	Sequence 168, App
409	14.8	74.0	1327	6	US-10-172-039A-170	Sequence 170, App	482	14.8	74.0	3143	3	US-09-978-191A-168	Sequence 168, App
410	14.8	74.0	1327	6	US-10-210-028-170	Sequence 170, App	483	14.8	74.0	3143	3	US-09-978-403A-168	Sequence 168, App
411	14.8	74.0	1327	6	US-10-017-085A-170	Sequence 170, App	484	14.8	74.0	3143	3	US-09-978-564A-168	Sequence 168, App
412	14.8	74.0	1327	6	US-10-013-916A-170	Sequence 170, App	485	14.8	74.0	3143	3	US-09-999-833A-168	Sequence 168, App
413	14.8	74.0	1327	6	US-10-143-026B-170	Sequence 170, App	486	14.8	74.0	3143	3	US-09-981-915A-168	Sequence 168, App
414	14.8	74.0	1327	6	US-10-013-918A-170	Sequence 170, App	487	14.8	74.0	3143	3	US-09-978-824-168	Sequence 168, App
415	14.8	74.0	1327	6	US-10-162-521A-170	Sequence 170, App	488	14.8	74.0	3143	3	US-09-918-585A-168	Sequence 168, App
416	14.8	74.0	1327	6	US-10-013-928A-170	Sequence 170, App	489	14.8	74.0	3143	3	US-09-999-834A-168	Sequence 168, App
417	14.8	74.0	1327	6	US-10-162-522A-170	Sequence 170, App	490	14.8	74.0	3143	3	US-09-978-433A-168	Sequence 168, App
418	14.8	74.0	1327	6	US-10-013-925A-170	Sequence 170, App	491	14.8	74.0	3143	3	US-09-978-133A-168	Sequence 168, App
419	14.8	74.0	1327	6	US-10-013-925A-170	Sequence 170, App	492	14.8	74.0	3143	3	US-09-999-830A-168	Sequence 168, App
420	14.8	74.0	1327	6	US-10-145-093A-170	Sequence 170, App	493	14.8	74.0	3143	3	US-09-978-757A-168	Sequence 168, App
421	14.8	74.0	1327	6	US-10-013-919A-170	Sequence 170, App	494	14.8	74.0	3143	3	US-09-978-187B-168	Sequence 168, App
422	14.8	74.0	1327	6	US-10-013-920A-170	Sequence 170, App	495	14.8	74.0	3143	3	US-09-978-643A-168	Sequence 168, App
423	14.8	74.0	1327	7	US-10-164-749A-170	Sequence 170, App	496	14.8	74.0	3143	3	US-09-978-375A-168	Sequence 168, App
424	14.8	74.0	1327	7	US-10-013-917A-170	Sequence 170, App	497	14.8	74.0	3143	3	US-09-978-288A-168	Sequence 168, App
425	14.8	74.0	1327	8	US-10-152-388B-170	Sequence 170, App	498	14.8	74.0	3143	3	US-09-978-188A-168	Sequence 168, App
426	14.8	74.0	1327	8	US-10-918-851-170	Sequence 170, App	499	14.8	74.0	3143	3	US-09-978-681A-168	Sequence 168, App
427	14.8	74.0	1327	8	US-10-805-667-170	Sequence 170, App	500	14.8	74.0	3143	3	US-09-999-829A-168	Sequence 168, App
428	14.8	74.0	1327	8	US-10-897-359-170	Sequence 170, App	501	14.8	74.0	3143	3	US-09-978-299A-168	Sequence 168, App
429	14.8	74.0	1327	8	US-10-893-802-170	Sequence 170, App	502	14.8	74.0	3143	3	US-09-978-544A-168	Sequence 168, App
430	14.8	74.0	1327	9	US-10-897-360-170	Sequence 170, App	503	14.8	74.0	3143	3	US-09-978-662A-168	Sequence 168, App
431	14.8	74.0	1327	9	US-10-165-036A-170	Sequence 170, App	504	14.8	74.0	3143	3	US-09-978-607A-168	Sequence 168, App
432	14.8	74.0	1327	9	US-10-165-036A-170	Sequence 170, App	505	14.8	74.0	3143	3	US-09-999-831A-168	Sequence 168, App
433	14.8	74.0	1327	10	US-11-129-762-170	Sequence 170, App	506	14.8	74.0	3143	3	US-09-978-824-168	Sequence 168, App
434	14.8	74.0	1356	8	US-10-357-930-258A1	Sequence 258A1, A	507	14.8	74.0	3143	3	US-10-017-081A-168	Sequence 168, App
435	14.8	74.0	1365	3	US-09-815-242-415A	Sequence 415A, Ap	508	14.8	74.0	3143	5	US-10-167-749-168	Sequence 168, App
436	14.8	74.0	1365	7	US-10-282-122A-7295	Sequence 7295, Ap	509	14.8	74.0	3143	5	US-10-013-921A-168	Sequence 168, App
437	14.8	74.0	1377	5	US-10-450-763-18993	Sequence 18993, A	510	14.8	74.0	3143	5	US-10-013-929A-168	Sequence 168, App
438	14.8	74.0	1386	9	US-10-044-090-684	Sequence 684, App	511	14.8	74.0	3143	5	US-10-016-127A-168	Sequence 168, App
439	14.8	74.0	1393	9	US-10-956-157-2623	Sequence 2623, Ap	512	14.8	74.0	3143	5	US-10-166-709A-168	Sequence 168, App
440	14.8	74.0	1400	9	US-10-956-157-5891	Sequence 5891, Ap	513	14.8	74.0	3143	6	US-10-143-031A-168	Sequence 168, App
441	14.8	74.0	1400	9	US-10-956-157-6144	Sequence 6144, Ap	514	14.8	74.0	3143	6	US-10-143-030A-168	Sequence 168, App
442	14.8	74.0	1400	9	US-10-956-157-6144	Sequence 6144, Ap	515	14.8	74.0	3143	6	US-10-002-967A-168	Sequence 168, App
443	14.8	74.0	1400	9	US-10-956-157-10090	Sequence 10090, A	516	14.8	74.0	3143	6	US-10-017-083A-168	Sequence 168, App
444	14.8	74.0	1665	7	US-10-282-122A-13A57	Sequence 13A57, A	517	14.8	74.0	3143	6	US-10-145-128A-168	Sequence 168, App
445	14.8	74.0	1803	3	US-10-467-434-25	Sequence 25, Appl	518	14.8	74.0	3143	6	US-10-017-191A-168	Sequence 168, App
446	14.8	74.0	1803	3	US-10-369-493-11120	Sequence 21929, A	519	14.8	74.0	3143	6	US-10-143-028A-168	Sequence 168, App
447	14.8	74.0	1899	6	US-10-369-493-11120	Sequence 31120, A	520	14.8	74.0	3143	6	US-10-143-028A-168	Sequence 168, App
448	14.8	74.0	2048	3	US-09-823-245A-356	Sequence 356, App	521	14.8	74.0	3143	6	US-10-145-089A-168	Sequence 168, App
449	14.8	74.0	2056	6	US-10-007-926A-264	Sequence 264, App	522	14.8	74.0	3143	6	US-10-145-067A-168	Sequence 168, App
450	14.8	74.0	2056	6	US-10-257-021-19	Sequence 19, Appl	523	14.8	74.0	3143	6	US-10-145-017A-168	Sequence 168, App
451	14.8	74.0	2056	6	US-10-956-157-909	Sequence 909, App	524	14.8	74.0	3143	6	US-10-013-926A-168	Sequence 168, App
452	14.8	74.0	2068	7	US-10-291-172-24	Sequence 24, Appl	525	14.8	74.0	3143	6	US-10-145-247A-168	Sequence 168, App
453	14.8	74.0	2079	6	US-10-291-172-23	Sequence 23, Appl	526	14.8	74.0	3143	6	US-10-145-124A-168	Sequence 168, App
454	14.8	74.0	2079	7	US-10-221-278-23	Sequence 23, Appl	527	14.8	74.0	3143	6	US-10-165-077A-168	Sequence 168, App
455	14.8	74.0	2079	7	US-10-369-493-28361	Sequence 28361, A	528	14.8	74.0	3143	6	US-10-160-502A-168	Sequence 168, App
456	14.8	74.0	2095	5	US-10-044-090-665	Sequence 665, App	529	14.8	74.0	3143	6	US-10-145-087A-168	Sequence 168, App
457	14.8	74.0	2098	6	US-10-291-172-25	Sequence 25, Appl	530	14.8	74.0	3143	6	US-10-017-086A-168	Sequence 168, App
458	14.8	74.0	2098	7	US-10-221-278-25	Sequence 25, Appl	531	14.8	74.0	3143	6	US-10-164-829A-168	Sequence 168, App
459	14.8	74.0	2120	6	US-10-119-428-26	Sequence 26, Appl	532	14.8	74.0	3143	6	US-10-164-929A-168	Sequence 168, App
460	14.8	74.0	2129	6	US-10-119-428-25	Sequence 25, Appl	533	14.8	74.0	3143	6	US-10-013-922A-168	Sequence 168, App
461	14.8	74.0	2150	6	US-10-119-428-27	Sequence 27, Appl	534	14.8	74.0	3143	6	US-10-013-922A-168	Sequence 168, App



535	14.8	74.0	3143	6	US-10-020-445A-168	Sequence 168, App	c 608	14.8	74.0	79256	7	US-10-332-281-167	Sequence 167, App
536	14.8	74.0	3143	6	US-10-013-924A-168	Sequence 168, App	c 609	14.8	74.0	88576	6	US-10-085-117-319	Sequence 319, App
537	14.8	74.0	3143	6	US-10-017-084A-168	Sequence 168, App	c 610	14.8	74.0	96389	3	US-10-052-482-181	Sequence 181, App
538	14.8	74.0	3143	6	US-10-145-016A-168	Sequence 168, App	c 611	14.8	74.0	96593	3	US-09-997-722-151	Sequence 151, App
539	14.8	74.0	3143	6	US-10-145-088A-168	Sequence 168, App	c 612	14.8	74.0	104062	5	US-10-087-192-916	Sequence 916, App
540	14.8	74.0	3143	6	US-10-145-095A-168	Sequence 168, App	c 613	14.8	74.0	105305	5	US-10-087-192-916	Sequence 1369, App
541	14.8	74.0	3143	6	US-10-145-129A-168	Sequence 168, App	c 614	14.8	74.0	107303	7	US-10-332-281-149	Sequence 249, App
542	14.8	74.0	3143	6	US-10-165-038A-168	Sequence 168, App	c 615	14.8	74.0	114793	6	US-10-148-806-3	Sequence 3, App11
543	14.8	74.0	3143	6	US-10-165-353A-168	Sequence 168, App	c 616	14.8	74.0	117793	6	US-10-859-792-3	Sequence 3, App11
544	14.8	74.0	3143	6	US-10-167-600-168	Sequence 168, App	c 617	14.8	74.0	117328	9	US-10-461-882-127	Sequence 127, App
545	14.8	74.0	3143	6	US-10-170-481A-168	Sequence 168, App	c 618	14.8	74.0	121128	9	US-10-332-281-587	Sequence 127, App
546	14.8	74.0	3143	6	US-10-172-039A-168	Sequence 168, App	c 619	14.8	74.0	141463	5	US-10-087-192-82	Sequence 22, App1
547	14.8	74.0	3143	6	US-10-210-028-168	Sequence 168, App	c 620	14.8	74.0	165961	6	US-10-085-117-741	Sequence 22, App1
548	14.8	74.0	3143	6	US-10-017-085A-168	Sequence 168, App	c 621	14.8	74.0	165961	5	US-10-087-192-955	Sequence 955, App
549	14.8	74.0	3143	6	US-10-013-916A-168	Sequence 168, App	c 622	14.8	74.0	166047	7	US-10-332-281-305	Sequence 305, App
550	14.8	74.0	3143	6	US-10-143-028B-168	Sequence 168, App	c 623	14.8	74.0	191597	8	US-10-719-993-8802	Sequence 8802, App
551	14.8	74.0	3143	6	US-10-013-918A-168	Sequence 168, App	c 624	14.8	74.0	240001	6	US-10-936-273-32	Sequence 32, App1
552	14.8	74.0	3143	6	US-10-162-521A-168	Sequence 168, App	c 625	14.8	74.0	744802	9	US-10-292-798-1369	Sequence 1369, App
553	14.8	74.0	3143	6	US-10-013-928A-168	Sequence 168, App	c 626	14.8	74.0	3186778	5	US-10-027-632-17961	Sequence 174961, App
554	14.8	74.0	3143	6	US-10-162-522A-168	Sequence 168, App	c 627	14.8	74.0	3186778	7	US-10-027-632-17961	Sequence 174961, App
555	14.8	74.0	3143	6	US-10-013-923A-168	Sequence 168, App	c 628	14.8	74.0	72.0	25	US-10-719-956-176532	Sequence 276532, App
556	14.8	74.0	3143	6	US-10-013-925A-168	Sequence 168, App	c 629	14.8	74.0	72.0	25	US-10-719-956-482311	Sequence 482311, App
557	14.8	74.0	3143	6	US-10-013-927A-168	Sequence 168, App	c 630	14.8	74.0	72.0	25	US-10-719-956-482311	Sequence 482311, App
558	14.8	74.0	3143	6	US-10-145-093A-168	Sequence 168, App	c 631	14.8	74.0	72.0	25	US-10-719-956-482311	Sequence 482311, App
559	14.8	74.0	3143	6	US-10-013-919A-168	Sequence 168, App	c 632	14.8	74.0	72.0	25	US-10-349-143-15	Sequence 145119, App
560	14.8	74.0	3143	7	US-10-013-920A-168	Sequence 168, App	c 633	14.8	74.0	72.0	215	US-09-933-797-584	Sequence 364, App1
561	14.8	74.0	3143	7	US-10-164-749A-168	Sequence 168, App	c 634	14.8	74.0	72.0	287	US-10-027-632-54948	Sequence 54948, App
562	14.8	74.0	3143	7	US-10-013-917A-168	Sequence 168, App	c 635	14.8	74.0	72.0	287	US-10-027-632-54948	Sequence 54948, App
563	14.8	74.0	3143	8	US-10-152-388B-168	Sequence 168, App	c 636	14.8	74.0	72.0	313	US-09-867-550-975	Sequence 975, App
564	14.8	74.0	3143	8	US-10-918-851-168	Sequence 168, App	c 637	14.8	74.0	72.0	319	US-10-425-115-13770	Sequence 135326, App
565	14.8	74.0	3143	8	US-10-805-667-168	Sequence 168, App	c 638	14.8	74.0	72.0	345	US-10-424-599-135526	Sequence 135526, App
566	14.8	74.0	3143	9	US-10-897-359-168	Sequence 168, App	c 639	14.8	74.0	72.0	360	US-09-864-408A-7183	Sequence 7183, App
567	14.8	74.0	3143	9	US-10-893-802-168	Sequence 168, App	c 640	14.8	74.0	72.0	360	US-09-925-065A-502200	Sequence 502200, App
568	14.8	74.0	3143	9	US-10-897-350-168	Sequence 168, App	c 641	14.8	74.0	72.0	436	US-10-857-294-313	Sequence 313, App
569	14.8	74.0	3143	9	US-10-165-036A-168	Sequence 168, App	c 642	14.8	74.0	72.0	436	US-09-867-701-7108	Sequence 7108, App
570	14.8	74.0	3143	10	US-11-129-762-168	Sequence 168, App	c 643	14.8	74.0	72.0	443	US-09-728-446-278	Sequence 278, App
571	14.8	74.0	3191	9	US-10-050-882-11	Sequence 11, App1	c 644	14.8	74.0	72.0	466	US-10-972-079-50596	Sequence 50596, App
572	14.8	74.0	3191	9	US-10-963-903-11	Sequence 11, App1	c 645	14.8	74.0	72.0	474	US-09-815-242-7821	Sequence 7821, App
573	14.8	74.0	3213	9	US-10-450-763-16155	Sequence 16155, App	c 646	14.8	74.0	72.0	498	US-11-097-143-5084	Sequence 5084, App
574	14.8	74.0	3410	3	US-09-823-245A-158	Sequence 158, App	c 647	14.8	74.0	72.0	509	US-10-702-075-941	Sequence 941, App1
575	14.8	74.0	3410	3	US-09-823-245A-158	Sequence 158, App	c 648	14.8	74.0	72.0	513	US-09-997-807-3	Sequence 3, App11
576	14.8	74.0	3410	3	US-09-823-245A-158	Sequence 158, App	c 649	14.8	74.0	72.0	513	US-10-370-370-3	Sequence 3, App11
577	14.8	74.0	3510	9	US-10-051-835-13	Sequence 13, App1	c 650	14.8	74.0	72.0	513	US-11-046-203-3	Sequence 3, App11
578	14.8	74.0	3570	6	US-10-956-157-4855	Sequence 157, App	c 651	14.8	74.0	72.0	514	US-09-925-065A-424597	Sequence 424597, App
579	14.8	74.0	3704	10	US-11-087-143-10183	Sequence 10183, App	c 652	14.8	74.0	72.0	519	US-10-925-065A-424597	Sequence 424597, App
580	14.8	74.0	3727	9	US-10-489-740-106	Sequence 106, App	c 653	14.8	74.0	72.0	574	US-10-972-079-50595	Sequence 50595, App
581	14.8	74.0	3727	9	US-10-956-157-656	Sequence 157, App	c 654	14.8	74.0	72.0	587	US-10-925-065A-288830	Sequence 288830, App
582	14.8	74.0	3734	3	US-09-814-353-20516	Sequence 20516, App	c 655	14.8	74.0	72.0	591	US-10-027-632-179660	Sequence 179660, App
583	14.8	74.0	3773	5	US-10-198-846-13361	Sequence 13361, App	c 656	14.8	74.0	72.0	593	US-09-925-065A-478143	Sequence 478143, App
584	14.8	74.0	3902	5	US-10-044-090-451	Sequence 451, App	c 657	14.8	74.0	72.0	593	US-09-925-065A-478143	Sequence 478143, App
585	14.8	74.0	3902	5	US-10-044-090-451	Sequence 451, App	c 658	14.8	74.0	72.0	610	US-09-925-065A-206702	Sequence 206702, App
586	14.8	74.0	4176	8	US-10-877-683-5	Sequence 260, App	c 659	14.8	74.0	72.0	610	US-09-925-065A-206702	Sequence 206702, App
587	14.8	74.0	4293	10	US-11-097-143-19082	Sequence 19082, App	c 660	14.8	74.0	72.0	612	US-09-925-065A-206704	Sequence 206704, App
588	14.8	74.0	4395	10	US-10-198-846-13574	Sequence 13574, App	c 661	14.8	74.0	72.0	612	US-09-925-065A-759912	Sequence 759912, App
589	14.8	74.0	4946	6	US-10-148-806-1	Sequence 1, App1	c 662	14.8	74.0	72.0	615	US-09-925-065A-653748	Sequence 653748, App
590	14.8	74.0	4946	6	US-10-388-350-371	Sequence 371, App	c 663	14.8	74.0	72.0	615	US-09-925-065A-653748	Sequence 653748, App
591	14.8	74.0	4946	6	US-10-859-792-1	Sequence 1, App1	c 664	14.8	74.0	72.0	615	US-09-925-065A-947517	Sequence 947517, App
592	14.8	74.0	4946	6	US-10-859-792-1	Sequence 1, App1	c 665	14.8	74.0	72.0	618	US-09-925-065A-947517	Sequence 947517, App
593	14.8	74.0	6034	10	US-11-097-143-16720	Sequence 16720, App	c 666	14.8	74.0	72.0	621	US-09-925-065A-946058	Sequence 946058, App
594	14.8	74.0	6663	3	US-09-037-657-28	Sequence 28, App1	c 667	14.8	74.0	72.0	624	US-10-425-115-140482	Sequence 140482, App
595	14.8	74.0	6663	3	US-11-097-143-19081	Sequence 19081, App	c 668	14.8	74.0	72.0	629	US-09-925-065A-518708	Sequence 518708, App
596	14.8	74.0	10925	10	US-11-097-143-38644	Sequence 38644, App	c 669	14.8	74.0	72.0	631	US-10-027-632-692	Sequence 692, App
597	14.8	74.0	11832	3	US-09-037-657-38	Sequence 38, App1	c 670	14.8	74.0	72.0	631	US-10-027-632-693	Sequence 693, App
598	14.8	74.0	21779	6	US-10-085-117-175	Sequence 175, App	c 671	14.8	74.0	72.0	631	US-10-027-632-694	Sequence 694, App
599	14.8	74.0	21898	6	US-10-034-650-7	Sequence 7, App1	c 672	14.8	74.0	72.0	631	US-10-027-632-695	Sequence 695, App
600	14.8	74.0	31703	6	US-10-085-117-172	Sequence 172, App	c 673	14.8	74.0	72.0	631	US-10-027-632-692	Sequence 692, App
601	14.8	74.0	33097	7	US-10-087-192-241	Sequence 241, App	c 674	14.8	74.0	72.0	631	US-10-027-632-693	Sequence 693, App
602	14.8	74.0	36048	7	US-10-052-482-127	Sequence 127, App	c 675	14.8	74.0	72.0	631	US-10-027-632-694	Sequence 694, App
603	14.8	74.0	39405	7	US-10-087-192-1285	Sequence 1285, App	c 676	14.8	74.0	72.0	631	US-10-027-632-695	Sequence 695, App
604	14.8	74.0	43914	7	US-10-332-281-299	Sequence 299, App	c 677	14.8	74.0	72.0	632	US-10-027-632-54947	Sequence 54947, App
605	14.8	74.0	69706	6	US-10-085-117-229	Sequence 229, App	c 678	14.8	74.0	72.0	632	US-10-027-632-313553	Sequence 313553, App
606	14.8	74.0	77530	7	US-10-332-281-265	Sequence 265, App	c 679	14.8	74.0	72.0	632	US-10-027-632-313554	Sequence 313554, App
607	14.8	74.0	79256	7	US-10-332-281-167	Sequence 167, App	c 680	14.8	74.0	72.0	632	US-10-027-632-313555	Sequence 313555, App

C 681	14.4	72.0	632	5	US-10-027-632-313556	Sequence 313556,
C 682	14.4	72.0	632	6	US-10-027-632-54947	Sequence 54947, A
C 683	14.4	72.0	632	6	US-10-027-632-113553	Sequence 313553,
C 684	14.4	72.0	632	6	US-10-027-632-113554	Sequence 313554,
C 685	14.4	72.0	632	6	US-10-027-632-113555	Sequence 313555,
C 686	14.4	72.0	632	6	US-10-027-632-113556	Sequence 313556,
C 687	14.4	72.0	644	7	US-10-437-963-33910	Sequence 33910, A
C 688	14.4	72.0	717	4	US-09-925-065A-671119	Sequence 671119, A
C 689	14.4	72.0	734	5	US-10-027-632-18318	Sequence 18318, A
C 690	14.4	72.0	734	6	US-10-027-632-20132	Sequence 20132, A
C 691	14.4	72.0	748	6	US-10-027-632-20132	Sequence 20132, A
C 692	14.4	72.0	748	6	US-09-925-065A-8490	Sequence 8490, Ap
C 693	14.4	72.0	778	4	US-10-027-632-155180	Sequence 155180,
C 694	14.4	72.0	811	5	US-10-027-632-155181	Sequence 155181,
C 695	14.4	72.0	811	6	US-10-027-632-155180	Sequence 155180,
C 696	14.4	72.0	811	6	US-10-027-632-155181	Sequence 155181,
C 697	14.4	72.0	811	6	US-10-027-632-155181	Sequence 155181,
C 698	14.4	72.0	813	5	US-10-027-632-8771	Sequence 8771, Ap
C 699	14.4	72.0	813	5	US-10-027-632-8771	Sequence 8771, Ap
C 700	14.4	72.0	813	6	US-10-027-632-8771	Sequence 8771, Ap
C 701	14.4	72.0	825	5	US-10-027-632-8772	Sequence 8772, Ap
C 702	14.4	72.0	825	5	US-10-027-632-154120	Sequence 154120,
C 703	14.4	72.0	825	5	US-10-027-632-154120	Sequence 154120,
C 704	14.4	72.0	825	5	US-10-156-761-2709	Sequence 2709, Ap
C 705	14.4	72.0	1146	6	US-10-027-632-118682	Sequence 118682,
C 706	14.4	72.0	1146	6	US-10-027-632-118682	Sequence 118682,
C 707	14.4	72.0	1147	9	US-10-764-420-2149	Sequence 2149, Ap
C 708	14.4	72.0	1333	6	US-10-369-493-45311	Sequence 45311, A
C 709	14.4	72.0	1333	6	US-09-925-065A-708564	Sequence 708564,
C 710	14.4	72.0	1407	6	US-10-369-493-44351	Sequence 44351, A
C 711	14.4	72.0	1467	6	US-10-369-493-339807	Sequence 339807, A
C 712	14.4	72.0	1589	6	US-09-778-844-159	Sequence 159, App
C 713	14.4	72.0	1605	6	US-10-369-493-39422	Sequence 39422, A
C 714	14.4	72.0	1605	6	US-10-369-493-39055	Sequence 39055, A
C 715	14.4	72.0	1636	10	US-11-097-143-1176	Sequence 1176, App
C 716	14.4	72.0	1704	10	US-11-097-143-332	Sequence 332, App
C 717	14.4	72.0	1809	9	US-09-778-844-158	Sequence 158, App
C 718	14.4	72.0	1809	9	US-10-764-420-2135	Sequence 2135, Ap
C 719	14.4	72.0	1865	3	US-09-747-155-430	Sequence 2, App1
C 720	14.4	72.0	1937	7	US-10-426-118-2	Sequence 1630, Ap
C 721	14.4	72.0	1937	3	US-09-764-864-1630	Sequence 1630, Ap
C 722	14.4	72.0	2002	3	US-09-17-800A-11319	Sequence 11319, A
C 723	14.4	72.0	2018	7	US-10-425-114-31162	Sequence 31162, A
C 724	14.4	72.0	2037	10	US-11-097-143-5615	Sequence 5615, Ap
C 725	14.4	72.0	2126	3	US-09-764-864-1631	Sequence 1631, Ap
C 726	14.4	72.0	2126	3	US-09-764-864-1633	Sequence 1633, Ap
C 727	14.4	72.0	2252	7	US-10-322-281-476	Sequence 476, App
C 728	14.4	72.0	2401	3	US-09-866-050A-439	Sequence 439, App
C 729	14.4	72.0	2401	3	US-10-152-661-439	Sequence 439, App1
C 730	14.4	72.0	2411	3	US-09-866-050A-75	Sequence 75, App1
C 731	14.4	72.0	2411	3	US-09-866-050A-256	Sequence 75, App1
C 732	14.4	72.0	2411	5	US-10-152-661-75	Sequence 256, App
C 733	14.4	72.0	2411	5	US-10-152-661-256	Sequence 256, App
C 734	14.4	72.0	2532	10	US-11-097-143-5083	Sequence 5083, Ap
C 735	14.4	72.0	2532	8	US-10-425-115-67374	Sequence 67374, A
C 736	14.4	72.0	2925	10	US-11-097-143-20803	Sequence 20803, A
C 737	14.4	72.0	3147	10	US-11-097-143-19394	Sequence 19394, A
C 738	14.4	72.0	3229	9	US-10-764-420-2636	Sequence 2636, Ap
C 739	14.4	72.0	3434	10	US-11-097-143-7219	Sequence 7219, Ap
C 740	14.4	72.0	3591	3	US-09-957-944-11	Sequence 11, App1
C 741	14.4	72.0	3591	10	US-11-099-059-11	Sequence 11, App1
C 742	14.4	72.0	3614	10	US-11-097-143-5068	Sequence 5068, Ap
C 743	14.4	72.0	3738	6	US-10-029-386-40677	Sequence 20677, A
C 744	14.4	72.0	3857	5	US-10-029-386-40677	Sequence 2057, Ap
C 745	14.4	72.0	3857	8	US-10-029-386-40677	Sequence 23, App1
C 746	14.4	72.0	4018	6	US-10-331-053-23	Sequence 23, App1
C 747	14.4	72.0	4160	10	US-11-097-143-175	Sequence 175, App
C 748	14.4	72.0	4550	3	US-09-901-484A-182	Sequence 182, App
C 749	14.4	72.0	4550	3	US-09-853-526-182	Sequence 182, App
C 750	14.4	72.0	4600	8	US-10-386-329-37	Sequence 1, App1
C 751	14.4	72.0	4600	8	US-10-386-329-37	Sequence 37, App1
C 752	14.4	72.0	4600	8	US-10-386-329-38	Sequence 38, App1
C 753	14.4	72.0	4848	9	US-10-450-763-3757	Sequence 3757, Ap
C 754	14.4	72.0	5008	10	US-11-097-143-361	Sequence 361, App
C 755	14.4	72.0	5190	10	US-11-097-143-5614	Sequence 5614, Ap
C 756	14.4	72.0	5307	9	US-10-502-332-1	Sequence 1, App1
C 757	14.4	72.0	7568	10	US-11-097-143-19393	Sequence 19393, A
C 758	14.4	72.0	10591	7	US-10-601-807-1	Sequence 1, App1
C 759	14.4	72.0	11546	8	US-10-876-285-9	Sequence 9, App1
C 760	14.4	72.0	13462	8	US-10-741-600-17938	Sequence 17938, A
C 761	14.4	72.0	16566	5	US-10-087-192-367	Sequence 367, App
C 762	14.4	72.0	20762	5	US-10-087-192-1819	Sequence 1819, App
C 763	14.4	72.0	21558	5	US-10-087-192-1735	Sequence 1735, Ap
C 764	14.4	72.0	21558	5	US-10-087-192-1735	Sequence 1735, Ap
C 765	14.4	72.0	22312	5	US-10-087-192-715	Sequence 715, App
C 766	14.4	72.0	22965	5	US-10-322-281-475	Sequence 475, App
C 767	14.4	72.0	23610	7	US-10-052-482-13	Sequence 13, App1
C 768	14.4	72.0	23611	7	US-10-322-281-61	Sequence 61, App1
C 769	14.4	72.0	23938	5	US-10-087-192-1933	Sequence 1933, Ap
C 770	14.4	72.0	23938	5	US-10-087-192-1933	Sequence 142, App
C 771	14.4	72.0	24495	7	US-10-367-094-142	Sequence 2056, App
C 772	14.4	72.0	24495	7	US-10-087-192-2056	Sequence 22, App1
C 773	14.4	72.0	24495	8	US-10-331-053-22	Sequence 1549, Ap
C 774	14.4	72.0	25469	5	US-10-087-192-1549	Sequence 1549, Ap
C 775	14.4	72.0	25469	5	US-10-087-192-1549	Sequence 1447, Ap
C 776	14.4	72.0	25469	5	US-10-087-192-1447	Sequence 439, App
C 777	14.4	72.0	26307	5	US-10-087-192-439	Sequence 133, App
C 778	14.4	72.0	27383	7	US-10-322-696-133	Sequence 1159, Ap
C 779	14.4	72.0	28027	5	US-10-087-192-1759	Sequence 1759, Ap
C 780	14.4	72.0	28903	5	US-10-087-192-1759	Sequence 757, App
C 781	14.4	72.0	28932	5	US-10-087-192-1711	Sequence 1711, App
C 782	14.4	72.0	29377	5	US-10-087-192-1711	Sequence 791, App
C 783	14.4	72.0	29560	7	US-10-322-281-191	Sequence 285, App
C 784	14.4	72.0	30140	6	US-10-085-117-105	Sequence 128, App
C 785	14.4	72.0	30304	6	US-10-367-094-128	Sequence 96, App1
C 786	14.4	72.0	30310	3	US-09-800-631-96	Sequence 96, App1
C 787	14.4	72.0	30310	6	US-10-293-783-36	Sequence 745, App
C 788	14.4	72.0	30310	6	US-10-388-263-745	Sequence 55, App1
C 789	14.4	72.0	30659	5	US-10-087-192-55	Sequence 745, App
C 790	14.4	72.0	30752	5	US-10-087-192-745	Sequence 745, App
C 791	14.4	72.0	30847	9	US-10-756-149-1452	Sequence 1452, App
C 792	14.4	72.0	31477	5	US-10-087-192-373	Sequence 373, App
C 793	14.4	72.0	31946	5	US-10-087-192-1909	Sequence 1909, Ap
C 794	14.4	72.0	32185	5	US-10-087-192-1135	Sequence 1135, Ap
C 795	14.4	72.0	32548	10	US-11-097-143-1164	Sequence 4464, A
C 796	14.4	72.0	33000	8	US-10-876-285-5	Sequence 5, App1
C 797	14.4	72.0	33551	8	US-10-087-192-283	Sequence 283, App
C 798	14.4	72.0	33551	8	US-10-417-375-41	Sequence 417, App1
C 799	14.4	72.0	34123	6	US-10-087-192-1783	Sequence 1783, Ap
C 800	14.4	72.0	34378	6	US-10-056-790-47	Sequence 47, App
C 801	14.4	72.0	34378	6	US-10-087-192-1639	Sequence 1639, App
C 802	14.4	72.0	35359	5	US-10-087-192-1639	Sequence 421, App
C 803	14.4	72.0	35828	6	US-10-384-893-17	Sequence 17, App1
C 804	14.4	72.0	35828	7	US-10-463-190-17	Sequence 17, App1
C 805	14.4	72.0	35828	7	US-10-095-248A-17	Sequence 17, App1
C 806	14.4	72.0	35828	7	US-10-085-117-103	Sequence 103, App
C 807	14.4	72.0	37459	6	US-10-085-117-103	Sequence 103, App
C 808	14.4	72.0	37723	6	US-10-087-192-1513	Sequence 1513, App
C 809	14.4	72.0	38646	5	US-10-087-192-1513	Sequence 1321, Ap
C 810	14.4	72.0	38977	5	US-10-087-192-1515	Sequence 1585, Ap
C 811	14.4	72.0	40463	5	US-10-087-192-1585	Sequence 1, App1
C 812	14.4	72.0	40633	5	US-10-087-192-1585	Sequence 1585, Ap
C 813	14.4	72.0	42179	5	US-10-087-192-1969	Sequence 1969, App
C 814	14.4	72.0	42514	5	US-10-087-192-475	Sequence 475, App
C 815	14.4	72.0	42962	7	US-10-322-281-835	Sequence 835, App
C 816	14.4	72.0	43292	7	US-10-087-192-835	Sequence 607, App
C 817	14.4	72.0	43769	5	US-10-087-192-607	Sequence 1081, App
C 818	14.4	72.0	44728	7	US-10-367-094-23	Sequence 23, App1
C 819	14.4	72.0	44972	5	US-10-087-192-349	Sequence 349, App
C 820	14.4	72.0	45364	7	US-10-322-281-235	Sequence 235, App
C 821	14.4	72.0	46338	7	US-10-322-281-235	Sequence 235, App
C 822	14.4	72.0	46338	5	US-10-087-192-265	Sequence 265, App
C 823	14.4	72.0	46635	6	US-10-087-192-265	Sequence 67, App1
C 824	14.4	72.0	47745	5	US-10-085-117-67	Sequence 469, App
C 825	14.4	72.0	50657	7	US-10-087-192-469	Sequence 469, App
C 826	14.4	72.0	51198	5	US-10-322-281-601	Sequence 601, App
					US-10-087-192-1729	Sequence 1729, Ap

C 827	14.4	72.0	51323	8	US-10-417-375-135	Sequence 135, App	900	14.4	72.0	155350	7	US-10-322-281-691	Sequence 691, App
C 828	14.4	72.0	51664	5	US-10-087-198-877	Sequence 827, App	901	14.4	72.0	158405	5	US-10-175-523-86	Sequence 86, App1
C 829	14.4	72.0	51705	5	US-10-052-482-229	Sequence 229, App	C 902	14.4	72.0	158405	5	US-10-175-523-86	Sequence 86, App1
C 830	14.4	72.0	52138	10	US-11-166-990-75	Sequence 75, App1	C 903	14.4	72.0	158405	10	US-11-099-266-86	Sequence 86, App1
C 831	14.4	72.0	52637	7	US-10-367-094-186	Sequence 186, App	C 904	14.4	72.0	158405	7	US-11-099-266-86	Sequence 86, App1
C 832	14.4	72.0	52920	7	US-10-322-281-661	Sequence 661, App	C 905	14.4	72.0	163701	10	US-10-322-281-639	Sequence 303, App
C 833	14.4	72.0	53381	5	US-10-087-192-1621	Sequence 1621, App	C 906	14.4	72.0	163701	7	US-10-322-281-639	Sequence 303, App
C 834	14.4	72.0	54037	5	US-10-322-281-1395	Sequence 395, App	C 907	14.4	72.0	164047	8	US-10-322-281-105	Sequence 105, App
C 835	14.4	72.0	54305	8	US-10-417-375-79	Sequence 79, App1	C 908	14.4	72.0	171936	6	US-10-388-838-1	Sequence 1, App1
C 836	14.4	72.0	54355	3	US-09-997-722-19	Sequence 19, App1	C 909	14.4	72.0	171936	6	US-10-265-071-24	Sequence 24, App1
C 837	14.4	72.0	55544	3	US-10-087-192-811	Sequence 811, App	C 910	14.4	72.0	171936	6	US-10-025-966A-24	Sequence 24, App1
C 838	14.4	72.0	56793	5	US-10-087-192-1697	Sequence 1897, App	C 911	14.4	72.0	171936	6	US-10-025-966A-24	Sequence 24, App1
C 839	14.4	72.0	58540	5	US-10-087-192-1189	Sequence 1189, App	C 912	14.4	72.0	171936	6	US-10-322-281-459	Sequence 459, App1
C 840	14.4	72.0	61791	7	US-10-322-281-645	Sequence 645, App	C 913	14.4	72.0	193992	9	US-10-461-862-95	Sequence 95, App1
C 841	14.4	72.0	63761	7	US-10-322-281-557	Sequence 557, App	C 914	14.4	72.0	193992	9	US-10-756-149-626	Sequence 626, App
C 842	14.4	72.0	64482	7	US-10-322-281-151	Sequence 151, App	C 915	14.4	72.0	193992	6	US-10-088-117-555	Sequence 355, App
C 843	14.4	72.0	64482	7	US-10-322-281-151	Sequence 151, App	C 916	14.4	72.0	193992	6	US-10-088-117-555	Sequence 355, App
C 844	14.4	72.0	65559	5	US-10-087-192-841	Sequence 841, App	C 917	14.4	72.0	193992	6	US-10-088-117-555	Sequence 355, App
C 845	14.4	72.0	65559	5	US-10-087-192-841	Sequence 841, App	C 918	14.4	72.0	193992	6	US-10-088-117-555	Sequence 355, App
C 846	14.4	72.0	66681	7	US-10-322-281-411	Sequence 411, App	C 919	14.4	72.0	193992	8	US-10-087-192-853	Sequence 853, App
C 847	14.4	72.0	66681	7	US-10-322-281-411	Sequence 411, App	C 920	14.4	72.0	193992	8	US-10-087-192-853	Sequence 853, App
C 848	14.4	72.0	66870	5	US-10-087-192-1765	Sequence 1765, App	C 921	14.4	72.0	202521	7	US-10-087-192-985	Sequence 985, App
C 849	14.4	72.0	68497	5	US-10-087-192-2047	Sequence 2047, App	C 922	14.4	72.0	202521	7	US-10-322-281-459	Sequence 459, App
C 850	14.4	72.0	69515	5	US-10-087-192-1219	Sequence 1219, App	C 923	14.4	72.0	202521	3	US-10-322-281-459	Sequence 459, App
C 851	14.4	72.0	70215	5	US-10-087-192-217	Sequence 217, App	C 924	14.4	72.0	202521	3	US-09-972-546-16	Sequence 16, App1
C 852	14.4	72.0	71553	8	US-10-719-993-7039	Sequence 7039, App	C 925	14.4	72.0	215980	3	US-09-972-546-16	Sequence 16, App1
C 853	14.4	72.0	71553	8	US-10-741-600-17960	Sequence 17960, App	C 926	14.4	72.0	215980	8	US-10-735-256-16	Sequence 16, App1
C 854	14.4	72.0	73507	5	US-10-087-192-1147	Sequence 1147, App	C 927	14.4	72.0	215980	8	US-10-735-256-16	Sequence 16, App1
C 855	14.4	72.0	76150	6	US-10-085-117-157	Sequence 157, App	C 928	14.4	72.0	225883	5	US-10-175-523-86	Sequence 86, App1
C 856	14.4	72.0	77530	6	US-10-322-281-265	Sequence 265, App	C 929	14.4	72.0	225883	5	US-10-175-523-86	Sequence 86, App1
C 857	14.4	72.0	79467	7	US-10-052-482-223	Sequence 223, App	C 930	14.4	72.0	233060	5	US-10-087-192-937	Sequence 937, App1
C 858	14.4	72.0	80321	5	US-10-087-192-1747	Sequence 1747, App	C 931	14.4	72.0	243060	7	US-10-322-281-131	Sequence 131, App
C 859	14.4	72.0	80420	5	US-10-367-094-41	Sequence 41, App1	C 932	14.4	72.0	250087	5	US-10-087-192-223	Sequence 223, App
C 860	14.4	72.0	83483	9	US-10-087-192-1405	Sequence 1405, App	C 933	14.4	72.0	250087	5	US-10-087-192-223	Sequence 223, App
C 861	14.4	72.0	83943	9	US-10-461-862-119	Sequence 119, App	C 934	14.4	72.0	250087	6	US-10-229-834A-6	Sequence 6, App1
C 862	14.4	72.0	84410	6	US-10-322-281-747	Sequence 747, App	C 935	14.4	72.0	250087	8	US-10-087-192-331	Sequence 331, App
C 863	14.4	72.0	85076	6	US-10-085-117-97	Sequence 97, App1	C 936	14.4	72.0	329112	8	US-10-812-232-3	Sequence 3, App1
C 864	14.4	72.0	88421	3	US-09-976-059-1	Sequence 1, App1	C 937	14.4	72.0	421609	7	US-10-367-094-41	Sequence 41, App1
C 865	14.4	72.0	88493	7	US-10-322-281-703	Sequence 703, App	C 938	14.4	72.0	421609	7	US-10-367-094-41	Sequence 41, App1
C 866	14.4	72.0	88493	7	US-10-322-281-703	Sequence 703, App	C 939	14.4	72.0	421609	8	US-10-719-993-681	Sequence 681, App
C 867	14.4	72.0	88853	5	US-10-087-192-85	Sequence 85, App1	C 940	14.4	72.0	775062	8	US-10-461-862-166	Sequence 166, App
C 868	14.4	72.0	89213	7	US-10-322-281-843	Sequence 843, App	C 941	14.4	72.0	783062	8	US-10-461-862-166	Sequence 166, App
C 869	14.4	72.0	89213	7	US-10-322-281-843	Sequence 843, App	C 942	14.4	72.0	1980090	8	US-10-719-993-681	Sequence 681, App
C 870	14.4	72.0	90351	7	US-10-367-094-166	Sequence 166, App	C 943	14.4	72.0	1980090	8	US-10-741-600-17676	Sequence 17676, App
C 871	14.4	72.0	90650	5	US-10-175-523-80	Sequence 80, App1	C 944	14.4	72.0	25	7	US-10-719-993-681	Sequence 681, App
C 872	14.4	72.0	90650	10	US-11-099-266-80	Sequence 80, App1	C 945	14.4	72.0	25	7	US-10-719-993-681	Sequence 681, App
C 873	14.4	72.0	91071	5	US-10-087-192-235	Sequence 235, App	C 946	14.4	72.0	25	7	US-10-719-993-681	Sequence 681, App
C 874	14.4	72.0	92076	7	US-10-322-281-465	Sequence 465, App	C 947	14.4	72.0	25	7	US-10-719-993-681	Sequence 681, App
C 875	14.4	72.0	94720	7	US-10-052-482-160	Sequence 160, App	C 948	14.4	72.0	25	8	US-10-719-993-681	Sequence 681, App
C 876	14.4	72.0	96389	7	US-10-052-482-181	Sequence 181, App	C 949	14.4	72.0	25	9	US-10-809-189-1066	Sequence 1066, App
C 877	14.4	72.0	96593	7	US-10-052-482-67	Sequence 67, App1	C 950	14.4	72.0	25	9	US-10-956-157-45765	Sequence 45765, App
C 878	14.4	72.0	98642	5	US-10-087-192-1105	Sequence 1105, App	C 951	14.4	72.0	25	9	US-10-956-157-45765	Sequence 45765, App
C 879	14.4	72.0	100554	5	US-10-087-192-1165	Sequence 1165, App	C 952	14.4	72.0	25	9	US-10-956-157-45765	Sequence 45765, App
C 880	14.4	72.0	101241	5	US-10-087-192-1339	Sequence 1339, App	C 953	14.4	72.0	25	10	US-11-036-317-6636	Sequence 6636, App
C 881	14.4	72.0	101241	5	US-10-087-192-1339	Sequence 1339, App	C 954	14.4	72.0	25	10	US-11-036-317-6636	Sequence 6636, App
C 882	14.4	72.0	105077	8	US-10-417-375-15	Sequence 15, App1	C 955	14.4	72.0	25	10	US-11-036-317-6636	Sequence 6636, App
C 883	14.4	72.0	108845	7	US-10-367-094-7	Sequence 7, App1	C 956	14.4	72.0	25	10	US-10-230-006-2645	Sequence 2645, App
C 884	14.4	72.0	110021	9	US-10-461-862-83	Sequence 83, App1	C 957	14.4	72.0	25	10	US-10-230-006-2645	Sequence 2645, App
C 885	14.4	72.0	110218	9	US-10-087-192-1345	Sequence 1345, App	C 958	14.4	72.0	25	10	US-10-424-599-106334	Sequence 106334, App
C 886	14.4	72.0	114633	5	US-10-087-192-727	Sequence 727, App	C 959	14.4	72.0	25	10	US-10-424-599-106334	Sequence 106334, App
C 887	14.4	72.0	117329	9	US-10-987-384-1	Sequence 1, App1	C 960	14.4	72.0	25	10	US-10-424-599-106334	Sequence 106334, App
C 888	14.4	72.0	123192	5	US-10-322-281-587	Sequence 587, App	C 961	14.4	72.0	201	8	US-10-741-600-18381	Sequence 18381, App
C 889	14.4	72.0	123192	5	US-10-175-523-71	Sequence 71, App1	C 962	14.4	72.0	201	8	US-10-741-600-18381	Sequence 18381, App
C 890	14.4	72.0	123192	10	US-11-099-266-71	Sequence 71, App1	C 963	14.4	72.0	201	8	US-10-741-600-18381	Sequence 18381, App
C 891	14.4	72.0	123920	5	US-10-087-192-1453	Sequence 1453, App	C 964	14.4	72.0	257	7	US-10-424-599-111001	Sequence 111001, App
C 892	14.4	72.0	124289	5	US-10-087-192-817	Sequence 817, App	C 965	14.4	72.0	262	3	US-10-796-632-6185	Sequence 6185, App
C 893	14.4	72.0	130427	5	US-10-175-523-87	Sequence 87, App1	C 966	14.4	72.0	262	6	US-10-040-862-6185	Sequence 6185, App
C 894	14.4	72.0	130427	10	US-11-099-266-87	Sequence 87, App1	C 967	14.4	72.0	262	6	US-10-040-862-6185	Sequence 6185, App
C 895	14.4	72.0	142976	5	US-10-367-094-99	Sequence 99, App1	C 968	14.4	72.0	262	8	US-10-764-324-6185	Sequence 6185, App
C 896	14.4	72.0	144179	5	US-10-087-192-511	Sequence 511, App	C 969	14.4	72.0	271	3	US-10-864-408A-1627	Sequence 1627, App
C 897	14.4	72.0	147443	5	US-10-087-192-1357	Sequence 1357, App	C 970	14.4	72.0	271	8	US-10-425-115-54674	Sequence 54674, App
C 898	14.4	72.0	153995	7	US-10-322-281-721	Sequence 721, App	C 971	14.4	72.0	272	3	US-09-796-692-3876	Sequence 3876, App
C 899	14.4	72.0	154504	7	US-10-322-281-696-67	Sequence 67, App1	C 972	14.4	72.0	272	5	US-10-040-862-3876	Sequence 3876, App

```

973 14.2 71.0 272 6 US-10-057-475B-3876 Sequence 3876, Ap
974 14.2 71.0 272 6 US-10-154-884B-3876 Sequence 3876, Ap
975 14.2 71.0 272 8 US-10-764-324-3876 Sequence 3876, Ap
976 14.2 71.0 277 7 US-10-424-599-9946 Sequence 9946, Ap
977 14.2 71.0 296 6 US-10-029-386-27061 Sequence 27061, A
978 14.2 71.0 307 8 US-10-425-115-71000 Sequence 71000, A
979 14.2 71.0 342 8 US-10-425-115-179790 Sequence 179790, A
980 14.2 71.0 367 8 US-10-425-115-19742 Sequence 19742, A
981 14.2 71.0 378 6 US-10-029-386-16309 Sequence 16309, A
982 14.2 71.0 385 9 US-10-950-009-169 Sequence 169, App
983 14.2 71.0 392 7 US-10-424-599-40113 Sequence 40113, A
984 14.2 71.0 408 3 US-09-803-719-1908 Sequence 1908, Ap
985 14.2 71.0 408 3 US-10-779-543-15178 Sequence 15178, A
986 14.2 71.0 423 4 US-09-925-065A-855911 Sequence 855911, A
987 14.2 71.0 423 9 US-10-779-543-13240 Sequence 13240, A
988 14.2 71.0 425 8 US-10-425-115-159641 Sequence 159641, A
989 14.2 71.0 435 3 US-09-876-889-1170 Sequence 1170, App
990 14.2 71.0 435 8 US-10-425-115-110738 Sequence 110738, A
991 14.2 71.0 447 8 US-10-425-115-13568 Sequence 13568, A
992 14.2 71.0 455 9 US-10-450-763-16178 Sequence 16178, A
993 14.2 71.0 458 8 US-10-425-115-43280 Sequence 43280, A
994 14.2 71.0 459 3 US-09-918-995-15779 Sequence 15779, A
995 14.2 71.0 460 5 US-10-198-846-6132 Sequence 6132, Ap
996 14.2 71.0 461 3 US-09-864-761-4406 Sequence 4406, Ap
997 14.2 71.0 472 3 US-09-918-995-13974 Sequence 13974, A
998 14.2 71.0 476 9 US-10-956-157-5119 Sequence 5119, Ap
999 14.2 71.0 476 9 US-10-956-157-10354 Sequence 10354, A
1000 14.2 71.0 480 4 US-09-925-065A-498925 Sequence 498925,

```

## ALIGNMENTS

## RESULT 1

```

US-09-888-326-68
; Sequence 68, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AMS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 68
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-888-326-68

```

```

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.2;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 AGGACAGCCAGGACUACGA 20
Db      1 AGGTACAGCCAGGACTACGA 20

```

## RESULT 2

```

US-09-776-479-391
; Sequence 391, Application US/09776479
; Publication No. US20030087846A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.

```

```

; APPLICANT: Fournon, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 391
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-391

```

```

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.2;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 AGGACAGCCAGGACUACGA 20
Db      1 AGGTACAGCCAGGACTACGA 20

```

## RESULT 3

```

US-09-776-479-391
; Sequence 391, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fournon, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 391
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-391

```

```

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.2;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 AGGACAGCCAGGACUACGA 20
Db      1 AGGTACAGCCAGGACTACGA 20

```

## RESULT 4

```

US-10-112-653-379
; Sequence 379, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Kriegl, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060 (AMS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29

```

PRIOR APPLICATION NUMBER: US 60/279,642  
PRIOR FILING DATE: 2001-03-29  
NUMBER OF SEQ ID NOS: 1040  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 379  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-112-653-379

Query Match 100.0%; Score 20; DB 5; Length 20;  
Best Local Similarity 90.0%; Pred. No. 3.2;  
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGUACAGCCAGACUACGA 20  
|||:|||||:|||||:|||||:  
Db 1 AGGTACAGCCAGACTACGA 20

RESULT 5  
US-10-017-995-391  
Sequence 391, Application US/10017995  
Publication No. US20030055014A1  
GENERAL INFORMATION:  
APPLICANT: Bratzler, Robert L.  
TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids  
FILE REFERENCE: C1037/7025 (HCL/MAT)  
CURRENT APPLICATION NUMBER: US/10/017,995  
CURRENT FILING DATE: 2001-12-18  
PRIOR APPLICATION NUMBER: US 60/255,534  
PRIOR FILING DATE: 2000-12-14  
NUMBER OF SEQ ID NOS: 1093  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 391  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Sequence  
US-10-017-995-391

Query Match 100.0%; Score 20; DB 5; Length 20;  
Best Local Similarity 90.0%; Pred. No. 3.2;  
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGUACAGCCAGACUACGA 20  
|||:|||||:|||||:|||||:  
Db 1 AGGTACAGCCAGACTACGA 20

RESULT 6  
US-10-314-578-391  
Sequence 391, Application US/10314578  
Publication No. US20030212026A1  
GENERAL INFORMATION:  
APPLICANT: Kries, Arthur M.  
APPLICANT: Schetter, Christian  
APPLICANT: Vollmer, Jorg  
TITLE OF INVENTION: Immunostimulatory Nucleic Acids  
FILE REFERENCE: C1039/7035 (HCL/MAT)  
CURRENT APPLICATION NUMBER: US/10/314,578  
PRIOR FILING DATE: 2002-12-09  
PRIOR APPLICATION NUMBER: US 60/156,113  
PRIOR FILING DATE: 1999-09-25  
PRIOR APPLICATION NUMBER: US 60/156,135  
PRIOR FILING DATE: 1999-09-27  
PRIOR APPLICATION NUMBER: US 60/227,436  
PRIOR FILING DATE: 2000-08-23  
NUMBER OF SEQ ID NOS: 1145  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 391

LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Sequence  
US-10-314-578-391

Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 90.0%; Pred. No. 3.2;  
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGUACAGCCAGACUACGA 20  
|||:|||||:|||||:|||||:  
Db 1 AGGTACAGCCAGACTACGA 20

RESULT 7  
US-10-831-778-391  
Sequence 391, Application US/10831778  
Publication No. US20040235774A1  
GENERAL INFORMATION:  
APPLICANT: Bratzler, Robert L.  
APPLICANT: Petersen, Deanna M.  
APPLICANT: Fouron, Yves  
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
TITLE OF INVENTION: Treatment of Asthma and Allergy  
FILE REFERENCE: C1037/7013 (HCL/MAT)  
CURRENT APPLICATION NUMBER: US/10/831,778  
CURRENT FILING DATE: 2004-04-23  
PRIOR APPLICATION NUMBER: US 60/179,991  
PRIOR FILING DATE: 2000-02-03  
NUMBER OF SEQ ID NOS: 1093  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 391  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Sequence  
US-10-831-778-391

Query Match 100.0%; Score 20; DB 8; Length 20;  
Best Local Similarity 90.0%; Pred. No. 3.2;  
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGUACAGCCAGACUACGA 20  
|||:|||||:|||||:|||||:  
Db 1 AGGTACAGCCAGACTACGA 20

RESULT 8  
US-10-800-926-3  
Sequence 3, Application US/10800926  
Publication No. US20050032731A1  
GENERAL INFORMATION:  
APPLICANT: MARSHALL, WILLIAM E.  
TITLE OF INVENTION: OLIGORIBONUCLEOTIDES ALERT THE IMMUNE SYSTEM OF ANIMALS  
FILE REFERENCE: P01936US06  
CURRENT APPLICATION NUMBER: US/10/800,926  
CURRENT FILING DATE: 2004-03-15  
PRIOR APPLICATION NUMBER: 09/883,550  
PRIOR FILING DATE: 2001-06-18  
PRIOR APPLICATION NUMBER: 09/193,653  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 08/739,264  
PRIOR FILING DATE: 1996-10-29  
PRIOR APPLICATION NUMBER: 08/517,016  
PRIOR FILING DATE: 1995-08-18  
PRIOR APPLICATION NUMBER: 08/376,175  
PRIOR FILING DATE: 1995-01-20  
PRIOR APPLICATION NUMBER: 08/059,745  
PRIOR FILING DATE: 1993-05-11

NUMBER OF SEQ ID NOS: 3  
SOFTWARE: Patentin Ver. 3.2  
SEQ ID NO 3  
LENGTH: 20  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-800-926-3

Query Match 100.0%; Score 20; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUACGA 20  
DB 1 AGGUACAGCCAGACUACGA 20

RESULT 9  
US-10-152-319A-532  
Sequence 532, Application US/10152319A  
Publication No. US20040072160A1  
GENERAL INFORMATION:  
APPLICANT: Mendrick, Donna  
APPLICANT: Porter, Mark  
APPLICANT: Johnson, Kory  
APPLICANT: Higgs, Brandon  
APPLICANT: Castle, Arthur  
APPLICANT: Blashoff, Michael  
TITLE OF INVENTION: Molecular Toxicology Modeling  
FILE REFERENCE: 44921-5089-US  
CURRENT APPLICATION NUMBER: US/10/152,319A  
CURRENT FILING DATE: 2002-05-22  
PRIOR APPLICATION NUMBER: US 60/292,335  
PRIOR FILING DATE: 2001-05-22  
PRIOR APPLICATION NUMBER: US 60/297,523  
PRIOR FILING DATE: 2001-06-13  
PRIOR APPLICATION NUMBER: US 60/298,925  
PRIOR FILING DATE: 2001-06-19  
PRIOR APPLICATION NUMBER: US 60/303,810  
PRIOR FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: US 60/303,807  
PRIOR FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: US 60/303,808  
PRIOR FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: US 60/315,047  
PRIOR FILING DATE: 2001-08-28  
PRIOR APPLICATION NUMBER: US 60/324,928  
PRIOR FILING DATE: 2001-09-27  
PRIOR APPLICATION NUMBER: US 60/330,867  
PRIOR FILING DATE: 2001-11-01  
PRIOR APPLICATION NUMBER: US 60/330,462  
PRIOR FILING DATE: 2001-10-22  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 2221  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 532  
LENGTH: 5253  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
FEATURE:  
OTHER INFORMATION: Genbank Accession No. AB012214  
US-10-152-319A-532

Query Match 90.0%; Score 18; DB 7; Length 5253;  
Best Local Similarity 88.9%; Pred. No. 30;  
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGACUACGA 19  
DB 2679 GGTAACAGCCAGACTACG 2696

RESULT 10  
US-10-425-115-14343  
Sequence 14343, Application US/10425115  
Publication No. US2004021472A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53222)B  
CURRENT APPLICATION NUMBER: US/10/425,115  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 369326  
SEQ ID NO 14343  
LENGTH: 281  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: MHT4577\_113070C.1  
US-10-425-115-14343

Query Match 84.0%; Score 16.8; DB 8; Length 281;  
Best Local Similarity 80.0%; Pred. No. 1.3e+02;  
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUACGA 20  
DB 160 AGGTACAGCCAGACTACGA 179

RESULT 11  
US-09-925-065A-693333/c  
Sequence 693333, Application US/09925065A  
Publication No. US20050228172A9  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 693333  
LENGTH: 605  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-693333

Query Match 84.0%; Score 16.8; DB 4; Length 605;  
Best Local Similarity 85.0%; Pred. No. 1.3e+02;  
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUACGA 20  
DB 398 AGGCACAGCCAGACTACGA 379

RESULT 12

US-09-925-065A-73830  
; Sequence 73830, Application US/09925065A  
; Publication No. US20050228172A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 73830  
; LENGTH: 740  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-73830

Query Match                    84.0%; Score 16.8; DB 4; Length 740;  
Best Local Similarity    80.0%; Pred. No. 1.3e+02;  
Matches    16; Conservative    2; Mismatches    2; Indels    0; Gaps    0;

QY                    1 AGTACAGCCAGGACTACGA 20  
                     |||:|||||:|:|  
DB                    66 AGTACAGCCAGGCTACGA 85

RESULT 13  
US-10-322-281-33  
; Sequence 33, Application US/10322281  
; Publication No. US20040126762A1  
; GENERAL INFORMATION:  
; APPLICANT: David W. Morris  
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer  
; FILE REFERENCE: 529452001000  
; CURRENT APPLICATION NUMBER: US/10/322,281  
; CURRENT FILING DATE: 2002-12-17  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 145068  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(145068)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-322-281-33

Query Match                    84.0%; Score 16.8; DB 7; Length 145068;  
Best Local Similarity    85.0%; Pred. No. 1.1e+02;  
Matches    17; Conservative    1; Mismatches    2; Indels    0; Gaps    0;

QY                    1 AGTACAGCCAGGACTACGA 20  
                     |||:|||||:|:|  
DB                    50545 AGTACTGCGCAGACACGA 50564

RESULT 14  
US-10-653-047-3156  
; Sequence 3156, Application US/10653047  
; Publication No. US20040229367A1

GENERAL INFORMATION:  
; APPLICANT: Randy M. Berka  
; APPLICANT: Michael W. Rey  
; APPLICANT: Jeffrey R. Shuster  
; APPLICANT: Sakari Kauppinen  
; APPLICANT: Ib Groth Clausen  
; APPLICANT: Peter Bjørke Olsen  
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene  
; FILE REFERENCE: 5849.200-US  
; CURRENT APPLICATION NUMBER: US/10/653,047  
; CURRENT FILING DATE: 2003-08-29  
; PRIOR APPLICATION NUMBER: US/09/533,559  
; PRIOR FILING DATE: 2000-03-22  
; PRIOR APPLICATION NUMBER: 09/273,623  
; PRIOR FILING DATE: 1999-03-22  
; NUMBER OF SEQ ID NOS: 7860  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3156  
; LENGTH: 246  
; TYPE: DNA  
; ORGANISM: Fusarium venenatum  
US-10-653-047-3156

Query Match                    82.0%; Score 16.4; DB 8; Length 246;  
Best Local Similarity    83.3%; Pred. No. 2.1e+02;  
Matches    15; Conservative    2; Mismatches    1; Indels    0; Gaps    0;

QY                    3 GTACAGCCAGGACTACGA 20  
                     |||:|||||:|:|  
DB                    154 GTACAGCCAGGACTACGA 171

RESULT 15  
US-09-925-065A-369463  
; Sequence 369463, Application US/09925065A  
; Publication No. US20050228172A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 369463  
; LENGTH: 586  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-369463

Query Match                    82.0%; Score 16.4; DB 4; Length 586;  
Best Local Similarity    83.3%; Pred. No. 2.1e+02;  
Matches    15; Conservative    2; Mismatches    1; Indels    0; Gaps    0;

QY                    1 AGTACAGCCAGGACTAC 18  
                     |||:|||||:|:|  
DB                    39 AGTACAGCCAGGACTAC 56

RESULT 16  
US-10-425-114-8343



```
Sequence 8343, Application US/10425114
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 8343
LENGTH: 1308
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 700748540_FLI
US-10-425-114-8343

Query Match      82.0%; Score 16.4; DB 7; Length 1308;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 GGUACGCCAGACGACUCG 19
DB      44 GATACGCGCAGGACTACG 61

RESULT 17
US-10-034-650-1/c
Sequence 1, Application US/10034650
GENERAL INFORMATION:
APPLICANT: Morris, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 529452000128
CURRENT APPLICATION NUMBER: US/10/034,650
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 09/474,377
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 61
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 31632
TYPE: DNA
ORGANISM: Mus musculus
US-10-034-650-1

Query Match      82.0%; Score 16.4; DB 6; Length 31632;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 AGGUACGCCAGGACUAC 18
DB      26940 AGGTACGCCAGGCTAC 26923

RESULT 18
US-09-997-722-199
Sequence 199, Application US/09997722
GENERAL INFORMATION:
APPLICANT: Morris, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
```

```
FILE REFERENCE: A-71171/RMS/DCF
CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
SOFTWARE: PatentIn version 3.1
SEQ ID NO 199
LENGTH: 96599
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc feature
LOCATION: (4189)..(4208)
OTHER INFORMATION: "n" at positions 4189 through 4208 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (9652)..(10001)
OTHER INFORMATION: "n" at positions 9652 through 10001 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (27805)..(27824)
OTHER INFORMATION: "n" at positions 27805 through 27824 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (54062)..(54139)
OTHER INFORMATION: "n" at positions 54062 through 54139 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (88386)..(88405)
OTHER INFORMATION: "n" at positions 88386 through 88405 can be any base.
US-09-997-722-199

Query Match      82.0%; Score 16.4; DB 3; Length 96599;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 AGGUACGCCAGGACUAC 18
DB      28454 AGGTACGCCAGGCTAC 28471

RESULT 19
US-10-085-117-250
Sequence 250, Application US/10085117
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: 529452000121
CURRENT APPLICATION NUMBER: US/10/085,117
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 250
LENGTH: 168749
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: variation
LOCATION: (1)..(168749)
OTHER INFORMATION: n = any nucleotide
US-10-085-117-250

Query Match      82.0%; Score 16.4; DB 6; Length 168749;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

Qy 1 AGUACAGCCAGGACUAC 18  
|||:|||||:|||||:  
Db 89636 AGGACGACTCAGGACTAC 89653

## RESULT 20

US-11-097-143-27752  
; Sequence 27752, Application US/11097143  
; Publication No. US20050208558A1  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; APPLICANT: et al.  
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; FILE REFERENCE: CL000728  
; CURRENT APPLICATION NUMBER: US/11/097,143  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: 60/157,832  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: 60/160,191  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/161,932  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 60/164,769  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/173,383  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/175,693  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/184,831  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/191,637  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 43008  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27752  
; LENGTH: 2550  
; TYPE: DNA  
; ORGANISM: DROSOPHILA  
US-11-097-143-27752

Query Match 80.0%; Score 16; DB 10; Length 2550;  
Best Local Similarity 87.5%; Pred. No. 3.2e+02;

Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GUACAGCCAGGACUAC 18  
|||:|||||:|||||:  
Db 1447 GTACAGCCAGGACTAC 1462

## RESULT 21

US-11-097-143-12095  
; Sequence 12095, Application US/11097143  
; Publication No. US20050208558A1  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; APPLICANT: et al.  
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; FILE REFERENCE: CL000728  
; CURRENT APPLICATION NUMBER: US/11/097,143  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: 60/157,832  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: 60/160,191  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/161,932  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 60/164,769  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/173,383

PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/175,693  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/184,831  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/191,637  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 43008  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12095  
; LENGTH: 2668  
; TYPE: DNA  
; ORGANISM: DROSOPHILA  
US-11-097-143-12095

## RESULT 22

US-11-097-143-27751/C  
; Sequence 27751, Application US/11097143  
; Publication No. US20050208558A1  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; APPLICANT: et al.  
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; FILE REFERENCE: CL000728  
; CURRENT APPLICATION NUMBER: US/11/097,143  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: 60/157,832  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: 60/160,191  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/161,932  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 60/164,769  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/173,383  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/175,693  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/184,831  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/191,637  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 43008  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27751  
; LENGTH: 4972  
; TYPE: DNA  
; ORGANISM: DROSOPHILA  
US-11-097-143-27751

## RESULT 23

US-11-097-143-12094/C  
; Sequence 12094, Application US/11097143

```
Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CLO000728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12094
LENGTH: 4989
TYPE: DNA
ORGANISM: DROSOPHILA
US-11-097-143-12094

Query Match      80.0%; Score 16; DB 10; Length 4989;
Best Local Similarity 87.5%; Pred. No. 3.2e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 GUACAGCCAGGACTAC 18
DB      2160 GTACAGCCAGGACTAC 2145

RESULT 24
US-09-997-722-85
Sequence 85, Application US/09997722
Publication No. US20040072154A1
GENERAL INFORMATION:
APPLICANT: Morris, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71171/RMS/DCP
CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
SOFTWARE: PatentIn version 3.1
SEQ ID NO 85
LENGTH: 96600
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc feature
LOCATION: (7785)..(7808)
OTHER INFORMATION: "n" at positions 7789 through 7808 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (9978)..(9997)
OTHER INFORMATION: "n" at positions 9978 through 9997 can be any base.
FEATURE:
```

```
NAME/KEY: misc feature
LOCATION: (14125)..(14144)
OTHER INFORMATION: "n" at positions 14125 through 14144 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (20780)..(20799)
OTHER INFORMATION: "n" at positions 20780 through 20799 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (27757)..(27816)
OTHER INFORMATION: "n" at positions 27797 through 27816 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (31149)..(31168)
OTHER INFORMATION: "n" at positions 31149 through 31168 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (33786)..(33805)
OTHER INFORMATION: "n" at positions 33786 through 33805 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (34873)..(34892)
OTHER INFORMATION: "n" at positions 34873 through 34892 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (45961)..(45980)
OTHER INFORMATION: "n" at positions 45961 through 45980 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (50121)..(50140)
OTHER INFORMATION: "n" at positions 50121 through 50140 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (53877)..(53896)
OTHER INFORMATION: "n" at positions 53877 through 53896 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (55271)..(55290)
OTHER INFORMATION: "n" at positions 55271 through 55290 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (57012)..(57031)
OTHER INFORMATION: "n" at positions 57012 through 57031 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (60915)..(60934)
OTHER INFORMATION: "n" at positions 60915 through 60934 can be any base.
FEATURE:
NAME/KEY: misc feature
LOCATION: (63387)..(63406)
OTHER INFORMATION: "n" at positions 63387 through 63406 can be any base.
US-09-997-722-85

Query Match      80.0%; Score 16; DB 3; Length 96600;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 GUACAGCCAGGACTAC 18
DB      91766 GTACAGCCAGGACTAC 91781

RESULT 25
US-10-624-149A-2/c
Sequence 2, Application US/10624149A
Publication No. US20040109873A1
GENERAL INFORMATION:
APPLICANT: Neubauer, Antoine
APPLICANT: Ziegler, Christine
TITLE OF INVENTION: gm-Negative EHV-Mutants without Heterologous Elements
FILE REFERENCE: 1/1372
CURRENT APPLICATION NUMBER: US/10/624,149A
CURRENT FILING DATE: 2003-07-21
```

PRIOR APPLICATION NUMBER: 60/403,282  
PRIOR FILING DATE: 2002-08-14  
PRIOR APPLICATION NUMBER: DE 10233064  
PRIOR FILING DATE: 2002-07-19  
PRIOR APPLICATION NUMBER: DE 10317008  
PRIOR FILING DATE: 2003-04-11  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: Patentin Version 3.0  
SEQ ID NO 2  
LENGTH: 145597  
TYPE: DNA  
ORGANISM: Equine herpesvirus 4  
PUBLICATION INFORMATION:  
AUTHORS: Telford, B.A.  
AUTHORS: Watson, M.S.  
AUTHORS: Perry, J.  
AUTHORS: Cullinane, A.A.  
AUTHORS: Davison, A.J.  
TITLE: The DNA sequence of equine herpesvirus-4  
JOURNAL: J. Gen. Virol.  
VOLUME: 79  
ISSUE: 5  
PAGES: 1197-1203  
DATE: MAY-1998  
DATABASE ACCESSION NUMBER: NC 001844, NCBI  
DATABASE ENTRY DATE: 2000-08-01  
US-10-624-149A-2

Query Match 80.0%; Score 16; DB 7; Length 145597;  
Best Local Similarity 87.5%; Pred. No. 2.9e+02;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 GGUACAGCCAGACUA 17  
DB 76347 GGTACAGCCAGACTA 76332

RESULT 26  
US-09-925-065A-132060/C  
Sequence 132060, Application US/09925065A  
Publication No. US20050228172A9  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
Nucleotide Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 132060  
LENGTH: 364  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-132060

Query Match 79.0%; Score 15.8; DB 4; Length 364;  
Best Local Similarity 78.9%; Pred. No. 4.3e+02;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 GGUACAGCCAGACUA 20  
DB 93 GGTACAGCCAGACTA 75

RESULT 27  
US-09-925-065A-290634/C  
Sequence 290634, Application US/09925065A  
Publication No. US20050228172A9  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
Nucleotide Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 290634  
LENGTH: 533  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-290634

Query Match 79.0%; Score 15.8; DB 4; Length 533;  
Best Local Similarity 78.9%; Pred. No. 4.2e+02;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 AGUACAGCCAGACUA 19  
DB 347 AAGTACAGCCAGACTAG 329

RESULT 28  
US-09-925-065A-290636/C  
Sequence 290636, Application US/09925065A  
Publication No. US20050228172A9  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
Nucleotide Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 290636  
LENGTH: 533  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-290636

Query Match 79.0%; Score 15.8; DB 4; Length 533;  
Best Local Similarity 78.9%; Pred. No. 4.2e+02;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGUAAGCCGAGACTUACG 19  
 ||:|||||||:|  
 Db 347 AAGTACAGCCAGACTATG 329

RESULT 29

US-10-357-930-15913/C  
 ; Sequence 15913, Application US/10357930  
 ; Publication No. US20040259086A1

GENERAL INFORMATION:

APPLICANT: Schlegel, Robert

APPLICANT: Endege, Wilson

APPLICANT: Monahan, John

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF

TITLE OF INVENTION: HUMAN PROSTATE CANCER

FILE REFERENCE: MRI-007BCN

CURRENT APPLICATION NUMBER: US/10/357, 930

PRIOR FILING DATE: 2003-02-04

PRIOR APPLICATION NUMBER: 09/785, 276

PRIOR FILING DATE: 2003-02-16

PRIOR APPLICATION NUMBER: 60/183, 319

PRIOR FILING DATE: 2000-02-17

PRIOR APPLICATION NUMBER: 60/189, 862

PRIOR FILING DATE: 2000-03-16

PRIOR APPLICATION NUMBER: 60/207, 454

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 60/211, 314

PRIOR FILING DATE: 2000-06-09

PRIOR APPLICATION NUMBER: 60/219, 007

PRIOR FILING DATE: 2000-07-18

PRIOR APPLICATION NUMBER: 60/255, 281

PRIOR FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 62232

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 15913

LENGTH: 542

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

LOCATION: 502\_516, 518, 525

OTHER INFORMATION: n = A,T,C or G

US-10-357-930-15913

Query Match 79.0%; Score 15.8; DB 8; Length 542;

Best Local Similarity 78.9%; Pred. No. 4.2e+02;

Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGUAAGCCGAGACTUACG 19  
 ||:|||||||:|  
 Db 90 AAGTACAGCCAGACTATG 72

RESULT 30

US-09-925-065A-813093

; Sequence 813093, Application US/09925065A

; Publication No. US2005028172A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925, 065A

PRIOR FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243, 096

PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/252, 147

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250, 092

PRIOR FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/261, 766

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289, 846  
 ; PRIOR FILING DATE: 2001-05-09  
 ; NUMBER OF SEQ ID NOS: 957086  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 813093  
 ; LENGTH: 572  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-925-065A-813093

Query Match 79.0%; Score 15.8; DB 4; Length 572;

Best Local Similarity 84.2%; Pred. No. 4.2e+02;

Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGUAAGCCGAGACTUACGA 20  
 ||:|||||||:|  
 Db 122 GGUAAGCCGAGACTUACGA 140

RESULT 31

US-10-357-930-45741/C

; Sequence 45741, Application US/10357930

; Publication No. US20040259086A1

GENERAL INFORMATION:

APPLICANT: Schlegel, Robert

APPLICANT: Endege, Wilson

APPLICANT: Monahan, John

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF

TITLE OF INVENTION: HUMAN PROSTATE CANCER

FILE REFERENCE: MRI-007BCN

CURRENT APPLICATION NUMBER: US/10/357, 930

PRIOR FILING DATE: 2003-02-04

PRIOR APPLICATION NUMBER: 09/785, 276

PRIOR FILING DATE: 2003-02-16

PRIOR APPLICATION NUMBER: 60/183, 319

PRIOR FILING DATE: 2000-02-17

PRIOR APPLICATION NUMBER: 60/189, 862

PRIOR FILING DATE: 2000-03-16

PRIOR APPLICATION NUMBER: 60/207, 454

PRIOR FILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 60/211, 314

PRIOR FILING DATE: 2000-06-09

PRIOR APPLICATION NUMBER: 60/219, 007

PRIOR FILING DATE: 2000-07-18

PRIOR APPLICATION NUMBER: 60/255, 281

PRIOR FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 62232

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 45741

LENGTH: 592

TYPE: DNA

ORGANISM: Homo sapiens

US-10-357-930-45741

Qy 1 AGGUAAGCCGAGACTUACG 19  
 ||:|||||||:|  
 Db 136 AAGTACAGCCAGACTATG 118

RESULT 32

US-10-767-701-25552

; Sequence 25552, Application US/10767701

; Publication No. US20040172684A1

GENERAL INFORMATION:

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

```
/ TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
/ FILE REFERENCE: 38-21(53535)B
/ CURRENT APPLICATION NUMBER: US/10/767,701
/ CURRENT FILING DATE: 2004-01-29
/ NUMBER OF SEQ ID NOS: 63128
/ SEQ ID NO 25552
/ LENGTH: 610
/ TYPE: DNA
/ ORGANISM: Sorghum bicolor
/ FEATURE:
/ OTHER INFORMATION: Clone ID: 30963281
/ US-10-767-701-25552

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 7; Length 610;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGGUAAGCCAGGAGCTACG 19
Db 334 AGGTCAGGAGGAGCTACG 352

RESULT 33
/ Sequence 59643, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 59643
/ LENGTH: 678
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)..(678)
/ OTHER INFORMATION: unsure at all n locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MWT4577_154393C.1
/ US-10-425-115-59643

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 8; Length 678;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGUAAGCCAGGAGCTACGA 20
Db 473 GGACAGCCAGGAGCAACA 491

RESULT 34
/ Sequence 25544, Application US/10450763
/ Publication No. US20050196754A1
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq, Inc
/ TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
/ FILE REFERENCE: 790CIP3/US
/ CURRENT APPLICATION NUMBER: US/10/450,763
/ CURRENT FILING DATE: 2003-06-11
/ PRIOR APPLICATION NUMBER: PCT/US01/08631
/ PRIOR FILING DATE: 2001-03-30
/ PRIOR APPLICATION NUMBER: 09/540,217
/ PRIOR FILING DATE: 2000-03-31
/ PRIOR APPLICATION NUMBER: 09/649,167
```

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/ PRIOR FILING DATE: 2000-08-23
/ NUMBER OF SEQ ID NOS: 60736
/ SOFTWARE: CuiCom
/ SEQ ID NO 25544
/ LENGTH: 693
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SIMILAR
/ LOCATION: (355)..(690)
/ OTHER INFORMATION: 96% homologous to Escherichia coli Hisp-1like nucleotide
/ OTHER INFORMATION: binding protein (phn), accession number J05260, Smith-Waterman sco
/ OTHER INFORMATION: =528.
/ US-10-450-763-25544

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 9; Length 693;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGUAAGCCAGGAGCTACGA 20
Db 186 GGACAGCCAGGAGCTAAGA 168

RESULT 35
/ Sequence 113386, Application US/10027632
/ Publication No. US20020198371A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 113386
/ LENGTH: 752
/ TYPE: DNA
/ ORGANISM: Human
/ US-10-027-632-113386

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 5; Length 752;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGUAAGCCAGGAGCTACGA 20
Db 451 GGACAGCCAGGAGCTAAGA 433

RESULT 36
/ Sequence 113387, Application US/10027632
/ Publication No. US20020198371A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
```

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; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113387
; LENGTH: 752
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-113387

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 6; Length 752;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGACUACGA 20
DB 451 GGCACAGCCAGACTAAGA 433

RESULT 37
US-10-027-632-113386/c
; Sequence 113386, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113386
; LENGTH: 752
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-113386

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 6; Length 752;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGACUACGA 20
DB 451 GGCACAGCCAGACTAAGA 433
```

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DB 451 GGCACAGCCAGACTAAGA 433

RESULT 38
US-10-027-632-113387/c
; Sequence 113387, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113387
; LENGTH: 752
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-113387

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 6; Length 752;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGACUACGA 20
DB 451 GGCACAGCCAGACTAAGA 433

RESULT 39
US-11-097-143-3449/c
; Sequence 3449, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
```



PRIOR APPLICATION NUMBER: 60/191,637  
PRIOR FILING DATE: 2000-03-23  
NUMBER OF SEQ ID NOS: 43008  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3449  
LENGTH: 978  
TYPE: DNA  
ORGANISM: DROSOPHILA  
US-11-097-143-3449

Query Match 79.0%; Score 15.8; DB 10; Length 978;  
Best Local Similarity 78.9%; Pred. No. 4.2e+02;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGUACAGCCAGGACUACG 19  
Db 236 AGGTATGACCGAGGATACG 218

RESULT 40  
US-10-389-647-172  
Sequence 172, Application US/10389647  
Publication No. US20040033549A1  
GENERAL INFORMATION:  
APPLICANT: GREENBERG, E. Peter  
APPLICANT: SCHUSTER, Martin  
APPLICANT: LOSTROH, Gerd  
TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA  
FILE REFERENCE: UI2-038CP  
CURRENT APPLICATION NUMBER: US/10/389,647  
CURRENT FILING DATE: 2003-03-14  
PRIOR APPLICATION NUMBER: 09/653730  
PRIOR FILING DATE: 2000-09-01  
PRIOR APPLICATION NUMBER: 60/153022  
PRIOR FILING DATE: 1999-09-03  
NUMBER OF SEQ ID NOS: 710  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 172  
LENGTH: 1023  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-10-389-647-172

Query Match 79.0%; Score 15.8; DB 7; Length 1023;  
Best Local Similarity 78.9%; Pred. No. 4.2e+02;  
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGUACAGCCAGGACUACG 19  
Db 166 AGCTACAGCCTGGAATACG 184

RESULT 41  
US-09-866-050A-18  
Sequence 18, Application US/09866050A  
Publication No. US20030040471A1  
GENERAL INFORMATION:  
APPLICANT: Watson, James D.  
APPLICANT: Strachan, Lorna  
APPLICANT: Sleeman, Matthew  
APPLICANT: Onrust, Rene  
APPLICANT: Murison, James G.  
TITLE OF INVENTION: Compositions Isolated From Skin Cells  
TITLE OF INVENTION: and Methods for Their Use  
FILE REFERENCE: 11000.1011c4U  
CURRENT APPLICATION NUMBER: US/09/866,050A  
CURRENT FILING DATE: 2001-05-24  
NUMBER OF SEQ ID NOS: 725  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 18  
LENGTH: 1057  
TYPE: DNA

ORGANISM: Rat  
US-09-866-050A-18

Query Match 79.0%; Score 15.8; DB 3; Length 1057;  
Best Local Similarity 84.2%; Pred. No. 4.2e+02;  
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGUACAGCCAGGACUACGA 20  
Db 1022 GCTACAGCCAGGACUACGA 1040

RESULT 42  
US-10-152-661-18  
Sequence 18, Application US/10152661  
Publication No. US20030022835A1  
GENERAL INFORMATION:  
APPLICANT: Watson, James D.  
APPLICANT: Strachan, Lorna  
APPLICANT: Sleeman, Matthew  
APPLICANT: Onrust, Rene  
APPLICANT: Murison, James G.  
TITLE OF INVENTION: Compositions Isolated From Skin Cells  
TITLE OF INVENTION: and Methods for Their Use  
FILE REFERENCE: 11000.1011c5  
CURRENT APPLICATION NUMBER: US/10/152,661  
CURRENT FILING DATE: 2002-05-20  
PRIOR APPLICATION NUMBER: 09/866,050  
PRIOR FILING DATE: 2001-05-24  
PRIOR APPLICATION NUMBER: 60/221,232  
PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: 60/206,650  
PRIOR FILING DATE: 2000-05-24  
PRIOR APPLICATION NUMBER: 09/312,283  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: PCT/NZ99/00051  
PRIOR FILING DATE: 1999-04-29  
PRIOR APPLICATION NUMBER: 09/188,930  
PRIOR FILING DATE: 1998-11-09  
PRIOR APPLICATION NUMBER: 09/069,726  
PRIOR FILING DATE: 1998-04-29  
NUMBER OF SEQ ID NOS: 725  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 18  
LENGTH: 1057  
TYPE: DNA  
ORGANISM: Rat  
US-10-152-661-18

Query Match 79.0%; Score 15.8; DB 5; Length 1057;  
Best Local Similarity 84.2%; Pred. No. 4.2e+02;  
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGUACAGCCAGGACUACGA 20  
Db 1022 GCTACAGCCAGGACUACGA 1040

RESULT 43  
US-09-866-050A-447  
Sequence 447, Application US/09866050A  
Publication No. US20030040471A1  
GENERAL INFORMATION:  
APPLICANT: Watson, James D.  
APPLICANT: Strachan, Lorna  
APPLICANT: Sleeman, Matthew  
APPLICANT: Onrust, Rene  
APPLICANT: Murison, James G.  
TITLE OF INVENTION: Compositions Isolated From Skin Cells  
TITLE OF INVENTION: and Methods for Their Use  
FILE REFERENCE: 11000.1011c4U

CURRENT APPLICATION NUMBER: US/09/866,050A  
CURRENT FILING DATE: 2001-05-24  
NUMBER OF SEQ ID NOS: 725  
SOFTWARE: FastSeq for Windows Version 4.0  
SRQ ID NO 447  
LENGTH: 1890  
TYPE: DNA  
ORGANISM: Rat  
US-09-866-050A-447

Query Match 79.0%; Score 15.8; DB 3; Length 1890;  
Best Local Similarity 84.2%; Pred. No. 4.1e+02;  
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGUACAGCCAGGACUACGA 20  
Db 881 GCTACAGCCAGGACUACGA 899

## RESULT 44

US-10-152-661-447  
Sequence 447, Application US/10152661  
Publication No. US20030022835A1  
GENERAL INFORMATION:  
APPLICANT: Watson, James D.  
APPLICANT: Strachan, Lorna  
APPLICANT: Sleeman, Matthew  
APPLICANT: Onrust, Rene  
APPLICANT: Muirson, James G.  
APPLICANT: Kumble, Krishanand D.  
TITLE OF INVENTION: Compositions Isolated From Skin Cells  
TITLE OF INVENTION: and Methods for Their Use  
FILE REFERENCE: 11000.1011c5  
CURRENT APPLICATION NUMBER: US/10/152,661  
CURRENT FILING DATE: 2002-05-20  
PRIOR APPLICATION NUMBER: 09/866,050  
PRIOR FILING DATE: 2001-05-24  
PRIOR APPLICATION NUMBER: 60/221,232  
PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: 60/206,650  
PRIOR FILING DATE: 2000-05-24  
PRIOR APPLICATION NUMBER: 09/312,283  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: PCT/NZ99/00051  
PRIOR FILING DATE: 1999-04-29  
PRIOR APPLICATION NUMBER: 09/188,930  
PRIOR FILING DATE: 1998-11-09  
PRIOR APPLICATION NUMBER: 09/069,726  
PRIOR FILING DATE: 1998-04-29  
NUMBER OF SEQ ID NOS: 725  
SOFTWARE: FastSeq for Windows Version 4.0  
SRQ ID NO 447  
LENGTH: 1890  
TYPE: DNA  
ORGANISM: Rat  
US-10-152-661-447

Query Match 79.0%; Score 15.8; DB 5; Length 1890;  
Best Local Similarity 84.2%; Pred. No. 4.1e+02;  
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGUACAGCCAGGACUACGA 20  
Db 881 GCTACAGCCAGGACUACGA 899

## RESULT 45

US-09-866-050A-230  
Sequence 230, Application US/09866050A  
Publication No. US20030040471A1  
GENERAL INFORMATION:  
APPLICANT: Watson, James D.  
APPLICANT: Strachan, Lorna

APPLICANT: Sleeman, Matthew  
APPLICANT: Onrust, Rene  
APPLICANT: Muirson, James G.  
APPLICANT: Kumble, Krishanand D.  
TITLE OF INVENTION: Compositions Isolated From Skin Cells  
TITLE OF INVENTION: and Methods for Their Use  
FILE REFERENCE: 11000.1011c4U  
CURRENT APPLICATION NUMBER: US/09/866,050A  
CURRENT FILING DATE: 2001-05-24  
NUMBER OF SEQ ID NOS: 725  
SOFTWARE: FastSeq for Windows Version 4.0  
SRQ ID NO 230  
LENGTH: 2004  
TYPE: DNA  
ORGANISM: Rat  
US-09-866-050A-230

Query Match 79.0%; Score 15.8; DB 3; Length 2004;  
Best Local Similarity 84.2%; Pred. No. 4.1e+02;  
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGUACAGCCAGGACUACGA 20  
Db 995 GCTACAGCCAGGACUACGA 1013

## RESULT 46

US-10-152-661-230  
Sequence 230, Application US/10152661  
Publication No. US20030022835A1  
GENERAL INFORMATION:  
APPLICANT: Watson, James D.  
APPLICANT: Strachan, Lorna  
APPLICANT: Sleeman, Matthew  
APPLICANT: Onrust, Rene  
APPLICANT: Muirson, James G.  
APPLICANT: Kumble, Krishanand D.  
TITLE OF INVENTION: Compositions Isolated From Skin Cells  
TITLE OF INVENTION: and Methods for Their Use  
FILE REFERENCE: 11000.1011c5  
CURRENT APPLICATION NUMBER: US/10/152,661  
CURRENT FILING DATE: 2002-05-20  
PRIOR APPLICATION NUMBER: 09/866,050  
PRIOR FILING DATE: 2001-05-24  
PRIOR APPLICATION NUMBER: 60/221,232  
PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: 60/206,650  
PRIOR FILING DATE: 2000-05-24  
PRIOR APPLICATION NUMBER: 09/312,283  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: PCT/NZ99/00051  
PRIOR FILING DATE: 1999-04-29  
PRIOR APPLICATION NUMBER: 09/188,930  
PRIOR FILING DATE: 1998-11-09  
PRIOR APPLICATION NUMBER: 09/069,726  
PRIOR FILING DATE: 1998-04-29  
NUMBER OF SEQ ID NOS: 725  
SOFTWARE: FastSeq for Windows Version 4.0  
SRQ ID NO 230  
LENGTH: 2004  
TYPE: DNA  
ORGANISM: Rat  
US-10-152-661-230

Query Match 79.0%; Score 15.8; DB 5; Length 2004;  
Best Local Similarity 84.2%; Pred. No. 4.1e+02;  
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGUACAGCCAGGACUACGA 20  
Db 995 GCTACAGCCAGGACUACGA 1013

```
RESULT 47
US-10-027-632-101774/c
; Sequence 101774, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101774
; LENGTH: 2407
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-101774

Query Match      79.0%; Score 15.8; DB 5; Length 2407;
Best Local Similarity 78.9%; Pred. No. 4.1e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy      1 AGGUAAGCCGAGGACUACG 19
Db      1660 AGGTAAGCCTGAGAGTACG 1642

RESULT 48
US-10-027-632-101774/c
; Sequence 101774, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101774
; LENGTH: 2407
; TYPE: DNA
; ORGANISM: Human
```

```
US-10-027-632-101774

Query Match      79.0%; Score 15.8; DB 6; Length 2407;
Best Local Similarity 78.9%; Pred. No. 4.1e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy      1 AGGUAAGCCGAGGACUACG 19
Db      1660 AGGTAAGCCTGAGAGTACG 1642

RESULT 49
US-10-282-122A-35246/c
; Sequence 35246, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyekind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA,034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PAM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35246
; LENGTH: 2412
; TYPE: DNA
; ORGANISM: Staphylococcus haemolyticus
US-10-282-122A-35246

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Best Local Similarity 78.9%; Pred. No. 4.1e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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RESULT 50
US-11-097-143-3448
; Sequence 3448, Application US/11097143
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; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: C0000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3448
; LENGTH: 3265
; TYPE: DNA
; ORGANISM: DROSOPHILA
; US-11-097-143-3448

Query Match      79.0%; Score 15.8; DB 10; Length 3265;
Best Local Similarity 78.9%; Pred. No. 4.1e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Search completed: March 19, 2006, 07:53:41
Job time : 3030.38 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

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35.104 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 8023312 seqs, 1165852854 residues

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Post-processing: Minimum Match 0%  
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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	16.8	84.0	740	US-09-925-065A-73830
5	16.4	82.0	586	US-09-925-065A-369463
6	16	80.0	1734	US-11-136-527-603
7	16	80.0	90616	US-10-330-773-713
8	15.8	79.0	364	US-09-925-065A-132060
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12	15.8	79.0	1098	US-10-933-182A-77115
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18	15.4	77.0	593	US-09-925-065A-135672
19	15.4	77.0	610	US-09-925-065A-768047
20	15.4	77.0	2208	US-11-121-438-5

21	15.4	77.0	2944	US-10-750-185-56251	Sequence 56251, A
22	15.4	77.0	2944	US-10-750-623-56251	Sequence 56251, A
23	15.4	77.0	137671	US-11-121-086-47	Sequence 47, Appl.
24	15.2	76.0	458	US-09-925-065A-591902	Sequence 591902, A
25	15.2	76.0	487	US-09-925-065A-226237	Sequence 226237, A
26	15.2	76.0	525	US-09-925-065A-20701	Sequence 20701, A
27	15.2	76.0	582	US-09-925-065A-502873	Sequence 502873, A
28	15.2	76.0	598	US-09-925-065A-191670	Sequence 191670, A
29	15.2	76.0	598	US-09-925-065A-544123	Sequence 544123, A
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37	15.2	76.0	101046	US-10-995-561-13330	Sequence 13330, A
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53	15	75.0	1803	US-10-750-185-38766	Sequence 38766, A
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55	15	75.0	44617	US-10-330-773-328	Sequence 328, Appl
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77	14.8	74.0	665	US-09-925-065A-486114	Sequence 486114, A
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C 96	14.8	74.0	3727	12	US-11-091-883-168	Sequence 168, App	169	14.2	71.0	25	12	US-11-135-527-32163	Sequence 32163, A
C 97	14.8	74.0	96128	7	US-10-985-561-13197	Sequence 13197, A	C 170	14.2	71.0	423	6	US-09-925-065A-85591	Sequence 85591, A
C 98	14.8	74.0	12279	7	US-10-330-773-29	Sequence 29, App	171	14.2	71.0	480	6	US-09-925-065A-48925	Sequence 48925, A
C 99	14.8	74.0	17460	7	US-10-330-773-497	Sequence 497, App	172	14.2	71.0	480	6	US-09-925-065A-48926	Sequence 48926, A
C 100	14.8	74.0	180026	7	US-10-330-773-729	Sequence 729, App	173	14.2	71.0	516	6	US-09-925-065A-608920	Sequence 608920, A
C 101	14.8	74.0	415117	10	US-11-101-244-1134892	Sequence 1134892, A	174	14.2	71.0	519	6	US-09-925-065A-763484	Sequence 763484, A
C 102	14.4	72.0	19	10	US-11-083-784-1134892	Sequence 1134892, A	175	14.2	71.0	537	6	US-09-925-065A-731146	Sequence 731146, A
C 103	14.4	72.0	19	11	US-09-925-065A-502200	Sequence 502200, A	C 176	14.2	71.0	545	6	US-09-925-065A-255405	Sequence 255405, A
C 104	14.4	72.0	360	12	US-11-128-061-5789	Sequence 5789, App	C 177	14.2	71.0	545	6	US-09-925-065A-552821	Sequence 552821, A
C 105	14.4	72.0	495	12	US-11-128-049-5789	Sequence 5789, App	178	14.2	71.0	586	6	US-09-925-065A-814628	Sequence 814628, A
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C 107	14.4	72.0	514	6	US-09-925-065A-2147	Sequence 2147, App	C 181	14.2	71.0	595	6	US-09-925-065A-139343	Sequence 139343, A
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C 111	14.4	72.0	593	6	US-09-925-065A-478144	Sequence 478144, A	C 185	14.2	71.0	606	6	US-09-925-065A-403422	Sequence 403422, A
C 112	14.4	72.0	600	8	US-10-750-623-3297	Sequence 3297, App	C 186	14.2	71.0	644	6	US-09-925-065A-98357	Sequence 98357, A
C 113	14.4	72.0	600	8	US-09-925-065A-206702	Sequence 206702, A	C 187	14.2	71.0	644	6	US-09-925-065A-98358	Sequence 98358, A
C 114	14.4	72.0	610	6	US-09-925-065A-206703	Sequence 206703, A	C 188	14.2	71.0	644	6	US-09-925-065A-772097	Sequence 772097, A
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C 129	14.4	72.0	2092	8	US-10-750-185-53152	Sequence 53152, A	C 203	14.2	71.0	1172	6	US-09-925-065A-26007	Sequence 26007, A
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C 131	14.4	72.0	42379	7	US-10-330-773-637	Sequence 637, App	C 205	14.2	71.0	1182	7	US-10-887-540-4	Sequence 540-4, A
C 132	14.4	72.0	43572	7	US-10-330-773-838	Sequence 838, App	C 206	14.2	71.0	1353	7	US-09-978-360A-69	Sequence 360A-69, A
C 133	14.4	72.0	50605	7	US-10-330-773-778	Sequence 778, App	C 207	14.2	71.0	1364	5	US-11-096-568A-11389	Sequence 11389, A
C 134	14.4	72.0	50605	7	US-10-330-773-669	Sequence 669, App	C 208	14.2	71.0	1391	9	US-11-096-568A-677260	Sequence 677260, A
C 135	14.4	72.0	53411	7	US-10-330-773-57	Sequence 57, App	C 209	14.2	71.0	1484	6	US-09-925-065A-18934	Sequence 18934, A
C 136	14.4	72.0	71594	7	US-10-330-773-738	Sequence 738, App	C 210	14.2	71.0	1557	8	US-10-750-185-59105	Sequence 59105, A
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C 141	14.4	72.0	88421	12	US-11-205-109-1	Sequence 1, App	C 215	14.2	71.0	1753	8	US-10-750-623-45812	Sequence 45812, A
C 142	14.4	72.0	88421	12	US-10-330-773-73	Sequence 73, App	C 216	14.2	71.0	1825	9	US-11-096-568A-18934	Sequence 18934, A
C 143	14.4	72.0	88421	12	US-10-330-773-73	Sequence 73, App	C 217	14.2	71.0	1825	9	US-11-186-284-88	Sequence 284-88, A
C 144	14.4	72.0	92969	7	US-10-330-773-625	Sequence 625, App	C 218	14.2	71.0	1840	12	US-11-115-877-1	Sequence 877-1, A
C 145	14.4	72.0	92969	7	US-10-330-773-178	Sequence 178, App	C 219	14.2	71.0	1840	12	US-10-932-182A-2146	Sequence 2146, App
C 146	14.4	72.0	95484	7	US-10-330-773-896	Sequence 896, App	C 220	14.2	71.0	1962	7	US-10-932-182A-2146	Sequence 2146, App
C 147	14.4	72.0	98638	7	US-10-330-773-896	Sequence 896, App	C 221	14.2	71.0	2017	7	US-10-821-234-107	Sequence 234-107, A
C 148	14.4	72.0	100864	7	US-10-330-773-839	Sequence 839, App	C 222	14.2	71.0	2017	7	US-10-932-182A-2146	Sequence 2146, App
C 149	14.4	72.0	114454	7	US-10-330-773-850	Sequence 850, App	C 223	14.2	71.0	2091	8	US-10-955-054A-37	Sequence 054A-37, A
C 150	14.4	72.0	118654	7	US-10-330-773-826	Sequence 826, App	C 224	14.2	71.0	2205	9	US-11-096-568A-19875	Sequence 19875, A
C 151	14.4	72.0	137454	7	US-10-330-773-365	Sequence 365, App	C 225	14.2	71.0	2205	9	US-11-024-958-152	Sequence 152, App
C 152	14.4	72.0	137454	7	US-10-330-773-365	Sequence 365, App	C 226	14.2	71.0	2347	12	US-11-112-908-16	Sequence 2301, App
C 153	14.4	72.0	171936	8	US-10-933-025-24	Sequence 24, App	C 227	14.2	71.0	4335	12	US-11-136-527-2301	Sequence 2788, App
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C 155	14.4	72.0	174600	7	US-10-330-773-497	Sequence 497, App	C 229	14.2	71.0	6474	7	US-10-693-483-27	Sequence 641, App
C 156	14.4	72.0	175603	7	US-10-330-773-531	Sequence 531, App	C 230	14.2	71.0	8280	12	US-11-000-688-641	Sequence 269, App
C 157	14.4	72.0	177175	12	US-11-121-086-79	Sequence 79, App	C 231	14.2	71.0	86149	7	US-10-330-773-269	Sequence 254, App
C 158	14.4	72.0	178024	7	US-10-330-773-698	Sequence 698, App	C 232	14.2	71.0	124972	12	US-11-121-086-100	Sequence 100, App
C 159	14.4	72.0	201990	8	US-10-775-169-52	Sequence 169, App	C 233	14.2	71.0	142605	12	US-11-121-086-64	Sequence 64, App
C 160	14.4	72.0	201990	8	US-10-995-561-13303	Sequence 13303, A	C 234	14.2	71.0	171182	12	US-11-112-908-38	Sequence 38, App
C 161	14.4	72.0	204803	7	US-10-330-773-325	Sequence 325, App	C 235	14.2	71.0	171182	12	US-11-112-908-60	Sequence 60, App
C 162	14.4	72.0	205388	7	US-10-330-773-537	Sequence 537, App	C 236	14.2	71.0	171457	12	US-11-114-798-48	Sequence 48, App
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C 165	14.4	72.0	358847	7	US-10-330-773-305	Sequence 305, App	C 239	14.2	71.0	1082144	12	US-11-117-187-211	Sequence 211, App

C 240	14.2	71.0	1125000	8	US-10-995-561-13286	Sequence 13286, A	C 313	13.8	69.0	618	6	US-09-925-065A-463684	Sequence 463684, A
C 241	14	70.0	50	12	US-11-175-859-55957	Sequence 55957, A	C 314	13.8	69.0	618	6	US-09-925-065A-771941	Sequence 771941, A
C 242	14	70.0	50	12	US-11-175-859-55957	Sequence 85379, A	C 315	13.8	69.0	622	6	US-09-925-065A-45899	Sequence 45899, A
C 243	14	70.0	521	6	US-09-925-065A-220524	Sequence 220524, A	C 316	13.8	69.0	622	6	US-09-925-065A-54012	Sequence 54012, A
C 244	14	70.0	528	6	US-09-925-065A-844115	Sequence 844115, A	C 317	13.8	69.0	626	6	US-09-925-065A-229555	Sequence 229555, A
C 245	14	70.0	599	6	US-09-925-065A-274234	Sequence 274234, A	C 318	13.8	69.0	626	6	US-09-925-065A-229555	Sequence 229555, A
C 246	14	70.0	599	6	US-09-925-065A-274235	Sequence 274235, A	C 319	13.8	69.0	627	6	US-09-925-065A-673911	Sequence 673911, A
C 247	14	70.0	603	6	US-09-925-065A-538164	Sequence 538164, A	C 320	13.8	69.0	632	6	US-09-925-065A-78636	Sequence 78636, A
C 248	14	70.0	632	6	US-09-925-065A-638193	Sequence 638193, A	C 321	13.8	69.0	632	6	US-09-925-065A-553362	Sequence 553362, A
C 249	14	70.0	1260	6	US-09-925-065A-64739	Sequence 64739, A	C 322	13.8	69.0	632	6	US-09-925-065A-570548	Sequence 570548, A
C 250	14	70.0	1260	6	US-09-925-065A-64740	Sequence 64740, A	C 323	13.8	69.0	637	6	US-09-925-065A-506223	Sequence 506223, A
C 251	14	70.0	2193	6	US-09-925-065A-92362	Sequence 92362, A	C 324	13.8	69.0	640	6	US-09-925-065A-780138	Sequence 780138, A
C 252	14	70.0	2193	6	US-09-925-065A-92363	Sequence 92363, A	C 325	13.8	69.0	644	6	US-09-925-065A-401138	Sequence 401138, A
C 253	14	70.0	2978	8	US-10-955-054A-55	Sequence 55, App1	C 326	13.8	69.0	649	6	US-09-925-065A-308983	Sequence 308983, A
C 254	14	70.0	13227	12	US-11-124-367A-5028	Sequence 5028, App	C 327	13.8	69.0	649	6	US-09-925-065A-509905	Sequence 509905, A
C 255	14	70.0	215308	12	US-11-121-086-77	Sequence 77, App1	C 328	13.8	69.0	653	6	US-09-925-065A-903905	Sequence 903905, A
C 256	13.8	69.0	19	11	US-11-083-784-1087909	Sequence 1087909, A	C 329	13.8	69.0	658	6	US-09-925-065A-916737	Sequence 916737, A
C 257	13.8	69.0	25	7	US-10-932-182A-73105	Sequence 73105, A	C 330	13.8	69.0	688	6	US-09-925-065A-72424	Sequence 72424, A
C 258	13.8	69.0	25	7	US-10-932-182A-73105	Sequence 73105, A	C 331	13.8	69.0	697	6	US-09-925-065A-887088	Sequence 887088, A
C 259	13.8	69.0	25	7	US-10-933-982-101531	Sequence 101531, A	C 332	13.8	69.0	697	6	US-09-925-065A-889988	Sequence 889988, A
C 260	13.8	69.0	25	7	US-10-933-982-160709	Sequence 160709, A	C 333	13.8	69.0	699	6	US-09-925-065A-866513	Sequence 866513, A
C 261	13.8	69.0	25	7	US-10-933-982-160710	Sequence 160710, A	C 334	13.8	69.0	714	8	US-10-750-623-55116	Sequence 55116, A
C 262	13.8	69.0	25	7	US-11-121-849-48078	Sequence 48078, A	C 335	13.8	69.0	743	8	US-10-750-623-55116	Sequence 55116, A
C 263	13.8	69.0	25	12	US-11-121-849-48078	Sequence 48078, A	C 336	13.8	69.0	743	8	US-10-750-623-55116	Sequence 55116, A
C 264	13.8	69.0	25	12	US-11-121-849-48078	Sequence 48078, A	C 337	13.8	69.0	755	8	US-10-750-623-55116	Sequence 55116, A
C 265	13.8	69.0	25	12	US-11-121-849-48078	Sequence 48078, A	C 338	13.8	69.0	755	8	US-10-750-623-55116	Sequence 55116, A
C 266	13.8	69.0	25	12	US-11-121-849-48078	Sequence 48078, A	C 339	13.8	69.0	842	6	US-09-925-065A-7632	Sequence 7632, App
C 267	13.8	69.0	25	12	US-11-121-849-48078	Sequence 48078, A	C 340	13.8	69.0	959	8	US-10-750-623-55116	Sequence 55116, A
C 268	13.8	69.0	67	8	US-10-310-914A-10237	Sequence 10237, A	C 341	13.8	69.0	959	8	US-10-750-623-55116	Sequence 55116, A
C 269	13.8	69.0	67	8	US-10-310-914A-10237	Sequence 10237, A	C 342	13.8	69.0	988	6	US-09-925-065A-84541	Sequence 84541, A
C 270	13.8	69.0	201	12	US-11-124-367A-25771	Sequence 25771, A	C 343	13.8	69.0	988	6	US-09-925-065A-84541	Sequence 84541, A
C 271	13.8	69.0	201	12	US-11-124-367A-25771	Sequence 25771, A	C 344	13.8	69.0	1015	6	US-09-925-065A-84541	Sequence 84541, A
C 272	13.8	69.0	360	9	US-11-021-492-317	Sequence 317, App	C 345	13.8	69.0	1021	6	US-09-925-065A-698686	Sequence 698686, A
C 273	13.8	69.0	420	7	US-10-932-182A-2480	Sequence 2480, App	C 346	13.8	69.0	1192	9	US-11-096-568A-2010	Sequence 2010, A
C 274	13.8	69.0	420	7	US-10-932-182A-2480	Sequence 2480, App	C 347	13.8	69.0	1239	6	US-09-925-065A-708005	Sequence 708005, A
C 275	13.8	69.0	446	6	US-09-925-065A-627584	Sequence 627584, A	C 348	13.8	69.0	1307	6	US-09-925-065A-711937	Sequence 711937, A
C 276	13.8	69.0	446	6	US-09-925-065A-528014	Sequence 528014, A	C 349	13.8	69.0	1307	6	US-09-925-065A-711938	Sequence 711938, A
C 277	13.8	69.0	451	6	US-09-925-065A-522088	Sequence 522088, A	C 350	13.8	69.0	1443	12	US-11-170-693-66	Sequence 66, App1
C 278	13.8	69.0	467	6	US-09-925-065A-257668	Sequence 257668, A	C 351	13.8	69.0	1544	8	US-10-750-623-60520	Sequence 60520, A
C 279	13.8	69.0	467	6	US-09-925-065A-257668	Sequence 257668, A	C 352	13.8	69.0	1544	8	US-10-750-623-60520	Sequence 60520, A
C 280	13.8	69.0	467	6	US-09-925-065A-257668	Sequence 257668, A	C 353	13.8	69.0	1559	8	US-10-750-623-45753	Sequence 45753, A
C 281	13.8	69.0	467	6	US-09-925-065A-257668	Sequence 257668, A	C 354	13.8	69.0	1559	8	US-10-750-623-45753	Sequence 45753, A
C 282	13.8	69.0	495	6	US-09-925-065A-227603	Sequence 227603, A	C 355	13.8	69.0	1625	8	US-10-750-623-25955	Sequence 25955, A
C 283	13.8	69.0	507	6	US-09-925-065A-588678	Sequence 588678, A	C 356	13.8	69.0	1625	8	US-10-750-623-25955	Sequence 25955, A
C 284	13.8	69.0	519	6	US-09-925-065A-829674	Sequence 829674, A	C 357	13.8	69.0	1625	8	US-10-750-623-25955	Sequence 25955, A
C 285	13.8	69.0	522	6	US-09-925-065A-842852	Sequence 842852, A	C 358	13.8	69.0	1675	8	US-10-750-623-40233	Sequence 40233, A
C 286	13.8	69.0	524	6	US-09-925-065A-654698	Sequence 654698, A	C 359	13.8	69.0	1755	8	US-10-750-623-40233	Sequence 40233, A
C 287	13.8	69.0	527	6	US-09-925-065A-858078	Sequence 858078, A	C 360	13.8	69.0	1780	6	US-09-925-065A-78692	Sequence 78692, A
C 288	13.8	69.0	533	6	US-09-925-065A-477710	Sequence 477710, A	C 361	13.8	69.0	1876	8	US-10-750-623-34164	Sequence 34164, A
C 289	13.8	69.0	533	6	US-09-925-065A-585475	Sequence 585475, A	C 362	13.8	69.0	1876	8	US-10-750-623-34164	Sequence 34164, A
C 290	13.8	69.0	534	6	US-09-925-065A-259219	Sequence 259219, A	C 363	13.8	69.0	1917	8	US-10-750-623-53627	Sequence 53627, A
C 291	13.8	69.0	534	6	US-09-925-065A-781816	Sequence 781816, A	C 364	13.8	69.0	1917	8	US-10-750-623-53627	Sequence 53627, A
C 292	13.8	69.0	556	6	US-09-925-065A-268742	Sequence 268742, A	C 365	13.8	69.0	1933	8	US-10-750-623-25283	Sequence 25283, A
C 293	13.8	69.0	559	6	US-09-925-065A-553657	Sequence 553657, A	C 366	13.8	69.0	1933	8	US-10-750-623-25283	Sequence 25283, A
C 294	13.8	69.0	560	6	US-09-925-065A-46136	Sequence 46136, A	C 367	13.8	69.0	2162	8	US-10-750-623-34194	Sequence 34194, A
C 295	13.8	69.0	560	6	US-09-925-065A-46136	Sequence 46136, A	C 368	13.8	69.0	2162	8	US-10-750-623-34194	Sequence 34194, A
C 296	13.8	69.0	563	6	US-09-925-065A-178442	Sequence 178442, A	C 369	13.8	69.0	2162	8	US-10-750-623-34194	Sequence 34194, A
C 297	13.8	69.0	568	6	US-09-925-065A-337281	Sequence 337281, A	C 370	13.8	69.0	2250	7	US-10-932-182A-3450	Sequence 3450, App
C 298	13.8	69.0	568	6	US-09-925-065A-337282	Sequence 337282, A	C 371	13.8	69.0	2250	7	US-10-932-182A-3450	Sequence 3450, App
C 299	13.8	69.0	577	6	US-09-925-065A-178454	Sequence 178454, A	C 372	13.8	69.0	2250	7	US-10-932-182A-3450	Sequence 3450, App
C 300	13.8	69.0	577	6	US-09-925-065A-178454	Sequence 178454, A	C 373	13.8	69.0	2339	12	US-11-136-527-2338	Sequence 2338, App
C 301	13.8	69.0	578	6	US-09-925-065A-422885	Sequence 422885, A	C 374	13.8	69.0	2400	7	US-10-932-182A-2510	Sequence 2510, App
C 302	13.8	69.0	579	6	US-09-925-065A-113642	Sequence 113642, A	C 375	13.8	69.0	2400	7	US-10-932-182A-2510	Sequence 2510, App
C 303	13.8	69.0	579	6	US-09-925-065A-113642	Sequence 113642, A	C 376	13.8	69.0	2400	7	US-10-932-182A-2510	Sequence 2510, App
C 304	13.8	69.0	579	6	US-09-925-065A-113642	Sequence 113642, A	C 377	13.8	69.0	2400	7	US-10-932-182A-2510	Sequence 2510, App
C 305	13.8	69.0	584	6	US-09-925-065A-434990	Sequence 434990, A	C 378	13.8	69.0	2960	8	US-10-750-623-42122	Sequence 42122, A
C 306	13.8	69.0	589	6	US-09-925-065A-152874	Sequence 152874, A	C 379	13.8	69.0	2960	8	US-10-750-623-42122	Sequence 42122, A
C 307	13.8	69.0	594	6	US-09-925-065A-198047	Sequence 198047, A	C 380	13.8	69.0	2960	8	US-10-750-623-42122	Sequence 42122, A
C 308	13.8	69.0	597	6	US-09-925-065A-455399	Sequence 455399, A	C 381	13.8	69.0	2961	8	US-10-750-623-37281	Sequence 37281, A
C 309	13.8	69.0	612	6	US-09-925-065A-868311	Sequence 868311, A	C 382	13.8	69.0	2990	9	US-11-072-512-595	Sequence 595, App
C 310	13.8	69.0	612	6	US-09-925-065A-868312	Sequence 868312, A	C 383	13.8	69.0	3107	8	US-10-750-623-51471	Sequence 51471, A
C 311	13.8	69.0	613	6	US-09-925-065A-568455	Sequence 568455, A	C 384	13.8	69.0	3107	8	US-10-750-623-51471	Sequence 51471, A
C 312	13.8	69.0	613	6	US-09-925-065A-568456	Sequence 568456, A	C 385	13.8	69.0	3654	7	US-10-750-623-51471	Sequence 51471, A



C 386	13.8	69.0	3684	8	US-10-750-185-51696	Sequence 51696, A	459	13.6	68.0	556	6	US-09-925-065A-431549	Sequence 431549, A
C 387	13.8	69.0	3684	8	US-10-750-623-51696	Sequence 51696, A	460	13.6	68.0	561	7	US-10-932-182A-4251	Sequence 4251, Ap
C 388	13.8	69.0	3790	8	US-10-750-185-50504	Sequence 50504, A	461	13.6	68.0	562	7	US-10-932-182A-4251	Sequence 4251, Ap
C 389	13.8	69.0	3790	8	US-10-750-623-50504	Sequence 50504, A	462	13.6	68.0	563	6	US-09-925-065A-521835	Sequence 521835, A
C 390	13.8	69.0	3946	9	US-11-230-180-4	Sequence 4, Appl1	463	13.6	68.0	564	6	US-09-925-065A-226763	Sequence 226763, A
C 391	13.8	69.0	4050	7	US-10-932-182A-6036	Sequence 6036, Ap	464	13.6	68.0	565	6	US-09-925-065A-634830	Sequence 634830, A
C 392	13.8	69.0	4050	7	US-10-932-182A-6036	Sequence 6036, Ap	465	13.6	68.0	566	6	US-09-925-065A-221668	Sequence 221668, A
C 393	13.8	69.0	4285	8	US-10-947-249-175	Sequence 175, App	466	13.6	68.0	567	6	US-09-925-065A-835167	Sequence 835167, A
C 394	13.8	69.0	4370	8	US-10-750-185-35839	Sequence 35839, A	467	13.6	68.0	567	6	US-09-925-065A-835168	Sequence 835168, A
C 395	13.8	69.0	4370	8	US-10-750-623-35839	Sequence 35839, A	468	13.6	68.0	570	6	US-09-925-065A-206181	Sequence 206181, A
C 396	13.8	69.0	7944	8	US-10-821-234-451	Sequence 451, App	469	13.6	68.0	573	6	US-09-925-065A-423954	Sequence 423954, A
C 397	13.8	69.0	11062	12	US-11-128-061-566	Sequence 566, App	470	13.6	68.0	573	6	US-09-925-065A-423955	Sequence 423955, A
C 398	13.8	69.0	11062	12	US-11-128-049-566	Sequence 566, App	471	13.6	68.0	575	6	US-09-925-065A-843955	Sequence 843955, A
C 399	13.8	69.0	11062	12	US-11-177-504-1	Sequence 1, Appl1	472	13.6	68.0	576	6	US-09-925-065A-785503	Sequence 785503, A
C 400	13.8	69.0	11121	9	US-11-200-710-1	Sequence 10, Appl1	473	13.6	68.0	576	6	US-09-925-065A-845009	Sequence 845009, A
C 401	13.8	69.0	11121	12	US-11-124-020A-10	Sequence 3, Appl1	474	13.6	68.0	576	6	US-09-925-065A-845010	Sequence 845010, A
C 402	13.8	69.0	11121	12	US-11-123-656A-3	Sequence 474, App	475	13.6	68.0	578	6	US-09-925-065A-119024	Sequence 119024, A
C 403	13.8	69.0	11121	12	US-10-330-773-474	Sequence 62, Appl1	476	13.6	68.0	578	6	US-09-925-065A-119025	Sequence 119025, A
C 404	13.8	69.0	21850	7	US-10-893-483-62	Sequence 62, Appl1	477	13.6	68.0	578	6	US-09-925-065A-119026	Sequence 119026, A
C 405	13.8	69.0	28672	7	US-10-893-483-62	Sequence 146, App	478	13.6	68.0	582	6	US-09-925-065A-654536	Sequence 654536, A
C 406	13.8	69.0	39700	12	US-11-124-020A-1	Sequence 1, Appl1	479	13.6	68.0	582	6	US-09-925-065A-761200	Sequence 761200, A
C 407	13.8	69.0	43445	12	US-11-124-020A-2	Sequence 2, Appl1	480	13.6	68.0	582	6	US-09-925-065A-663345	Sequence 663345, A
C 408	13.8	69.0	43445	12	US-11-124-020A-2	Sequence 2892, Ap	481	13.6	68.0	583	6	US-09-925-065A-663345	Sequence 663345, A
C 409	13.8	69.0	50484	7	US-10-893-483-63	Sequence 63, Appl1	482	13.6	68.0	585	6	US-09-925-065A-129784	Sequence 129784, A
C 410	13.8	69.0	50833	7	US-10-330-773-188	Sequence 188, App	483	13.6	68.0	587	6	US-09-925-065A-745630	Sequence 745630, A
C 411	13.8	69.0	72352	7	US-10-330-773-43	Sequence 43, Appl1	484	13.6	68.0	591	6	US-09-925-065A-297548	Sequence 297548, A
C 412	13.8	69.0	109974	12	US-11-117-187-204	Sequence 105, App	485	13.6	68.0	591	6	US-09-925-065A-734060	Sequence 734060, A
C 413	13.8	69.0	124285	7	US-10-893-483-105	Sequence 13262, A	486	13.6	68.0	593	6	US-09-925-065A-779044	Sequence 779044, A
C 414	13.8	69.0	141121	8	US-10-995-561-13262	Sequence 90, Appl1	487	13.6	68.0	594	6	US-09-925-065A-153801	Sequence 153801, A
C 415	13.8	69.0	172111	12	US-11-121-086-28	Sequence 28, Appl1	488	13.6	68.0	594	6	US-09-925-065A-534972	Sequence 534972, A
C 416	13.8	69.0	172111	12	US-11-121-086-28	Sequence 664, App	489	13.6	68.0	594	6	US-09-925-065A-534973	Sequence 534973, A
C 417	13.8	69.0	179487	7	US-10-330-773-664	Sequence 54, Appl1	490	13.6	68.0	598	6	US-09-925-065A-850507	Sequence 850507, A
C 418	13.8	69.0	195958	8	US-10-995-561-13489	Sequence 13489, A	491	13.6	68.0	599	6	US-09-925-065A-88610	Sequence 88610, A
C 419	13.8	69.0	195958	8	US-11-121-086-9	Sequence 9, Appl1	492	13.6	68.0	600	8	US-10-750-185-11954	Sequence 11954, A
C 420	13.8	69.0	196200	12	US-11-121-086-10	Sequence 10, Appl1	493	13.6	68.0	600	8	US-10-750-185-11954	Sequence 11954, A
C 421	13.8	69.0	196200	12	US-10-330-773-119	Sequence 119, App	494	13.6	68.0	600	8	US-10-750-623-21954	Sequence 21954, A
C 422	13.8	69.0	228006	7	US-10-330-773-111	Sequence 111, App	495	13.6	68.0	600	8	US-10-750-623-4489	Sequence 4489, A
C 423	13.8	69.0	254481	8	US-10-310-914A-677076	Sequence 677076, A	496	13.6	68.0	601	8	US-10-750-185-4744	Sequence 4744, Ap
C 424	13.6	68.0	25	12	US-11-136-527-357805	Sequence 357805, A	497	13.6	68.0	601	8	US-10-750-623-4744	Sequence 4744, Ap
C 425	13.6	68.0	336	7	US-10-932-182A-173501	Sequence 173501, A	499	13.6	68.0	602	6	US-09-925-065A-258134	Sequence 258134, A
C 426	13.6	68.0	336	7	US-10-932-182A-173501	Sequence 173501, A	500	13.6	68.0	604	6	US-09-925-065A-13715	Sequence 13715, A
C 427	13.6	68.0	387	12	US-11-043-752-4275	Sequence 4275, Ap	501	13.6	68.0	604	6	US-09-925-065A-13716	Sequence 13716, A
C 428	13.6	68.0	387	12	US-10-769-744-499	Sequence 499, App	502	13.6	68.0	604	6	US-09-925-065A-13717	Sequence 13717, A
C 429	13.6	68.0	396	12	US-11-096-191-607	Sequence 607, App	503	13.6	68.0	604	6	US-09-925-065A-198853	Sequence 198853, A
C 430	13.6	68.0	441	6	US-09-925-065A-486543	Sequence 486543, A	504	13.6	68.0	606	6	US-09-925-065A-308956	Sequence 308956, A
C 431	13.6	68.0	441	6	US-09-925-065A-486544	Sequence 486544, A	505	13.6	68.0	606	6	US-09-925-065A-177055	Sequence 177055, A
C 432	13.6	68.0	444	6	US-09-925-065A-650636	Sequence 650636, A	506	13.6	68.0	607	6	US-09-925-065A-192849	Sequence 192849, A
C 433	13.6	68.0	444	6	US-09-925-065A-15458	Sequence 15458, A	507	13.6	68.0	608	6	US-09-925-065A-816737	Sequence 816737, A
C 434	13.6	68.0	455	6	US-09-925-065A-423887	Sequence 423887, A	508	13.6	68.0	609	6	US-09-925-065A-439546	Sequence 439546, A
C 435	13.6	68.0	471	6	US-10-932-182A-959	Sequence 959, App	509	13.6	68.0	616	6	US-09-925-065A-340969	Sequence 340969, A
C 436	13.6	68.0	480	7	US-10-932-182A-959	Sequence 959, App	510	13.6	68.0	623	6	US-09-925-065A-758947	Sequence 758947, A
C 437	13.6	68.0	480	7	US-10-932-182A-959	Sequence 348077, A	511	13.6	68.0	624	6	US-09-925-065A-47243	Sequence 47243, A
C 438	13.6	68.0	485	6	US-09-925-065A-472268	Sequence 472268, A	512	13.6	68.0	624	6	US-09-925-065A-756590	Sequence 756590, A
C 439	13.6	68.0	485	6	US-09-925-065A-54398	Sequence 54398, A	513	13.6	68.0	626	6	US-09-925-065A-255869	Sequence 255869, A
C 440	13.6	68.0	514	6	US-09-925-065A-284463	Sequence 284463, A	514	13.6	68.0	626	6	US-09-925-065A-553611	Sequence 553611, A
C 441	13.6	68.0	514	6	US-09-925-065A-267826	Sequence 267826, A	515	13.6	68.0	627	6	US-09-925-065A-359785	Sequence 359785, A
C 442	13.6	68.0	519	6	US-09-925-065A-214374	Sequence 214374, A	516	13.6	68.0	630	6	US-09-925-065A-758947	Sequence 758947, A
C 443	13.6	68.0	527	6	US-09-925-065A-129788	Sequence 129788, A	517	13.6	68.0	631	6	US-09-925-065A-876535	Sequence 876535, A
C 444	13.6	68.0	527	6	US-09-925-065A-129788	Sequence 129788, A	518	13.6	68.0	632	6	US-09-925-065A-905711	Sequence 905711, A
C 445	13.6	68.0	529	6	US-09-925-065A-821038	Sequence 821038, A	519	13.6	68.0	633	6	US-09-925-065A-497701	Sequence 497701, A
C 446	13.6	68.0	529	6	US-09-925-065A-821038	Sequence 921809, A	520	13.6	68.0	633	6	US-09-925-065A-3346	Sequence 3346, Ap
C 447	13.6	68.0	541	6	US-09-925-065A-921810	Sequence 921810, A	521	13.6	68.0	641	6	US-09-925-065A-679325	Sequence 679325, A
C 448	13.6	68.0	541	6	US-09-925-065A-921810	Sequence 921810, A	522	13.6	68.0	641	6	US-09-925-065A-753719	Sequence 753719, A
C 449	13.6	68.0	541	6	US-09-925-065A-921826	Sequence 921826, A	523	13.6	68.0	641	6	US-09-925-065A-753719	Sequence 753719, A
C 450	13.6	68.0	541	6	US-09-925-065A-921826	Sequence 921826, A	524	13.6	68.0	651	6	US-09-925-065A-900379	Sequence 900379, A
C 451	13.6	68.0	541	6	US-09-925-065A-946735	Sequence 946735, A	525	13.6	68.0	651	6	US-09-925-065A-669642	Sequence 669642, A
C 452	13.6	68.0	541	6	US-09-925-065A-946735	Sequence 946735, A	526	13.6	68.0	655	6	US-09-925-065A-669643	Sequence 669643, A
C 453	13.6	68.0	541	6	US-09-925-065A-946742	Sequence 946742, A	527	13.6	68.0	655	6	US-09-925-065A-19668	Sequence 19668, A
C 454	13.6	68.0	541	6	US-09-925-065A-946742	Sequence 946742, A	528	13.6	68.0	720	6	US-09-925-065A-13669	Sequence 13669, A
C 455	13.6	68.0	545	6	US-09-925-065A-604819	Sequence 604819, A	529	13.6	68.0	720	6	US-09-925-065A-13669	Sequence 13669, A
C 456	13.6	68.0	552	12	US-11-136-527-3480	Sequence 3480, Ap	530	13.6	68.0	726	6	US-09-925-065A-53322	Sequence 53322, A
C 457	13.6	68.0	552	12	US-11-136-527-3480	Sequence 3480, Ap	531	13.6	68.0	726	6	US-09-925-065A-53322	Sequence 53322, A
C 458	13.6	68.0	554	6	US-09-925-065A-199532	Sequence 199532, A	532	13.6	68.0	750	7	US-10-330-773-126	Sequence 126, App

532	13.6	68.0	765	8	US-10-750-185-49132	Sequence 49132, A	605	13.6	68.0	2446	9	US-11-051-720-1489	Sequence 1489, Ap
533	13.6	68.0	765	8	US-10-750-623-49132	Sequence 49132, A	606	13.6	68.0	2514	9	US-11-051-720-1610	Sequence 1610, Ap
534	13.6	68.0	775	6	US-09-925-065A-951648	Sequence 951648, A	607	13.6	68.0	2532	8	US-10-750-185-62974	Sequence 62974, A
535	13.6	68.0	788	6	US-09-925-065A-109095	Sequence 709095, A	608	13.6	68.0	2532	8	US-10-750-623-62974	Sequence 62974, A
536	13.6	68.0	788	6	US-09-925-065A-109096	Sequence 709096, A	609	13.6	68.0	2605	9	US-11-051-720-1486	Sequence 1486, Ap
537	13.6	68.0	916	6	US-09-925-065A-87409	Sequence 87409, A	610	13.6	68.0	2611	9	US-11-051-720-1488	Sequence 1488, Ap
538	13.6	68.0	923	6	US-09-925-065A-682543	Sequence 682543, A	611	13.6	68.0	2690	12	US-11-000-688-771	Sequence 771, Ap
539	13.6	68.0	923	6	US-09-925-065A-682544	Sequence 682544, A	612	13.6	68.0	2706	9	US-11-051-720-1611	Sequence 1611, Ap
540	13.6	68.0	923	6	US-09-925-065A-682545	Sequence 682545, A	613	13.6	68.0	2735	6	US-09-925-065A-30287	Sequence 30287, A
541	13.6	68.0	923	6	US-09-925-065A-682546	Sequence 682546, A	614	13.6	68.0	2735	6	US-09-925-065A-30288	Sequence 30288, A
542	13.6	68.0	923	6	US-09-925-065A-682547	Sequence 682547, A	615	13.6	68.0	2744	12	US-11-091-883-95	Sequence 95, Ap
543	13.6	68.0	923	6	US-09-925-065A-682548	Sequence 682548, A	616	13.6	68.0	2763	7	US-10-932-182A-77850	Sequence 77850, A
544	13.6	68.0	932	6	US-09-925-065A-671999	Sequence 671999, A	617	13.6	68.0	2763	7	US-10-932-182A-77850	Sequence 77850, A
545	13.6	68.0	932	6	US-09-925-065A-672000	Sequence 672000, A	618	13.6	68.0	2763	7	US-10-932-182A-77850	Sequence 77850, A
546	13.6	68.0	932	6	US-09-925-065A-672001	Sequence 672001, A	619	13.6	68.0	2797	6	US-09-925-065A-67328	Sequence 67328, A
547	13.6	68.0	932	6	US-09-925-065A-672002	Sequence 672002, A	620	13.6	68.0	2797	6	US-11-051-720-1484	Sequence 1484, Ap
548	13.6	68.0	1043	9	US-11-096-568A-3190	Sequence 3190, Ap	621	13.6	68.0	2833	7	US-10-501-035-137	Sequence 137, Ap
549	13.6	68.0	1046	8	US-10-750-185-27261	Sequence 27261, A	622	13.6	68.0	2871	12	US-11-000-688-1515	Sequence 1515, Ap
550	13.6	68.0	1046	8	US-10-750-623-27261	Sequence 27261, A	623	13.6	68.0	2875	12	US-11-000-688-780	Sequence 780, Ap
551	13.6	68.0	1090	6	US-09-925-065A-35831	Sequence 35831, A	624	13.6	68.0	2885	9	US-11-072-512-510	Sequence 510, Ap
552	13.6	68.0	1090	6	US-09-925-065A-35832	Sequence 35832, A	625	13.6	68.0	2918	8	US-10-750-185-25928	Sequence 25928, A
553	13.6	68.0	1092	6	US-09-925-065A-82409	Sequence 82409, A	626	13.6	68.0	2918	8	US-10-750-623-25928	Sequence 25928, A
554	13.6	68.0	1138	8	US-10-972-587-29	Sequence 29, Ap	627	13.6	68.0	2962	9	US-11-051-720-1485	Sequence 1485, Ap
555	13.6	68.0	1168	8	US-10-750-185-49322	Sequence 49322, A	628	13.6	68.0	3043	6	US-09-925-065A-713947	Sequence 713947, A
556	13.6	68.0	1168	8	US-10-750-623-49322	Sequence 49322, A	629	13.6	68.0	3128	8	US-10-750-185-19637	Sequence 19637, A
557	13.6	68.0	1201	8	US-11-122-329-55	Sequence 55, Ap	630	13.6	68.0	3128	8	US-10-750-623-39637	Sequence 39637, A
558	13.6	68.0	1201	8	US-10-750-623-54871	Sequence 54871, A	631	13.6	68.0	3204	6	US-09-925-065A-81426	Sequence 81426, A
559	13.6	68.0	1256	6	US-09-925-065A-72187	Sequence 72187, A	632	13.6	68.0	3204	6	US-09-925-065A-81427	Sequence 81427, A
560	13.6	68.0	1258	8	US-10-750-185-34378	Sequence 34378, A	633	13.6	68.0	3213	7	US-10-932-182A-77018	Sequence 77018, A
561	13.6	68.0	1258	8	US-10-750-623-34378	Sequence 34378, A	634	13.6	68.0	3213	7	US-10-932-182A-77018	Sequence 77018, A
562	13.6	68.0	1259	8	US-10-821-234-28	Sequence 28, Ap	635	13.6	68.0	3225	7	US-10-932-182A-79745	Sequence 79745, A
563	13.6	68.0	1285	9	US-11-096-568A-18281	Sequence 25346, A	636	13.6	68.0	3225	7	US-10-932-182A-79745	Sequence 79745, A
564	13.6	68.0	1335	6	US-09-925-065A-676467	Sequence 676467, A	637	13.6	68.0	3501	12	US-11-124-367A-10745	Sequence 10745, Ap
565	13.6	68.0	1413	6	US-09-925-065A-69174	Sequence 69174, A	638	13.6	68.0	3940	8	US-10-750-185-17144	Sequence 17144, A
566	13.6	68.0	1413	6	US-09-925-065A-69175	Sequence 69175, A	639	13.6	68.0	3940	8	US-10-750-623-77144	Sequence 77144, A
567	13.6	68.0	1429	6	US-09-925-065A-680505	Sequence 680505, A	640	13.6	68.0	4029	8	US-10-750-185-25438	Sequence 25438, A
568	13.6	68.0	1432	6	US-09-925-065A-667585	Sequence 667585, A	641	13.6	68.0	4029	8	US-10-750-623-25438	Sequence 25438, A
569	13.6	68.0	1486	8	US-10-750-185-42740	Sequence 42740, A	642	13.6	68.0	4070	8	US-10-750-185-53638	Sequence 53638, A
570	13.6	68.0	1486	8	US-10-750-623-42740	Sequence 42740, A	643	13.6	68.0	4070	8	US-10-750-623-53638	Sequence 53638, A
571	13.6	68.0	1486	8	US-10-750-623-42740	Sequence 42740, A	644	13.6	68.0	4119	7	US-10-501-035-53	Sequence 53, Ap
572	13.6	68.0	1486	8	US-10-750-623-42740	Sequence 42740, A	645	13.6	68.0	4299	8	US-10-750-185-67932	Sequence 67932, A
573	13.6	68.0	1494	8	US-10-750-185-62383	Sequence 62383, A	646	13.6	68.0	4563	8	US-10-750-623-67932	Sequence 67932, A
574	13.6	68.0	1494	8	US-10-750-623-62383	Sequence 62383, A	647	13.6	68.0	4563	8	US-10-750-623-67932	Sequence 67932, A
575	13.6	68.0	1496	8	US-10-750-185-33443	Sequence 33443, A	648	13.6	68.0	5250	8	US-10-750-185-25037	Sequence 25037, A
576	13.6	68.0	1496	8	US-10-750-623-33443	Sequence 33443, A	649	13.6	68.0	5250	8	US-10-750-623-25037	Sequence 25037, A
577	13.6	68.0	1523	8	US-10-750-185-35737	Sequence 35737, A	650	13.6	68.0	5313	12	US-11-103-957-22	Sequence 22, Ap
578	13.6	68.0	1523	8	US-10-750-623-35737	Sequence 35737, A	651	13.6	68.0	5313	12	US-10-453-372-113	Sequence 113, Ap
579	13.6	68.0	1530	12	US-11-094-519A-1	Sequence 1, Ap	652	13.6	68.0	8160	8	US-10-453-372-113	Sequence 113, Ap
580	13.6	68.0	1635	6	US-09-925-065A-29391	Sequence 29391, A	653	13.6	68.0	8575	8	US-10-453-372-167	Sequence 167, Ap
581	13.6	68.0	1635	6	US-09-925-065A-29392	Sequence 29392, A	654	13.6	68.0	8689	12	US-11-136-527-1254	Sequence 1254, Ap
582	13.6	68.0	1635	6	US-09-925-065A-29393	Sequence 29393, A	655	13.6	68.0	9668	8	US-10-453-372-135	Sequence 135, Ap
583	13.6	68.0	1635	6	US-09-925-065A-29394	Sequence 29394, A	656	13.6	68.0	9729	8	US-10-453-372-147	Sequence 147, Ap
584	13.6	68.0	1635	6	US-09-925-065A-29395	Sequence 29395, A	657	13.6	68.0	9756	8	US-10-453-372-145	Sequence 145, Ap
585	13.6	68.0	1673	8	US-10-750-185-64018	Sequence 64018, A	658	13.6	68.0	9823	8	US-10-453-372-141	Sequence 141, Ap
586	13.6	68.0	1673	8	US-10-750-623-64018	Sequence 64018, A	659	13.6	68.0	9823	8	US-10-453-372-153	Sequence 153, Ap
587	13.6	68.0	1728	8	US-10-750-185-33421	Sequence 33421, A	660	13.6	68.0	9826	8	US-10-453-372-149	Sequence 149, Ap
588	13.6	68.0	1728	8	US-10-750-623-33421	Sequence 33421, A	661	13.6	68.0	9852	8	US-10-453-372-115	Sequence 115, Ap
589	13.6	68.0	1739	8	US-09-925-065A-76183	Sequence 76183, A	662	13.6	68.0	11807	7	US-10-893-483-103	Sequence 103, Ap
590	13.6	68.0	1813	7	US-10-980-722-1	Sequence 1, Ap	663	13.6	68.0	16658	7	US-10-893-483-104	Sequence 104, Ap
591	13.6	68.0	1896	6	US-09-925-065A-83341	Sequence 83341, A	664	13.6	68.0	16668	7	US-10-893-483-100	Sequence 100, Ap
592	13.6	68.0	1903	9	US-11-072-512-1266	Sequence 1266, Ap	665	13.6	68.0	24777	7	US-10-893-483-96	Sequence 96, Ap
593	13.6	68.0	1979	8	US-10-750-185-57702	Sequence 57702, A	666	13.6	68.0	26727	12	US-11-124-368A-2923	Sequence 2923, Ap
594	13.6	68.0	2115	6	US-10-750-623-57702	Sequence 57702, A	667	13.6	68.0	42823	12	US-11-066-723-18	Sequence 18, Ap
595	13.6	68.0	2115	6	US-09-925-065A-80438	Sequence 80438, A	668	13.6	68.0	48443	7	US-10-330-773-125	Sequence 125, Ap
596	13.6	68.0	2181	6	US-09-925-065A-711065	Sequence 711065, A	669	13.6	68.0	77358	12	US-11-124-368A-29217	Sequence 2917, Ap
597	13.6	68.0	2181	6	US-09-925-065A-75374	Sequence 75374, A	670	13.6	68.0	81230	12	US-10-995-561-13295	Sequence 13295, A
598	13.6	68.0	2188	6	US-09-925-065A-75375	Sequence 75375, A	671	13.6	68.0	81463	7	US-10-330-773-659	Sequence 659, Ap
599	13.6	68.0	2188	6	US-09-925-065A-75376	Sequence 75376, A	672	13.6	68.0	81656	7	US-10-330-773-853	Sequence 853, Ap
600	13.6	68.0	2254	9	US-11-051-720-1487	Sequence 1487, Ap	673	13.6	68.0	100000	12	US-11-124-367A-5024	Sequence 5024, Ap
601	13.6	68.0	2259	7	US-10-932-182A-274	Sequence 274, Ap	674	13.6	68.0	117722	8	US-10-330-773-278	Sequence 278, Ap
602	13.6	68.0	2259	7	US-10-932-182A-274	Sequence 274, Ap	675	13.6	68.0	141171	7	US-10-995-561-13262	Sequence 13262, A
603	13.6	68.0	2271	8	US-10-689-742-129	Sequence 129, Ap	676	13.6	68.0	142605	12	US-11-121-086-64	Sequence 64, Ap
604	13.6	68.0	2386	12	US-11-136-527-72	Sequence 72, Ap	677	13.6	68.0	149382	8	US-10-995-561-13272	Sequence 13272, A

C 678	13.6	68.0	160213	12	US-11-121-086-103	Sequence 103, App	751	13.4	67.0	441	6	US-09-925-065A-620744	Sequence 620744,
679	13.6	68.0	162085	12	US-11-121-086-7	Sequence 7, Appl	752	13.4	67.0	448	6	US-09-925-065A-171302	Sequence 171302,
680	13.6	68.0	169495	12	US-11-121-086-61	Sequence 61, Appl	753	13.4	67.0	458	6	US-09-925-065A-259881	Sequence 259881,
681	13.6	68.0	169725	12	US-11-121-086-63	Sequence 63, Appl	754	13.4	67.0	468	6	US-09-925-065A-528570	Sequence 528570,
C 682	13.6	68.0	168750	9	US-11-114-798-56	Sequence 56, Appl	C 755	13.4	67.0	476	12	US-11-000-463-77	Sequence 77, Appl
683	13.6	68.0	210920	7	US-10-330-773-99	Sequence 99, Appl	C 756	13.4	67.0	491	6	US-09-925-065A-404260	Sequence 404260,
C 684	13.6	68.0	214000	8	US-10-768-744-1	Sequence 1, Appl	C 757	13.4	67.0	494	6	US-09-925-065A-415627	Sequence 415627,
C 685	13.6	68.0	214000	12	US-11-096-191-1	Sequence 261, App	C 758	13.4	67.0	494	6	US-09-925-065A-415628	Sequence 415628,
686	13.6	68.0	215248	7	US-10-330-773-261	Sequence 261, App	C 759	13.4	67.0	507	12	US-11-108-172-171	Sequence 171, App
687	13.6	68.0	236246	7	US-10-330-773-567	Sequence 567, App	760	13.4	67.0	519	6	US-09-925-065A-29932	Sequence 29932, A
C 688	13.6	68.0	272022	7	US-10-330-773-102	Sequence 102, App	761	13.4	67.0	520	6	US-09-925-065A-82488	Sequence 82488,
689	13.6	68.0	387780	8	US-10-995-561-13259	Sequence 13259, A	762	13.4	67.0	520	6	US-09-925-065A-82488	Sequence 82488,
C 690	13.6	68.0	1080000	8	US-10-928-446A-1	Sequence 1, Appl	763	13.4	67.0	523	6	US-09-925-065A-486571	Sequence 486571,
C 691	13.6	68.0	1080000	8	US-10-928-446A-181	Sequence 181, App	764	13.4	67.0	523	6	US-09-925-065A-186656	Sequence 186656,
C 692	13.6	68.0	1080000	8	US-10-928-446A-181	Sequence 181, App	765	13.4	67.0	524	6	US-09-925-065A-186656	Sequence 186656,
C 693	13.6	68.0	1080000	8	US-10-928-446A-181	Sequence 183, App	766	13.4	67.0	528	6	US-09-925-065A-105649	Sequence 105649,
C 694	13.6	68.0	1080000	8	US-10-928-446A-183	Sequence 183, App	767	13.4	67.0	530	6	US-09-925-065A-440337	Sequence 440337,
C 695	13.6	68.0	1080000	8	US-10-928-446A-185	Sequence 185, App	768	13.4	67.0	535	6	US-09-925-065A-186655	Sequence 186655,
C 696	13.6	68.0	1080000	8	US-10-928-446A-185	Sequence 185, App	769	13.4	67.0	535	6	US-09-925-065A-186655	Sequence 186655,
C 697	13.6	68.0	1080000	8	US-10-928-446A-187	Sequence 187, App	770	13.4	67.0	549	6	US-09-925-065A-126755	Sequence 126755,
C 698	13.6	68.0	1080000	8	US-10-928-446A-187	Sequence 187, App	771	13.4	67.0	550	6	US-09-925-065A-177278	Sequence 177278,
C 699	13.6	68.0	1080000	8	US-10-928-446A-189	Sequence 189, App	772	13.4	67.0	550	6	US-09-925-065A-400034	Sequence 400034,
C 700	13.6	68.0	1080000	8	US-10-928-446A-189	Sequence 189, App	773	13.4	67.0	554	6	US-09-925-065A-492491	Sequence 492491,
C 701	13.6	68.0	1080000	8	US-10-928-446A-191	Sequence 191, App	774	13.4	67.0	554	6	US-09-925-065A-928132	Sequence 928132,
C 702	13.6	68.0	1080000	8	US-10-928-446A-191	Sequence 191, App	775	13.4	67.0	560	6	US-09-925-065A-46138	Sequence 46138, A
C 703	13.6	68.0	1080000	8	US-10-928-446A-191	Sequence 191, App	776	13.4	67.0	560	6	US-09-925-065A-734692	Sequence 734692,
C 704	13.6	68.0	1080000	8	US-10-928-446A-193	Sequence 193, App	777	13.4	67.0	563	6	US-09-925-065A-105653	Sequence 105653,
C 705	13.6	68.0	1080000	8	US-10-928-446A-193	Sequence 193, App	778	13.4	67.0	565	6	US-09-925-065A-105654	Sequence 105654,
C 706	13.6	68.0	1080000	8	US-10-928-446A-195	Sequence 195, App	C 779	13.4	67.0	565	6	US-09-925-065A-105655	Sequence 105655,
C 707	13.6	68.0	1080000	8	US-10-928-446A-195	Sequence 195, App	C 780	13.4	67.0	565	6	US-09-925-065A-385159	Sequence 385159,
C 708	13.6	68.0	1080000	8	US-10-928-446A-197	Sequence 197, App	781	13.4	67.0	565	6	US-09-925-065A-521517	Sequence 521517,
C 709	13.6	68.0	1080000	8	US-10-928-446A-197	Sequence 197, App	782	13.4	67.0	568	6	US-09-925-065A-833705	Sequence 833705,
C 710	13.6	68.0	1080000	8	US-10-928-446A-199	Sequence 199, App	783	13.4	67.0	568	6	US-11-128-061-243	Sequence 243, App
C 711	13.6	68.0	1080000	8	US-10-928-446A-199	Sequence 199, App	C 784	13.4	67.0	570	12	US-11-128-061-243	Sequence 243, App
C 712	13.6	68.0	1080000	8	US-10-928-446A-201	Sequence 201, App	C 785	13.4	67.0	570	12	US-11-128-061-243	Sequence 243, App
C 713	13.6	68.0	1080000	8	US-10-928-446A-201	Sequence 201, App	C 786	13.4	67.0	570	12	US-11-128-061-243	Sequence 243, App
C 714	13.6	68.0	1080000	8	US-10-928-446A-201	Sequence 201, App	C 787	13.4	67.0	570	12	US-11-128-061-243	Sequence 243, App
C 715	13.6	68.0	169140	12	US-11-091-018-1	Sequence 1, Appl	C 788	13.4	67.0	573	8	US-09-925-065A-834490	Sequence 834490,
C 716	13.4	67.0	19	10	US-11-101-244-133519	Sequence 133519,	789	13.4	67.0	573	8	US-09-925-065A-834490	Sequence 834490,
C 717	13.4	67.0	19	10	US-11-101-244-822723	Sequence 822723,	790	13.4	67.0	590	6	US-09-925-065A-486225	Sequence 486225,
C 718	13.4	67.0	19	10	US-11-101-244-133754	Sequence 133754,	791	13.4	67.0	592	6	US-09-925-065A-48713	Sequence 48713,
719	13.4	67.0	19	10	US-11-101-244-1337142	Sequence 1337142,	C 792	13.4	67.0	595	6	US-09-925-065A-218061	Sequence 218061,
720	13.4	67.0	19	10	US-11-101-244-1337159	Sequence 1337159,	793	13.4	67.0	595	6	US-09-925-065A-218062	Sequence 218062,
C 721	13.4	67.0	19	11	US-11-083-784-193519	Sequence 193519,	C 794	13.4	67.0	598	6	US-09-925-065A-18062	Sequence 18062,
C 722	13.4	67.0	19	11	US-11-083-784-822723	Sequence 822723,	795	13.4	67.0	600	6	US-09-925-065A-226756	Sequence 226756,
C 723	13.4	67.0	19	11	US-11-083-784-123945	Sequence 123945,	796	13.4	67.0	601	6	US-09-925-065A-226756	Sequence 226756,
C 724	13.4	67.0	19	11	US-11-083-784-135754	Sequence 135754,	C 797	13.4	67.0	603	6	US-09-925-065A-168863	Sequence 168863,
725	13.4	67.0	19	11	US-11-083-784-1537142	Sequence 1537142,	798	13.4	67.0	604	6	US-09-925-065A-592174	Sequence 592174,
726	13.4	67.0	19	11	US-11-083-784-1537159	Sequence 1537159,	C 799	13.4	67.0	605	6	US-09-925-065A-125243	Sequence 125243,
727	13.4	67.0	21	8	US-10-310-914A-312749	Sequence 312749,	800	13.4	67.0	608	6	US-09-925-065A-125243	Sequence 125243,
728	13.4	67.0	21	8	US-10-310-914A-312753	Sequence 312753,	801	13.4	67.0	608	6	US-09-925-065A-125243	Sequence 125243,
729	13.4	67.0	21	8	US-10-310-914A-433380	Sequence 433380,	802	13.4	67.0	609	6	US-09-925-065A-728433	Sequence 728433,
730	13.4	67.0	21	8	US-10-310-914A-433382	Sequence 433382,	803	13.4	67.0	610	6	US-09-925-065A-434058	Sequence 434058,
C 731	13.4	67.0	30	7	US-10-831-386A-21239	Sequence 21239, A	804	13.4	67.0	610	6	US-09-925-065A-434058	Sequence 434058,
C 732	13.4	67.0	30	12	US-11-175-859-90317	Sequence 90317, A	C 805	13.4	67.0	612	6	US-09-925-065A-301872	Sequence 301872,
C 733	13.4	67.0	201	8	US-10-995-561-34166	Sequence 34166, A	C 806	13.4	67.0	612	6	US-09-925-065A-301872	Sequence 301872,
C 734	13.4	67.0	201	8	US-10-995-561-34168	Sequence 34168, A	807	13.4	67.0	612	6	US-09-925-065A-733135	Sequence 733135,
C 735	13.4	67.0	201	8	US-10-995-561-34170	Sequence 34170, A	808	13.4	67.0	617	6	US-09-925-065A-152542	Sequence 152542,
C 736	13.4	67.0	201	8	US-10-995-561-38539	Sequence 38539, A	809	13.4	67.0	617	6	US-09-925-065A-1528084	Sequence 1528084,
C 737	13.4	67.0	201	8	US-10-995-561-38543	Sequence 38543, A	810	13.4	67.0	617	6	US-09-925-065A-1528085	Sequence 1528085,
C 738	13.4	67.0	201	8	US-10-995-561-38544	Sequence 38544, A	C 811	13.4	67.0	621	6	US-09-925-065A-528086	Sequence 528086,
C 739	13.4	67.0	201	8	US-10-995-561-38850	Sequence 38850, A	812	13.4	67.0	621	6	US-09-925-065A-528086	Sequence 528086,
C 740	13.4	67.0	201	8	US-10-995-561-38852	Sequence 38852, A	C 813	13.4	67.0	621	6	US-09-925-065A-950767	Sequence 950767,
C 741	13.4	67.0	201	8	US-10-995-561-38854	Sequence 38854, A	814	13.4	67.0	622	6	US-09-925-065A-210711	Sequence 210711,
742	13.4	67.0	201	8	US-10-995-561-75790	Sequence 75790, A	C 815	13.4	67.0	625	6	US-09-925-065A-74804	Sequence 74804, A
743	13.4	67.0	201	8	US-10-995-561-84690	Sequence 84690, A	C 816	13.4	67.0	625	6	US-09-925-065A-936844	Sequence 936844,
C 744	13.4	67.0	284	6	US-09-925-065A-482445	Sequence 482445,	817	13.4	67.0	627	6	US-09-925-065A-936844	Sequence 936844,
C 745	13.4	67.0	290	12	US-11-108-172-794	Sequence 794, App	C 818	13.4	67.0	632	6	US-09-925-065A-154972	Sequence 154972,
C 746	13.4	67.0	399	12	US-11-084-085-29	Sequence 29, Appl	819	13.4	67.0	632	6	US-09-925-065A-154972	Sequence 154972,
C 747	13.4	67.0	414	12	US-11-108-172-662	Sequence 662, App	820	13.4	67.0	635	6	US-09-925-065A-914221	Sequence 914221,
C 748	13.4	67.0	423	6	US-09-925-065A-486741	Sequence 486741,	821	13.4	67.0	635	6	US-09-925-065A-914221	Sequence 914221,
C 749	13.4	67.0	428	6	US-09-925-065A-656377	Sequence 656377,	822	13.4	67.0	636	6	US-09-925-065A-93485	Sequence 93485,
C 750	13.4	67.0	429	12	US-11-000-463-549	Sequence 549, App	823	13.4	67.0	658	6	US-09-925-065A-93485	Sequence 93485,

C 824	13.4	67.0	670	6	US-09-925-065A-667685	Sequence 867685,
825	13.4	67.0	725	6	US-09-925-065A-524067	Sequence 524067,
826	13.4	67.0	725	6	US-09-925-065A-524068	Sequence 524068,
827	13.4	67.0	751	8	US-10-750-185-40790	Sequence 40790, A
828	13.4	67.0	751	8	US-10-750-185-40790	Sequence 40790, A
C 829	13.4	67.0	799	6	US-09-925-065A-68972	Sequence 68972, A
C 830	13.4	67.0	799	6	US-10-750-185-51000	Sequence 51000, A
C 831	13.4	67.0	799	8	US-10-750-185-51000	Sequence 51000, A
C 832	13.4	67.0	821	6	US-09-925-065A-65875	Sequence 65875, A
C 833	13.4	67.0	828	8	US-10-750-185-3733	Sequence 3733, A
C 834	13.4	67.0	828	8	US-10-750-623-3733	Sequence 3733, A
C 835	13.4	67.0	840	6	US-09-925-065A-7575	Sequence 7575, A
C 836	13.4	67.0	840	6	US-09-925-065A-7575	Sequence 7575, A
C 837	13.4	67.0	849	6	US-09-925-065A-38398	Sequence 38398, A
C 838	13.4	67.0	849	6	US-09-925-065A-38399	Sequence 38399, A
C 839	13.4	67.0	849	6	US-09-925-065A-71122	Sequence 71122, A
C 840	13.4	67.0	899	8	US-10-750-185-33850	Sequence 33850, A
C 841	13.4	67.0	899	8	US-10-750-623-32850	Sequence 32850, A
C 842	13.4	67.0	926	6	US-09-925-065A-723294	Sequence 723294, A
C 843	13.4	67.0	926	6	US-09-925-065A-723295	Sequence 723295, A
C 844	13.4	67.0	935	6	US-09-925-065A-22627	Sequence 22626, A
C 845	13.4	67.0	935	6	US-09-925-065A-22627	Sequence 22626, A
C 846	13.4	67.0	939	6	US-09-925-065A-67249	Sequence 67249, A
C 847	13.4	67.0	959	6	US-09-925-065A-67250	Sequence 67250, A
C 848	13.4	67.0	1006	7	US-10-501-035-12	Sequence 12, Appl
C 849	13.4	67.0	1056	8	US-10-972-587-21	Sequence 21, Appl
C 850	13.4	67.0	1056	8	US-11-108-172-1054	Sequence 1054, A
C 851	13.4	67.0	1109	12	US-11-108-172-1096	Sequence 1096, A
C 852	13.4	67.0	1142	8	US-10-750-185-28672	Sequence 28672, A
C 853	13.4	67.0	1142	8	US-10-750-623-28672	Sequence 28672, A
C 854	13.4	67.0	1182	7	US-10-933-182A-1214	Sequence 1214, A
C 855	13.4	67.0	1182	7	US-10-933-182A-1214	Sequence 1214, A
C 856	13.4	67.0	1213	6	US-09-925-065A-297915	Sequence 297915, A
C 857	13.4	67.0	1253	8	US-10-750-185-64768	Sequence 64768, A
C 858	13.4	67.0	1253	8	US-10-750-623-64768	Sequence 64768, A
C 859	13.4	67.0	1293	6	US-09-925-065A-19496	Sequence 19496, A
C 860	13.4	67.0	1299	6	US-10-821-234-611	Sequence 611, A
C 861	13.4	67.0	1314	6	US-09-925-065A-52116	Sequence 52116, A
C 862	13.4	67.0	1367	9	US-11-096-568A-12591	Sequence 12591, A
C 863	13.4	67.0	1438	8	US-10-821-234-432	Sequence 432, A
C 864	13.4	67.0	1484	8	US-10-750-185-37159	Sequence 37159, A
C 865	13.4	67.0	1484	8	US-10-750-623-37159	Sequence 37159, A
C 866	13.4	67.0	1633	9	US-11-096-568A-19469	Sequence 19469, A
C 867	13.4	67.0	1692	8	US-10-750-185-56918	Sequence 56918, A
C 868	13.4	67.0	1692	8	US-10-750-623-56918	Sequence 56918, A
C 869	13.4	67.0	1847	6	US-09-925-065A-24516	Sequence 24516, A
C 870	13.4	67.0	2002	6	US-09-925-065A-42155	Sequence 42155, A
C 871	13.4	67.0	2002	6	US-09-925-065A-42156	Sequence 42156, A
C 872	13.4	67.0	2002	6	US-09-925-065A-42157	Sequence 42157, A
C 873	13.4	67.0	2043	12	US-11-136-527-2325	Sequence 2325, A
C 874	13.4	67.0	2057	6	US-09-925-065A-90227	Sequence 90227, A
C 875	13.4	67.0	2261	6	US-09-925-065A-466	Sequence 466, A
C 876	13.4	67.0	2261	6	US-09-925-065A-467	Sequence 467, A
C 877	13.4	67.0	2356	5	US-09-978-360A-32	Sequence 32, Appl
C 878	13.4	67.0	2461	9	US-11-245-147-158	Sequence 158, A
C 879	13.4	67.0	2461	9	US-11-245-147-230	Sequence 230, A
C 880	13.4	67.0	2524	6	US-09-925-065A-5183	Sequence 5183, A
C 881	13.4	67.0	2524	6	US-09-925-065A-5184	Sequence 5184, A
C 882	13.4	67.0	2524	6	US-09-925-065A-5185	Sequence 5185, A
C 883	13.4	67.0	2524	6	US-09-925-065A-5186	Sequence 5186, A
C 884	13.4	67.0	2524	6	US-09-925-065A-73589	Sequence 73589, A
C 885	13.4	67.0	2761	6	US-09-925-065A-73590	Sequence 73590, A
C 886	13.4	67.0	2761	6	US-09-925-065A-73591	Sequence 73591, A
C 887	13.4	67.0	2863	9	US-11-072-512-610	Sequence 610, A
C 888	13.4	67.0	2889	9	US-11-096-568A-24459	Sequence 24459, A
C 889	13.4	67.0	3010	8	US-10-750-185-41676	Sequence 41676, A
C 890	13.4	67.0	3010	8	US-10-750-623-41676	Sequence 41676, A
C 891	13.4	67.0	3067	7	US-10-511-538-90	Sequence 90, Appl
C 892	13.4	67.0	3102	8	US-10-750-185-60482	Sequence 60482, A
C 893	13.4	67.0	3102	8	US-10-750-623-60482	Sequence 60482, A
C 894	13.4	67.0	3284	9	US-11-072-512-1317	Sequence 1317, A
C 895	13.4	67.0	3392	8	US-10-750-185-60479	Sequence 60479, A
C 896	13.4	67.0	3392	8	US-10-750-623-60479	Sequence 60479, A
C 897	13.4	67.0	3419	12	US-11-000-688-424	Sequence 424, A
C 898	13.4	67.0	3457	8	US-10-750-185-50627	Sequence 50627, A
C 899	13.4	67.0	3457	8	US-10-750-623-50627	Sequence 50627, A
C 900	13.4	67.0	3462	9	US-11-096-568A-30387	Sequence 30387, A
C 901	13.4	67.0	3626	8	US-10-821-234-245	Sequence 245, A
C 902	13.4	67.0	3626	12	US-11-128-061-672	Sequence 672, A
C 903	13.4	67.0	3960	12	US-11-128-049-672	Sequence 672, A
C 904	13.4	67.0	4022	9	US-11-181-330-7	Sequence 7, Appl
C 905	13.4	67.0	4233	8	US-10-750-185-39432	Sequence 39432, A
C 906	13.4	67.0	4233	8	US-10-750-623-39432	Sequence 39432, A
C 907	13.4	67.0	7450	12	US-11-124-367A-103	Sequence 103, A
C 908	13.4	67.0	7786	11	US-11-096-051-9	Sequence 9, Appl
C 909	13.4	67.0	8362	11	US-11-096-051-9	Sequence 9, Appl
C 910	13.4	67.0	8645	11	US-11-096-051-7	Sequence 7, Appl
C 911	13.4	67.0	8657	11	US-11-096-051-7	Sequence 7, Appl
C 912	13.4	67.0	9630	12	US-11-124-367A-102	Sequence 102, A
C 913	13.4	67.0	10166	12	US-11-147-606-3	Sequence 3, Appl
C 914	13.4	67.0	10326	7	US-10-893-483-123	Sequence 123, A
C 915	13.4	67.0	14154	8	US-10-995-561-13282	Sequence 13282, A
C 916	13.4	67.0	17004	12	US-11-176-253-1	Sequence 1, Appl
C 917	13.4	67.0	20492	12	US-11-095-668-2	Sequence 2, Appl
C 918	13.4	67.0	20865	12	US-11-124-367A-5021	Sequence 5021, A
C 919	13.4	67.0	23433	12	US-11-153-238-7	Sequence 7, Appl
C 920	13.4	67.0	23672	8	US-10-995-561-13267	Sequence 13267, A
C 921	13.4	67.0	24231	7	US-10-330-773-353	Sequence 353, A
C 922	13.4	67.0	27032	8	US-10-995-561-13468	Sequence 13468, A
C 923	13.4	67.0	27936	12	US-11-124-367A-5042	Sequence 5042, A
C 924	13.4	67.0	30625	12	US-11-153-238-5	Sequence 5, Appl
C 925	13.4	67.0	30676	12	US-11-153-238-8	Sequence 8, Appl
C 926	13.4	67.0	31337	7	US-10-330-773-7	Sequence 7, Appl
C 927	13.4	67.0	34116	12	US-11-124-367A-5020	Sequence 5020, A
C 928	13.4	67.0	41309	8	US-10-995-561-13467	Sequence 13467, A
C 929	13.4	67.0	43256	7	US-10-330-773-713	Sequence 713, A
C 930	13.4	67.0	43975	8	US-10-995-561-13279	Sequence 13279, A
C 931	13.4	67.0	46752	8	US-10-995-561-13410	Sequence 13410, A
C 932	13.4	67.0	53916	7	US-10-330-773-65	Sequence 65, A
C 933	13.4	67.0	71594	7	US-10-330-773-738	Sequence 738, A
C 934	13.4	67.0	90141	7	US-10-330-773-844	Sequence 844, A
C 935	13.4	67.0	90739	7	US-10-330-773-902	Sequence 902, A
C 936	13.4	67.0	107432	7	US-10-330-773-137	Sequence 137, A
C 937	13.4	67.0	116856	12	US-11-143-980-1	Sequence 1, Appl
C 938	13.4	67.0	116856	12	US-11-143-980-1	Sequence 1, Appl
C 939	13.4	67.0	118063	7	US-10-330-773-156	Sequence 156, A
C 940	13.4	67.0	126552	7	US-11-121-086-1	Sequence 1, Appl
C 941	13.4	67.0	135050	7	US-10-330-773-954	Sequence 954, A
C 942	13.4	67.0	146733	7	US-10-330-773-387	Sequence 387, A
C 943	13.4	67.0	155083	7	US-10-330-773-868	Sequence 868, A
C 944	13.4	67.0	155462	7	US-10-330-773-371	Sequence 371, A
C 945	13.4	67.0	175603	7	US-10-330-773-531	Sequence 531, A
C 946	13.4	67.0	176771	7	US-10-330-773-143	Sequence 143, A
C 947	13.4	67.0	181172	12	US-11-121-086-41	Sequence 41, Appl
C 948	13.4	67.0	189519	12	US-11-121-086-16	Sequence 16, Appl
C 949	13.4	67.0	201309	9	US-11-121-086-2	Sequence 2, Appl
C 950	13.4	67.0	201309	9	US-11-121-086-2	Sequence 2, Appl
C 951	13.4	67.0	210920	7	US-10-330-773-99	Sequence 99, A
C 952	13.4	67.0	210920	12	US-11-121-086-8	Sequence 8, Appl
C 953	13.4	67.0	226960	7	US-10-330-773-23	Sequence 23, Appl
C 954	13.4	67.0	333323	19	US-10-310-914A-1078950	Sequence 1078950, A
C 955	13.2	66.0	19	8	US-10-310-914A-1078950	Sequence 1078950, A
C 956	13.2	66.0	19	10	US-11-101-244-204675	Sequence 204675, A
C 957	13.2	66.0	19	10	US-11-101-244-803692	Sequence 803692, A
C 958	13.2	66.0	19	10	US-11-101-244-803692	Sequence 803692, A
C 959	13.2	66.0	19	10	US-11-101-244-803692	Sequence 803692, A
C 960	13.2	66.0	19	10	US-11-101-244-803692	Sequence 803692, A
C 961	13.2	66.0	19	10	US-11-101-244-803692	Sequence 803692, A
C 962	13.2	66.0	19	11	US-11-083-78A-204675	Sequence 204675, A
C 963	13.2	66.0	19	11	US-11-083-78A-803692	Sequence 803692, A
C 964	13.2	66.0	19	11	US-11-083-78A-1246485	Sequence 1246485, A
C 965	13.2	66.0	19	11	US-11-083-78A-1414797	Sequence 1414797, A
C 966	13.2	66.0	19	11	US-11-083-78A-1414896	Sequence 1414896, A
C 967	13.2	66.0	21	8	US-10-310-914A-43817	Sequence 43817, A
C 968	13.2	66.0	23	8	US-10-310-914A-235238	Sequence 235238, A
C 969	13.2	66.0	23	8	US-10-310-914A-1258113	Sequence 1258113, A
C 970	13.2	66.0	23	8	US-10-310-914A-1258130	Sequence 1258130, A

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770 13.2 66.0 24 8 US-10-310-914A-628616 Sequence 628616,
771 13.2 66.0 24 8 US-10-310-914A-779901 Sequence 779901,
772 13.2 66.0 25 7 US-10-932-182A-66721, A Sequence 66721, A
773 13.2 66.0 25 7 US-10-932-182A-161588 Sequence 161588,
774 13.2 66.0 25 7 US-10-932-182A-178713 Sequence 178713, A
775 13.2 66.0 25 7 US-10-932-182A-66721, A Sequence 66721, A
776 13.2 66.0 25 7 US-10-932-182A-161588 Sequence 161588,
777 13.2 66.0 25 7 US-10-932-182A-178713 Sequence 178713, A
778 13.2 66.0 25 7 US-10-932-182A-161588 Sequence 161588, A
779 13.2 66.0 25 7 US-10-932-182A-178713 Sequence 178713, A
780 13.2 66.0 25 7 US-10-932-182A-161588 Sequence 161588,
781 13.2 66.0 25 7 US-10-932-182A-178713 Sequence 178713, A
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783 13.2 66.0 25 7 US-10-932-182A-178713 Sequence 178713, A
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785 13.2 66.0 25 7 US-10-932-182A-178713 Sequence 178713, A
786 13.2 66.0 25 7 US-10-932-182A-161588 Sequence 161588,
787 13.2 66.0 25 7 US-10-932-182A-178713 Sequence 178713, A
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790 13.2 66.0 25 7 US-10-932-182A-161588 Sequence 161588,
791 13.2 66.0 25 7 US-10-932-182A-178713 Sequence 178713, A
792 13.2 66.0 25 7 US-10-932-182A-161588 Sequence 161588,
793 13.2 66.0 25 7 US-10-932-182A-178713 Sequence 178713, A
794 13.2 66.0 25 7 US-10-932-182A-161588 Sequence 161588,
795 13.2 66.0 25 7 US-10-932-182A-178713 Sequence 178713, A
796 13.2 66.0 25 7 US-10-932-182A-161588 Sequence 161588,
797 13.2 66.0 25 7 US-10-932-182A-178713 Sequence 178713, A
798 13.2 66.0 25 7 US-10-932-182A-161588 Sequence 161588,
799 13.2 66.0 25 7 US-10-932-182A-178713 Sequence 178713, A
1000 13.2 66.0 25 7 US-10-932-182A-161588 Sequence 161588,
Sequence 354760,
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## ALIGNMENTS

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RESULT 1
US-11-127-654-379
; Sequence 379, Application US/11127654
; Publication No. US20050250726A1
; GENERAL INFORMATION:
; APPLICANT: Kitley, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC
; TITLE OF INVENTION: INFLAMMATORY DISEASES
; FILE REFERENCE: C1039.70060US01
; CURRENT APPLICATION NUMBER: US/11/127,654
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/112,653
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 379
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-379
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Query Match 100.0%; Score 20; DB 12; Length 20;
Best Local Similarity 90.0%; Pred. No. 0.44;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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OY 1 AGGACAGCCAGGAGCAGCAGCA 20
|||:|||||:|||||:|||||:
Db 1 AGGACAGCCAGGAGCAGCAGCA 20
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; Sequence 481, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 481
; LENGTH: 5308
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-481
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Query Match 90.0%; Score 18; DB 12; Length 5308;
Best Local Similarity 88.9%; Pred. No. 10;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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OY 2 GGACAGCCAGGAGCAGCAGCA 19
|||:|||||:|||||:|||||:
Db 2734 GGACAGCCAGGAGCAGCAGCA 2751
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RESULT 3
US-09-925-065A-693333/C
; Sequence 693333, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: PatSeqSO for Windows Version 4.0
; SEQ ID NO 693333
; LENGTH: 605
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-693333
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Query Match 84.0%; Score 16.8; DB 6; Length 605;
Best Local Similarity 85.0%; Pred. No. 35;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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OY 1 AGGACAGCCAGGAGCAGCAGCA 20
|||:|||||:|||||:|||||:
Db 398 AGGACAGCCAGGAGCAGCAGCA 379
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RESULT 4
US-09-925-065A-73830
; Sequence 73830, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
```

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; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73830
; LENGTH: 740
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-73830

Query Match      84.0%; Score 16,8; DB 6; Length 740;
Best Local Similarity 80.0%; Pred. No. 36;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 AGTACAGCCAGGACGACGAC 20
        |||:|||||:|||||:|:|
DB      66 AGGTACAGCCAGGCGCTAGGA 85

RESULT 5
; US-09-925-065A-369463
; Sequence 369463, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 369463
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-369463

Query Match      82.0%; Score 16,4; DB 6; Length 586;
Best Local Similarity 83.3%; Pred. No. 56;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 AGTACAGCCAGGACGACGAC 18
        |||:|||||:|||||:|:|
DB      39 AGTACAGCCAGGACGACGAC 56

RESULT 6
; US-11-136-527-603
; Sequence 603, Application US/11136527
; Publication No. US20050287570A1
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; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William M
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 603
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-11-136-527-603

Query Match      80.0%; Score 16; DB 12; Length 1734;
Best Local Similarity 87.5%; Pred. No. 1,1e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 GTACAGCCAGGACGACGAC 18
        |||:|||||:|||||:|:|
DB      1042 GTACAGCCAGGACGACGAC 1057

RESULT 7
; US-10-330-773-573
; Sequence 573, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 573
; LENGTH: 90616
; TYPE: DNA
; ORGANISM: Mus musculus
; PEATRE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(90616)
; OTHER INFORMATION: n = A,T,C or G
; US-10-330-773-573

Query Match      80.0%; Score 16; DB 7; Length 90616;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 GUACAGCCAGGACGACGAC 18
        |||:|||||:|||||:|:|
DB      39970 GTACAGCCAGGACGACGAC 39985

RESULT 8
; US-09-925-065A-132060/C
; Sequence 132060, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
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; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132060
; LENGTH: 364
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-132060

Query Match          79.0%; Score 15.8; DB 6; Length 364;
Best Local Similarity 78.9%; Pred. No. 1.2e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2  GGUACAGCCAGGACUACGA 20
Db      93  GGTCAGCCAGGCGCTACGA 75

RESULT 9
US-09-925-065A-290634/c
; Sequence 290634, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 290634
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-290634

Query Match          79.0%; Score 15.8; DB 6; Length 533;
Best Local Similarity 78.9%; Pred. No. 1.2e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1  AGUACAGCCAGGACUACG 19
Db      347  AAGTACAGCCAGGACTACG 329

RESULT 10
US-09-925-065A-290636/c
; Sequence 290636, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
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; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 290636
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-290636

Query Match          79.0%; Score 15.8; DB 6; Length 533;
Best Local Similarity 78.9%; Pred. No. 1.2e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1  AGUACAGCCAGGACTACG 19
Db      347  AAGTACAGCCAGGACTACG 329

RESULT 11
US-09-925-065A-813093
; Sequence 813093, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 813093
; LENGTH: 572
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-813093

Query Match          79.0%; Score 15.8; DB 6; Length 572;
Best Local Similarity 84.2%; Pred. No. 1.2e+02;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2  GGUACAGCCAGGACUACGA 20
Db      122  GGACAGCCAGGACTACGA 140

RESULT 12
US-10-932-182A-77115
; Sequence 77115, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHITIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
```



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; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 77115
; LENGTH: 1098
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-77115

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 7; Length 1098;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGUACAGCCAGACUACG 19
DB 726 AGGTACACTAGACTACG 744

RESULT 13
US-10-932-182A-77115
; Sequence 77115, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 77115
; LENGTH: 1098
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-77115

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 7; Length 1098;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGUACAGCCAGACUACG 19
DB 726 AGGTACACTAGACTACG 744

RESULT 14
US-10-330-773-713
; Sequence 713, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 713
; LENGTH: 43256
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(43256)
```

```

; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-713

Query Match
Best Local Similarity 79.0%; Score 15.8; DB 7; Length 43256;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGACUACGA 20
DB 27866 GGGACAGCCAGACTACCA 27884

RESULT 15
US-09-925-065A-173502
; Sequence 173502, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 173502
; LENGTH: 363
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-173502

Query Match
Best Local Similarity 77.0%; Score 15.4; DB 6; Length 363;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGUACAGCCAGACUACG 17
DB 41 ATGTACAGCCAGACTA 57

RESULT 16
US-09-925-065A-90145
; Sequence 90145, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 957086
```

SEQ ID NO 90145  
LENGTH: 538  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-90145

Query Match 77.0%; Score 15.4; DB 6; Length 538;  
Best Local Similarity 82.4%; Pred. No. 1.9e+02;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGAGACTCC 18  
DB 494 GGTAACGCGCAGACTCC 510

## RESULT 17

US-09-925-065A-90146  
Sequence 90146, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 90146  
LENGTH: 538  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-90146

Query Match 77.0%; Score 15.4; DB 6; Length 538;  
Best Local Similarity 82.4%; Pred. No. 1.9e+02;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGAGACTCC 18  
DB 494 GGTAACGCGCAGACTCC 510

## RESULT 18

US-09-925-065A-135672  
Sequence 135672, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 135672  
LENGTH: 593  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-135672

Query Match 77.0%; Score 15.4; DB 6; Length 593;  
Best Local Similarity 82.4%; Pred. No. 1.9e+02;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 UACAGCCAGAGACTCC 20  
DB 70 TACAGCCAGAGACTCC 86

## RESULT 19

US-09-925-065A-768047  
Sequence 768047, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 768047  
LENGTH: 610  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-768047

Query Match 77.0%; Score 15.4; DB 6; Length 610;  
Best Local Similarity 82.4%; Pred. No. 1.9e+02;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGAGACTCC 18  
DB 581 GGTAACGCGCAGACTCC 597

## RESULT 20

US-11-121-438-5  
Sequence 5, Application US/11121438  
Publication No. US20060014173A1  
GENERAL INFORMATION:  
APPLICANT: Huang, Shi  
TITLE OF INVENTION: PR/SET- Domain Containing Nucleic Acids,  
Polypeptides, Antibodies and Methods of Use  
FILE REFERENCE: P-Id 5301  
CURRENT APPLICATION NUMBER: US/11/121,438  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: US/10/200,012  
PRIOR FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: US 09/910,478  
PRIOR FILING DATE: 2001-07-18  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: FastSeq for Windows Version 4.0

US-11-121-438-5  
Sequence 5, Application US/11121438  
Publication No. US20060014173A1  
GENERAL INFORMATION:  
APPLICANT: Huang, Shi  
TITLE OF INVENTION: PR/SET- Domain Containing Nucleic Acids,  
Polypeptides, Antibodies and Methods of Use  
FILE REFERENCE: P-Id 5301  
CURRENT APPLICATION NUMBER: US/11/121,438  
CURRENT FILING DATE: 2005-05-03  
PRIOR APPLICATION NUMBER: US/10/200,012  
PRIOR FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: US 09/910,478  
PRIOR FILING DATE: 2001-07-18  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5  
LENGTH: 2208  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (250)...(1761)  
US-11-121-438-5

Query Match 77.0% Score 15.4; DB 12; Length 2208,  
Best Local Similarity 82.4%; Pred. No. 2.3e+02;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGUACAGCCAGGACUAC 18  
DB 1001 GGTACAGCCAGGACTAC 1017

RESULT 21  
US-10-750-185-56251

Sequence 56251, Application US/10750185  
Publication No. US2005026063A1  
GENERAL INFORMATION:  
APPLICANT: MMI GENOMICS, INC.  
APPLICANT: DENISE, Sue K.  
APPLICANT: KERR, Richard  
APPLICANT: ROSENFIELD, David  
APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen  
APPLICANT: PANTIN, Dennis  
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
FILE REFERENCE: MM11100-2  
CURRENT APPLICATION NUMBER: US/10/750,185  
CURRENT FILING DATE: 2003-12-31  
PRIOR APPLICATION NUMBER: US 60/437,482  
PRIOR FILING DATE: 2002-12-31  
NUMBER OF SEQ ID NOS: 64922  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 56251  
LENGTH: 2944  
TYPE: DNA  
ORGANISM: Bovine  
US-10-750-185-56251

Query Match 77.0% Score 15.4; DB 8; Length 2944;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGGACUAC 17  
DB 2293 AGGACAGCCAGGACTA 2309

RESULT 22  
US-10-750-623-56251

Sequence 56251, Application US/10750623  
Publication No. US20050287531A1  
GENERAL INFORMATION:  
APPLICANT: MMI GENOMICS, INC.  
APPLICANT: DENISE, Sue K.  
APPLICANT: KERR, Richard  
APPLICANT: ROSENFIELD, David  
APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen  
APPLICANT: PANTIN, Dennis  
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
FILE REFERENCE: MM11100-1  
CURRENT APPLICATION NUMBER: US/10/750,623  
CURRENT FILING DATE: 2003-12-31  
PRIOR APPLICATION NUMBER: US 60/437,482  
PRIOR FILING DATE: 2002-12-31  
NUMBER OF SEQ ID NOS: 64922  
SOFTWARE: PatentIn version 3.1

SEQ ID NO 56251  
LENGTH: 2944  
TYPE: DNA  
ORGANISM: Bovine  
US-10-750-623-56251

Query Match 77.0% Score 15.4; DB 8; Length 2944;  
Best Local Similarity 88.2%; Pred. No. 2.4e+02;  
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGGACUAC 17  
DB 2293 AGGACAGCCAGGACTA 2309

RESULT 23  
US-11-121-086-47/c

Sequence 47, Application US/1121086  
Publication No. US20050266459A1  
GENERAL INFORMATION:  
APPLICANT: FOUTSSEN, TIM S.  
APPLICANT: NIELSEN, KIRSTEN V.  
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES  
FILE REFERENCE: 09138.6000-00000  
CURRENT APPLICATION NUMBER: US/11/121,086  
CURRENT FILING DATE: 2005-05-04  
PRIOR APPLICATION NUMBER: 60/567,570  
PRIOR FILING DATE: 2004-05-04  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 47  
LENGTH: 137671  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-121-086-47

Query Match 77.0% Score 15.4; DB 12; Length 137671;  
Best Local Similarity 82.4%; Pred. No. 3.8e+02;  
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 UACAGCCAGGACUACGA 20  
DB 96035 TACAGCCAGGACTAGA 96019

RESULT 24  
US-09-925-065A-591902/c

Sequence 591902, Application US/0925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
Nucleotide Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: PastSeq for Windows Version 4.0  
SEQ ID NO 591902  
LENGTH: 458  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-591902

Query Match 76.0%; Score 15.2; DB 6; Length 458;  
Best Local Similarity 75.0%; Pred. No. 2.4e+02;  
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUACGA 20  
|||:|||||:|||||:  
DB 227 AGTTACAGCCAGACTGACGA 208

## RESULT 25

US-09-925-065A-226237  
; Sequence 226237, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 226237  
; LENGTH: 487  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-226237

Query Match 76.0%; Score 15.2; DB 6; Length 487;  
Best Local Similarity 75.0%; Pred. No. 2.4e+02;  
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUACGA 20  
|||:|||||:|||||:  
DB 68 AGGTGACGCCAGGCTGCCA 87

## RESULT 26

US-09-925-065A-20701  
; Sequence 20701, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20701  
; LENGTH: 525

; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-20701

Query Match 76.0%; Score 15.2; DB 6; Length 525;  
Best Local Similarity 80.0%; Pred. No. 2.4e+02;  
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUACGA 20  
|||:|||||:|||||:  
DB 445 AGGCGCAGCCAGACTTCGA 464

## RESULT 27

US-09-925-065A-502873/c  
; Sequence 502873, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 502873  
; LENGTH: 582  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-502873

Query Match 76.0%; Score 15.2; DB 6; Length 582;  
Best Local Similarity 80.0%; Pred. No. 2.5e+02;  
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUACGA 20  
|||:|||||:|||||:  
DB 264 AGGTACAGCCAGACACAAAGA 245

## RESULT 28

US-09-925-065A-191670  
; Sequence 191670, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 191670  
LENGTH: 598  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-191670

Query Match 76.0%; Score 15.2; DB 6; Length 598;  
Best Local Similarity 75.0%; Pred. No. 2.5e+02;  
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUAACGCCAGACUACGA 20  
|||:|||||:|  
DB 254 AGGTAGACGCCAGACTGCA 273

RESULT 29  
US-09-925-065A-544123/c  
Sequence 544123, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 544123  
LENGTH: 598  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-544123

Query Match 76.0%; Score 15.2; DB 6; Length 598;  
Best Local Similarity 75.0%; Pred. No. 2.5e+02;  
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUAACGCCAGACUACGA 20  
|||:|||||:|  
DB 495 AGGTGACGCCAGGCTTACA 476

RESULT 30  
US-10-467-657-2197  
Sequence 2197, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:  
APPLICANT: CHIRON SPA  
APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASIGNANI Vega  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
PRIOR FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8  
PRIOR FILING DATE: 2001-02-12  
NUMBER OF SEQ ID NOS: 9218  
SOFTWARE: SeqWin99, version 1.04  
SEQ ID NO 2197

LENGTH: 807  
TYPE: DNA  
ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-2197

Query Match 76.0%; Score 15.2; DB 8; Length 807;  
Best Local Similarity 75.0%; Pred. No. 2.6e+02;  
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUAACGCCAGACUACGA 20  
|||:|||||:|  
DB 6 AGTACTGCCATGATACGA 25

RESULT 31  
US-10-467-657-2199/c  
Sequence 2199, Application US/10467657  
Publication No. US20050260581A1  
GENERAL INFORMATION:  
APPLICANT: CHIRON SPA  
APPLICANT: FONTANA Maria Rita  
APPLICANT: PIZZA Mariagrazia  
APPLICANT: MASIGNANI Vega  
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/467,657  
PRIOR FILING DATE: 2003-08-11  
PRIOR APPLICATION NUMBER: GB-0103424.8  
PRIOR FILING DATE: 2001-02-12  
NUMBER OF SEQ ID NOS: 9218  
SOFTWARE: SeqWin99, version 1.04  
SEQ ID NO 2199  
LENGTH: 828  
TYPE: DNA  
ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-2199

Query Match 76.0%; Score 15.2; DB 8; Length 828;  
Best Local Similarity 75.0%; Pred. No. 2.6e+02;  
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUAACGCCAGACUACGA 20  
|||:|||||:|  
DB 793 AGTACTGCCATGATACGA 774

RESULT 32  
US-09-925-065A-15531  
Sequence 15531, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15531  
LENGTH: 2049  
TYPE: DNA

ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(2049)  
OTHER INFORMATION: n = A,T,C or G  
US-09-925-065A-15531

Query Match 76.0%; Score 15.2; DB 6; Length 2049;  
Best Local Similarity 75.0%; Pred. No. 2.9e+02;  
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUACGA 20  
|||:|||||:|:|  
DB 148 AGGTACAGCCAGATTAGCA 167

RESULT 33

US-10-932-182A-4937  
; Sequence 4937, Application US/10932182A  
; Publication No. US20060046253A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIRO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: 030685-043  
; CURRENT APPLICATION NUMBER: US/10/932,182A  
; CURRENT FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 4937  
; LENGTH: 3090  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-10-932-182A-4937

Query Match 76.0%; Score 15.2; DB 7; Length 3090;  
Best Local Similarity 80.0%; Pred. No. 3e+02;  
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUACGA 20  
|||:|||||:|:|  
DB 647 AGGACAGCAGACTACCA 666

RESULT 34

US-10-932-182A-4937  
; Sequence 4937, Application US/10932182A  
; Publication No. US20060046253A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIRO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: 030685-043  
; CURRENT APPLICATION NUMBER: US/10/932,182A  
; CURRENT FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 4937  
; LENGTH: 3090  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-10-932-182A-4937

Query Match 76.0%; Score 15.2; DB 7; Length 3090;  
Best Local Similarity 80.0%; Pred. No. 3e+02;  
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUACGA 20  
|||:|||||:|:|  
DB 647 AGGACAGCAGACTACCA 666

RESULT 35

US-10-330-773-511/C  
; Sequence 511, Application US/10330773  
; Publication No. US20060040262A1  
; GENERAL INFORMATION:  
; APPLICANT: David W. Morris  
; APPLICANT: Marc Malandro  
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer  
; FILE REFERENCE: 529452001300  
; CURRENT APPLICATION NUMBER: US/10/330,773  
; CURRENT FILING DATE: 2002-12-27  
; NUMBER OF SEQ ID NOS: 981  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 511  
; LENGTH: 58687  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(58687)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-330-773-511

Query Match 76.0%; Score 15.2; DB 7; Length 58687;  
Best Local Similarity 80.0%; Pred. No. 4.4e+02;  
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUACGA 20  
|||:|||||:|:|  
DB 17509 AGGAAAGCAGACTACCA 17490

RESULT 36

US-10-330-773-620/C  
; Sequence 620, Application US/10330773  
; Publication No. US20060040262A1  
; GENERAL INFORMATION:  
; APPLICANT: David W. Morris  
; APPLICANT: Marc Malandro  
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer  
; FILE REFERENCE: 529452001300  
; CURRENT APPLICATION NUMBER: US/10/330,773  
; CURRENT FILING DATE: 2002-12-27  
; NUMBER OF SEQ ID NOS: 981  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 620  
; LENGTH: 100137  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(100137)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-330-773-620

Query Match 76.0%; Score 15.2; DB 7; Length 100137;  
Best Local Similarity 75.0%; Pred. No. 4.7e+02;  
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGACUACGA 20  
|||:|||||:|:|  
DB 5669 AGATACAGCCAGACTACCA 5650

RESULT 37

US-10-995-561-1330/C  
; Sequence 1330, Application US/10995561  
; Publication No. US20050272054A1

```

; GENERAL INFORMATION: Michele et al.
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13330
; LENGTH: 101046
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(101046)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13330

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 8; Length 101046;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGUACAGCCAGACGACUACGA 20
Db 53538 AGGTACACACAGACTAGAGA 53519

RESULT 38
US-10-330-773-76/c
; Sequence 76, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 118544
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-773-76

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 7; Length 118544;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGUACAGCCAGACGACUACGA 20
Db 16256 AGGCACAGCCAGACTGTGA 16237

RESULT 39
US-11-091-018-1
; Sequence 1, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: Greteardottir, Solveig
; APPLICANT: Thorleifsson, Gudmar
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; FILE REFERENCE: 2345.2010-016
; CURRENT APPLICATION NUMBER: US/11/091,018
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: PCT/US03/29906
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 10/255,120
```

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; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 10/419,723
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 10/650,120
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 10/067,514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/811,352
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1691140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1691140)
; OTHER INFORMATION: n=A,T,C or G
US-11-091-018-1

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 12; Length 1691140;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGUACAGCCAGACGACUACGA 20
Db 734050 AGGTACAGCCAGACTGTGGA 734069

RESULT 40
US-11-175-859-84034
; Sequence 84034, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 84034
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-84034

Query Match
Best Local Similarity 75.0%; Score 15; DB 12; Length 50;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGUACAGCCAGACGACUACGA 17
Db 19 ATGTACARCCAGACTA 35

RESULT 41
US-11-124-368A-16998
; Sequence 16998, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
```



```

1  APPLICANT: Wang, David G.
2  TITLE OF INVENTION: Identification and Mapping of Single
3  Nucleotide Polymorphisms in the Human Genome
4  TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
5  FILE REFERENCE: 108827.135
6  CURRENT APPLICATION NUMBER: US/09/925,065A
7  CURRENT FILING DATE: 2001-08-08

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PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 361016  
LENGTH: 532  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-361016

Query Match 75.0%; Score 15; DB 6; Length 532;  
Best Local Similarity 93.3%; Pred. No. 3.1e+02;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGGAC 15  
DB 291 AGGTACAGCCAGGAC 277

RESULT 46  
US-09-925-065A-361019/c  
Sequence 361019, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
Nucleotide Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 361019  
LENGTH: 532  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-361019

Query Match 75.0%; Score 15; DB 6; Length 532;  
Best Local Similarity 93.3%; Pred. No. 3.1e+02;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGGAC 15  
DB 291 AGGTACAGCCAGGAC 277

RESULT 47  
US-09-925-065A-178453  
Sequence 178453, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
Nucleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 178453  
LENGTH: 577  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-178453

Query Match 75.0%; Score 15; DB 6; Length 577;  
Best Local Similarity 76.5%; Pred. No. 3.1e+02;  
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGGAC 17  
DB 243 AGGTACAGCCAGGAC 259

RESULT 48  
US-09-925-065A-361017/c  
Sequence 361017, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
Nucleotide Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 361017  
LENGTH: 577  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-361017

Query Match 75.0%; Score 15; DB 6; Length 577;  
Best Local Similarity 93.3%; Pred. No. 3.1e+02;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGUACAGCCAGGAC 15  
DB 252 AGGTACAGCCAGGAC 238

RESULT 49  
US-09-925-065A-361018/c  
Sequence 361018, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:

```

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 361018
; LENGTH: 577
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-361018

```

```

Query Match          75.0%; Score 15; DB 6; Length 577;
Best Local Similarity 93.3%; Pred. No. 3.1e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 AGGACAGCCAGGAC 15
      |||:|||||
DB      252 AGGTACAGCCAGGAC 238

```

```

RESULT 50
US-09-925-065A-636833
; Sequence 636833, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 636833
; LENGTH: 638
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-636833

```

```

Query Match          75.0%; Score 15; DB 6; Length 638;
Best Local Similarity 93.3%; Pred. No. 3.2e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 AGGACAGCCAGGAC 15
      |||:|||||
DB      202 AGGTACAGCCAGGAC 216

```

Job completed: March 19, 2006, 05:42:58  
 Time: 1355.46 secs